

Access DB# 73546

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval  
 Reference Librarian  
 Biotechnology & Chemical Library  
 CM1 1E07 - 703-308-4498  
 jan.delaval@uspto.gov

### STAFF USE ONLY

Searcher: <u>Jan</u>	Type of Search	Vendors and cost where applicable
Searcher Phone #: <u>4498</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
Searcher Location: _____	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Date Searcher Picked Up: <u>8/19/02</u>	Structure (#) _____	Questel/Orbit _____
Date Completed: <u>8/21/02</u>	Bibliographic _____	Dr.Link _____
Searcher Prep & Review Time: _____	Litigation _____	Lexis/Nexis _____
Clerical Prep Time: <u>20</u>	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Online Time: <u>15</u>	Patent Family _____	WWW/Internet _____
	Other _____	Other (specify) _____

GenCore version 4.5  
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OM protein - protein search, using sw model

Run On: August 19, 2002, 06:14:39 ; Search time 78.53 seconds  
(without alignments)  
12.236 Million cell updates/sec

Title: US-09-339-922A-34  
Perfect score: 53  
Sequence: 1 GFTFSSYDMS 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	94	2 S14580	Ig heavy chain V r
2	49	92.5	97	2 S26890	Ig heavy chain V r
3	48	90.6	113	2 S26468	Ig heavy chain V r
4	48	90.6	117	1 HVMS34	Ig heavy chain pre
5	48	90.6	121	2 D27888	Ig heavy chain V r
6	48	90.6	124	2 C27888	Ig heavy chain V r
7	46	86.8	40	2 S33406	Ig heavy chain V r
8	46	86.8	83	2 C25913	Ig heavy chain V r
9	46	86.8	98	2 S26891	Ig heavy chain V r
10	46	86.8	108	2 PL0248	Ig heavy chain V r
11	46	86.8	108	2 PH1006	Ig heavy chain V r
12	46	86.8	117	1 HVMS84	Ig heavy chain pre
13	46	86.8	117	2 PL0249	Ig heavy chain V r
14	46	86.8	117	2 PL0252	Ig heavy chain V r
15	46	86.8	119	2 E27888	Ig heavy chain V r
16	46	86.8	122	2 E27888	Ig heavy chain V r
17	46	86.8	138	2 S02258	Ig heavy chain V r
18	45	84.9	92	2 S56009	Ig heavy chain var
19	45	84.9	92	2 S56008	Ig heavy chain var
20	45	84.9	97	1 HVMS91	Ig heavy chain V r
21	45	84.9	97	2 PH0872	Ig heavy chain V r
22	45	84.9	98	2 S26889	Ig heavy chain V r
23	45	84.9	100	2 D48223	Ig heavy chain V r
24	45	84.9	102	2 S14581	Ig heavy chain V r
25	45	84.9	108	2 PH1648	Ig heavy chain V r
26	45	84.9	108	2 PH1011	Ig heavy chain V r
27	45	84.9	109	2 PH1649	Ig heavy chain V r
28	45	84.9	111	2 PH1659	Ig heavy chain V r
29	45	84.9	111	2 S40090	Ig heavy chain - m

30	45	84.9	111	2 PH1007	Ig heavy chain V r
31	45	84.9	112	2 S26327	Ig heavy chain V r
32	45	84.9	112	2 PH1647	Ig heavy chain V r
33	45	84.9	113	2 S25571	Ig heavy chain V r
34	45	84.9	117	1 H3H026	Ig heavy chain pre
35	45	84.9	117	2 A45953	Ig heavy chain pre
36	45	84.9	117	2 B34964	Ig heavy chain pre
37	45	84.9	117	2 S34012	Ig heavy chain V r
38	45	84.9	118	2 S31121	Ig heavy chain - h
39	45	84.9	119	2 C36005	Ig heavy chain V r
40	45	84.9	119	2 D36005	Ig heavy chain V r
41	45	84.9	119	2 S31107	Ig heavy chain - h
42	45	84.9	119	2 S31108	Ig heavy chain - h
43	45	84.9	120	2 S48798	Ig heavy chain V r
44	45	84.9	120	2 S55538	Ig heavy chain V r
45	45	84.9	120	2 S55539	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S14580  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S14580  
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.  
submitted to the EMBL Data Library, March 1991  
A:Description: Natural polyclonal antibodies differ from Ag-induced antibodies in V  
A:Reference number: S14484  
A:Accession: S14580  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-94 <CHE>  
A:Cross-references: EMBL:X58652; NID:g51293; PIDN:CAA41509.1; PID:g51294  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 53; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. No. 0.0047;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GFTFSSYDMS 10  
| | | | | | | | | |  
Db 18 GFTFSSYDMS 27

RESULT 2

S26890  
Ig heavy chain V region (DP-48) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S26890  
R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o  
A:Reference number: S26885; MUID:93021117  
A:Accession: S26890  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-97 <TOM>  
A:Cross-references: EMBL:Z12348; NID:g32916; PIDN:CAA78218.1; PID:g32917  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 92.5%; Score 49; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.028; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 GFTFSSYDM 9  
 |||||  
 Db 26 GFTFSSYDM 34

## RESULT 3

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J.

Submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 &lt;KAV&gt;

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

90.6%; Score 48; DB 2; Length 113;

Best Local Similarity 90.0%; Pred. No. 0.051;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 10

|||||

Db 22 GFAFSSYDM 31

## RESULT 4

HVMS34

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 31-Mar-1997

C:Accession: J70502

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: J70501; MUID:89279149

A:Accession: J70502

A&gt;Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 &lt;LEV&gt;

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence status predicted &lt;SIG&gt;

F:20-117/Product: Ig heavy chain V region (345) #status predicted &lt;MAT&gt;

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;

F:41-115/Disulfide bonds: #status predicted

## Query Match

90.6%; Score 48; DB 1; Length 117;

Best Local Similarity 90.0%; Pred. No. 0.053;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 10

|||||

Db 45 GFAFSSYDM 54

## RESULT 5

D27888

Ig heavy chain V region (H37-60) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996

C:Accession: D27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658

A:Accession: D27888

A:Molecule type: DNA

A:Residues: 1-121 &lt;CAT&gt;

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

90.6%; Score 48; DB 2; Length 121;

Best Local Similarity 90.0%; Pred. No. 0.055;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 10

|||||

Db 26 GFAFSSYDM 35

## RESULT 6

C27888

Ig heavy chain V region (H37-62) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996

C:Accession: C27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658

A:Accession: C27888

A:Molecule type: DNA

A:Residues: 1-124 &lt;CAT&gt;

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

## Query Match

90.6%; Score 48; DB 2; Length 124;

Best Local Similarity 90.0%; Pred. No. 0.056;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 10

|||||

Db 26 GFAFSSYDM 35

## RESULT 7

S33406

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 17-Jul-1998

C:Accession: S33406

R:Kettlborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.

Eur. J. Immunol. 23, 206-211, 1993

A:Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes

A:Reference number: S33391; MUID:93122092

A:Accession: S33406

A:Molecule type: mRNA

A:Residues: 1-40 &lt;KET&gt;

A:Cross-references: EMBL:X73009

A:Experimental source: strain BALB/c

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-40/Domain: immunoglobulin homology (fragment) &lt;IMM&gt;

Query Match 86.8%; Score 46; DB 2; Length 40;  
 Best Local Similarity 90.0%; Pred. No. 0.04; 1; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10  
 Db 26 GFTFSSYTMS 35

RESULT 8  
 C25913  
 Ig heavy chain V region (BFL14) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 16-Aug-1996  
 C:Accession: C25913  
 R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987  
 A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes  
 A:Reference number: A94148; MUID:87175892  
 A:Accession: C25913  
 A:Molecule type: DNA  
 A:Residues: 1-83 <LAW>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 86.8%; Score 46; DB 2; Length 83;  
 Best Local Similarity 90.0%; Pred. No. 0.088;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10  
 Db 11 GFTFSSYGMS 20

RESULT 9  
 S26891  
 Ig heavy chain V region (DP-58) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S26891  
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
 J. Mol. Biol. 227, 778-798, 1992  
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
 A:Reference number: S26885; MUID:93021117  
 A:Accession: S26891  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-98 <TOM>  
 A:Cross-references: EMBL:Z12358; NID:g32935; PIDN:CAA78228.1; PID:g32936  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 46; DB 2; Length 98;  
 Best Local Similarity 80.0%; Pred. No. 0.1;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10  
 Db 26 GFTFSSYEMN 35

RESULT 10  
 PL0248  
 Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
 C:Accession: PL0248  
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
 J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat  
 A:Reference number: PL0231; MUID:90111618  
 A:Accession: PL0248  
 A:Molecule type: mRNA  
 A:Residues: 1-108 <SHL>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-24/Region: framework 1  
 F:9-92/Domain: immunoglobulin homology <IMM>  
 F:25-29/Region: complementarity-determining 1  
 F:30-43/Region: framework 2  
 F:44-60/Region: complementarity-determining 2  
 F:61-92/Region: framework 3  
 F:93-99/Region: complementarity-determining 3  
 F:100-108/Region: framework 4

Query Match 86.8%; Score 46; DB 2; Length 108;  
 Best Local Similarity 90.0%; Pred. No. 0.12; 1; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10  
 Db 20 GFTFSSYTMS 29

RESULT 11  
 PH1006  
 Ig heavy chain V region (clone 202.33) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PH1006  
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective  
 A:Reference number: PH0971; MUID:92381444  
 A:Accession: PH1006  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-108 <TTL>  
 A:Experimental source: B cell, strain [N2B x N2W]F1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 46; DB 2; Length 108;  
 Best Local Similarity 90.0%; Pred. No. 0.12; 1; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10  
 Db 21 GFTFSSYGMS 30

RESULT 12  
 HVMS84  
 Ig heavy chain precursor V region (5-84) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 31-Mar-1997  
 C:Accession: JT0505  
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
 J. Exp. Med. 169, 2007-2019, 1989  
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar  
 A:Reference number: JT0501; MUID:89279149  
 A:Accession: JT0505  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-117 <LEV>  
 A:Experimental source: strain BALB/cJ  
 A:Note: this sequence belongs to the VH7183 subfamily  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>  
 F:34-117/Domain: immunoglobulin homology <IMM>  
 F:41-115/Disulfide bonds: #status predicted

Query Match 86.8%; Score 46; DB 1; Length 117;  
 Best Local Similarity 90.0%; Pred. No. 0.13;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
 ||||| ||  
 Db 45 GFTFSSYTMS 54

## RESULT 13

PL0249  
 Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
 C:Accession: PL0249  
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
 J. Exp. Med. 171, 265-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A:Reference number: PL0231; MUID:90111618  
 A:Accession: PL0249  
 A:Molecule type: mRNA  
 A:Residues: 1-117 <SHL>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-30/Region: framework 1  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:36-49/Region: framework 2  
 F:50-66/Region: complementarity-determining 2  
 F:67-98/Region: framework 3  
 F:99-108/Region: complementarity-determining 3  
 F:109-117/Region: framework 4

Query Match 86.8%; Score 46; DB 2; Length 117;  
 Best Local Similarity 90.0%; Pred. No. 0.13;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
 ||||| ||  
 Db 26 GFTFSSYTMS 35

## RESULT 14

PL0252  
 Ig heavy chain V region (anti-DNA, clones 2E3VH, 6B8VH, and 3G9VH) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
 C:Accession: PL0252; PL0251  
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
 J. Exp. Med. 171, 265-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A:Reference number: PL0231; MUID:90111618  
 A:Accession: PL0252  
 A:Molecule type: mRNA  
 A:Residues: 1-117 <SHL>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-30/Region: framework 1  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:36-49/Region: framework 2  
 F:50-66/Region: complementarity-determining 2  
 F:67-98/Region: framework 3  
 F:99-108/Region: complementarity-determining 3  
 F:109-117/Region: framework 4

Query Match 86.8%; Score 46; DB 2; Length 117;  
 Best Local Similarity 90.0%; Pred. No. 0.13;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
 ||||| ||  
 Db 26 GFTFSSYTMS 35

## RESULT 15

F27888  
 Ig heavy chain V region (H158-89H4) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
 C:Accession: F27888  
 R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
 EMBO J. 5, 1577-1587, 1986  
 A:Title: Structural and functional implications of a restricted antibody response to  
 A:Reference number: A91043; MUID:86300658  
 A:Accession: F27888  
 A:Molecule type: DNA  
 A:Residues: 1-119 <CAT>  
 A:Experimental source: strain Balb/c  
 A:Note: this sequence was determined from the germline gene  
 C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 46; DB 2; Length 119;  
 Best Local Similarity 90.0%; Pred. No. 0.13;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
 ||||| ||  
 Db 26 GFTFSSYTMS 35

Search completed: August 19, 2002, 06:36:03  
 Job time: 1284 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:15 ; Search time 51.81 Seconds  
(without alignments)  
7.473 Million cell updates/sec

Title: US-09-339-922A-34  
Perfect score: 53  
Sequence: 1 GFTFSSYDMS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	90.6	117	1 HV55_MOUSE	P18526 mus musculus
2	46	86.8	117	1 HV54_MOUSE	P18525 mus musculus
3	45	84.9	97	1 HV56_MOUSE	P18527 mus musculus
4	45	84.9	117	1 HV3C_HUMAN	P01764 homo sapien
5	44	83.0	117	1 HV53_MOUSE	P18524 mus musculus
6	43	81.1	117	1 HV59_MOUSE	P18530 mus musculus
7	41	77.4	115	1 HV3D_HUMAN	P01765 homo sapien
8	40	75.5	117	1 HV52_MOUSE	P06327 mus musculus
9	39	73.6	114	1 HV00_MOUSE	P01741 mus musculus
10	39	73.6	114	1 HV01_CANFA	P01784 canis famil
11	39	73.6	116	1 HV1A_RABIT	P01826 oryctolagus
12	39	73.6	117	1 HV2B_RABIT	P01828 oryctolagus
13	39	73.6	120	1 HV3E_HUMAN	P01766 homo sapien
14	39	73.6	121	1 HV3J_HUMAN	P01771 homo sapien
15	38	71.7	114	1 HV3B_HUMAN	P01763 homo sapien
16	38	71.7	117	1 HV58_MOUSE	P18529 mus musculus
17	38	71.7	122	1 HV3C_HUMAN	P01768 homo sapien
18	38	71.7	136	1 HV16_MOUSE	P01783 mus musculus
19	37	69.8	111	1 HV35_MOUSE	P01804 mus musculus
20	37	69.8	113	1 HV27_MOUSE	P01796 mus musculus
21	37	69.8	113	1 HV28_MOUSE	P01797 mus musculus
22	37	69.8	113	1 HV29_MOUSE	P01798 mus musculus
23	37	69.8	113	1 HV30_MOUSE	P01799 mus musculus
24	37	69.8	113	1 HV31_MOUSE	P01800 mus musculus
25	37	69.8	113	1 HV34_MOUSE	P01803 mus musculus
26	37	69.8	115	1 HV32_MOUSE	P01801 mus musculus
27	37	69.8	115	1 HV33_MOUSE	P01802 mus musculus
28	37	69.8	117	1 HV02_CANFA	P01785 canis famil
29	37	69.8	117	1 HV17_MOUSE	P01786 mus musculus
30	36	67.9	98	1 HV57_MOUSE	P18528 mus musculus
31	36	67.9	119	1 HV3M_HUMAN	P01774 homo sapien
32	35	66.0	117	1 HV02_CAICR	P03981 calman croc
33	35	66.0	117	1 HV03_CARAU	P19180 carassius a

#### ALIGNMENTS

RESULT 1

HV55\_MOUSE 35 56.0 126 1 HV3K\_HUMAN P01772 homo sapien  
AC P18526; 35 56.0 142 1 HV01\_RAT P01805 rattus norv  
DT 01-NOV-1990 (Rel. 16, Last sequence update) O83084 treponema p  
DT 01-NOV-1990 (Rel. 16, Last sequence update) P33573 petromyzon  
DT 15-JUL-1999 (Rel. 38, Last annotation update) Q9pa86 xylella fas  
DE Ig heavy chain V region 345 precursor. P01813 calman croc  
OS Mus musculus (Mouse). P01758 mus musculus  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; P01743 homo sapien  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. P01769 homo sapien  
OX NCBI\_TaxID=10090; P75227 mycoplasma  
RN [1] P25294 saccharomyc  
RC SEQUENCE FROM N.A.  
RC STRAIN=BALBYCJ;  
RX MEDLINE=89279149; PubMed=2499654;  
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during  
the primary immune response";  
RL J. Exp. Med. 169:2007-2019(1989).  
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.  
DR PIR; JT0502; HVMS34.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION 345.  
FT CHAIN 20 117 FRAMEWORK-1.  
FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 50 54 FRAMEWORK-2.  
FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 69 85 FRAMEWORK-3.  
FT DISULFID 86 117 BY SIMILARITY.  
FT NON\_TER 41 115  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 90.6%; Score 48; DB 1; Length 117;

Best Local Similarity 90.08; Pred. No. 0.015; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 1;

Qy 1 GFTFSSYDMS 10

Db 45 GFTFSSYDMS 54

RESULT 2

HV54\_MOUSE 35 56.0 126 1 HV54\_MOUSE P18525; PRT; 117 AA.  
AC P18525;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 5-84 precursor.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0505; HVMS84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 86.8%; Score 46; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTSSYDMS 10
DB 45 GFTSSYMS 54

RESULT 3
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0504; HVMS91.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin v region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB333FF55DA893 CRC64;

Query Match 84.9%; Score 45; DB 1; Length 97;
Best Local Similarity 90.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTSSYDMS 10
DB 26 GFTSSYAMS 35

RESULT 4
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -----
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DR EMBL; J00236; AAA53516.1; -
DR EMBL; M35415; AAA58735.1; -
DR PIR; A02047; H3HU26.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; B826733F1A3CB0F1 CRC64;

Query Match 84.9%; Score 45; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTSSYDMS 10
DB 45 GFTSSYAMS 54

RESULT 5
HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;

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RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during  
 the primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.  
 DR PIR: JTO503; HVMSRF.  
 DR HSSP: P01810; 2FBJ.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 KW Immunoglobulin V region; Hybridoma; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION RE..  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 83.0%; Score 44; DB 1; Length 117;  
 Best Local Similarity 90.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
 DB 45 GFTFSSYMS 54

RESULT 6  
 HV59\_MOUSE STANDARD; PRT; 117 AA.  
 AC P18530;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 7-39 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/CJ;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during  
 the primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.  
 DR PIR: JTO507; HVMS39.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 81.1%; Score 43; DB 1; Length 117;  
 Best Local Similarity 80.0%; Pred. No. 0.14;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GFTFSSYDMS 10  
 DB 45 GFTFSSYMS 54

RESULT 7  
 HV3D\_HUMAN STANDARD; PRT; 115 AA.  
 AC P01765;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-III region TIL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=78005528; PubMed=409716;  
 RA Wang A.-C., Wang I.Y., Fudenberg H.H.;  
 RT "Immunoglobulin structure and genetics. Identity between variable  
 regions of a mu and a gamma2 chain.";  
 RL J. Biol. Chem. 252:7192-7199(1977).  
 CC -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS  
 OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL  
 GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO  
 IDENTICAL.

PIR: A02048; H3HUTL.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 KW Immunoglobulin V region.  
 FT NON\_TER 115 115  
 SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 77.4%; Score 41; DB 1; Length 115;  
 Best Local Similarity 80.0%; Pred. No. 0.33;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
 DB 26 GFTFSSYMS 35

RESULT 8  
 HV52\_MOUSE STANDARD; PRT; 117 AA.  
 AC P06327;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region VH558 Al/A4 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85099340; PubMed=2578321;  
 RA Yancopoulos G.D., Alt F.W.;  
 RT "Developmentally controlled and tissue-specific expression of  
 unrearranged VH gene segments.";  
 RL Cell 40:271-281(1985).

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 CC EMBL; M13787; AAA38499.1; -.  
 DR PIR; A02029; HVMSAL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/44.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 75.5%; Score 40; DB 1; Length 117;  
 Best Local Similarity 60.0%; Pred. No. 0.53; Indels 0; Gaps 0;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
 Db 45 GYTFTSYDIN 54  
 I:|||||:

RESULT 9  
 HV00\_MOUSE  
 ID HV00\_MOUSE STANDARD; PRT; 114 AA.  
 AC P01741.  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last annotation update)  
 DE Ig heavy chain V region (Anti-arsenate antibody).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=A/J;  
 RX MEDLINE=79195438; PubMed=109536;  
 RA Capra J.D., Nisonoff A.;  
 RT "Structural studies on induced antibodies with defined idiotypic  
 RT specificities. VII. The complete amino acid sequence of the heavy  
 RT chain variable region of anti-p-azophenylarsenate antibodies from A/J  
 RT mice bearing a cross-reactive idiotype.";  
 RL J. Immunol. 123:279-284(1979).  
 CC -!- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF  
 CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V  
 CC REGION SEQUENCE.  
 DR PIR; A02022; G1MSAA.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Antiarsenate antibody.  
 FT NON\_TER 114 114  
 SQ SEQUENCE 114 AA; 12555 MW; 99D8F0B6A69F4BE CRC64;

Query Match 73.6%; Score 39; DB 1; Length 114;  
 Best Local Similarity 66.7%; Pred. No. 0.8; Indels 0; Gaps 0;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9  
 Db 26 GYTFTSYEL 34  
 I:|||||:

RESULT 10  
 HV01\_CANFA  
 ID HV01\_CANFA STANDARD; PRT; 114 AA.  
 AC P01784;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region GOM.  
 DE Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77242268; PubMed=407924;  
 RA Wasserman R.L., Capra J.D.;  
 RT "Primary structure of the variable regions of two canine  
 RT immunoglobulin heavy chains.";  
 RL Biochemistry 16:3160-3168(1977).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR; A02067; AVDGM.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region.  
 FT NON\_TER 114 114  
 SQ SEQUENCE 114 AA; 12430 MW; BID4745D2C4E13C4 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 114;  
 Best Local Similarity 77.8%; Pred. No. 0.8; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9  
 Db 26 GITFSGYDM 34  
 I:|||||:

RESULT 11  
 HV1A\_RABIT  
 ID HV1A\_RABIT STANDARD; PRT; 116 AA.  
 AC P01826;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-A1 region BS-5.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE OF 1-69.  
 RX MEDLINE=73220191; PubMed=4146279;  
 RA Jaton J.-C., Braun D.G.;  
 RT "Amino acid sequence of the N-terminal sixty-nine residues of heavy  
 RT chain derived from a homogeneous rabbit antibody.";  
 RL Biochem. J. 130:539-546(1972).  
 RN [2]  
 RP SEQUENCE OF 64-116.  
 RX MEDLINE=75183340; PubMed=4142749;  
 RA Jaton J.-C.;  
 RT "Completion of the analysis of the primary structure of the variable  
 RT domain of a homogeneous rabbit antibody to type III pneumococcal  
 RT polysaccharide.";  
 RL Biochem. J. 143:723-732(1974).  
 CC -!- MISCELLANEOUS: THIS GAMMA CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE  
 CC III PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE

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CC RABBIT.
DR PIR: A02102; GARB15
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12349 MW; 95C6FAC93C788C42 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 116;
Best Local Similarity 77.8%; Pred. No. 0.82;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9
DB 25 GFSLSYDM 33

RESULT 12
HV2B_RABBIT
ID HV2B_RABBIT STANDARD; PRT; 117 AA.
AC P01828;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain V-A2 region K-25.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=76039436; PubMed=2411319;
RA Jaton J.-C.;
RT "Comparison of the amino acid sequences of the variable domains of
RT two homogeneous rabbit antibodies to type III pneumococcal
RT polysaccharide.";
RL Biochem. J. 147:235-247(1975).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM THE SERUM OF A SINGLE RABBIT.
CC PNEUMOCOCCI AND WAS ISOLATED FROM ANTI BODY TO TYPE III
DR PIR: A02104; GARB2K.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 21 91
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12580 MW; 28DD87FDB7AE9B8 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 0.83;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 10
DB 25 GFSLSYDM 34

RESULT 13
HV3E_HUMAN
ID HV3E_HUMAN STANDARD; PRT; 120 AA.
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain V-III region BRO.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77117674; PubMed=65324;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monotypic IgM lambda and IgG kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the IgM paraprotein.";
RL Immunochimistry 13:995-999(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
CC TYPE.
DR PIR: A02049; M3HUBW.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2E6410 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 120;
Best Local Similarity 70.0%; Pred. No. 0.85;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 10
DB 26 GFTFSSYNNM 35

RESULT 14
HV3J_HUMAN
ID HV3J_HUMAN STANDARD; PRT; 121 AA.
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain V-III region HIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RT cryoimmunoglobulin IgG HIL.";
RL Biochemistry 18:553-560(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
DR PIR: A02054; G1HUHL.
DR HSSP: P01772; 2FBA.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 73.6%; Score 39; DB 1; Length 121;
Best Local Similarity 77.8%; Pred. No. 0.86;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9
DB 26 GFTFSSNYGM 34

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RESULT 15
HV3B_HUMAN
ID HV3B_HUMAN STANDARD; PRT; 114 AA.
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A02046; M3HUNE.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12256 MW; . D88294FB418A07B7 CRC64;

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Query Match      71.7%; Score 38; DB 1; Length 114;
Best Local Similarity 70.0%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSYDMS 10
DB 26 GFTFSANDMN 35

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Search completed: August 19, 2002, 06:59:05  
Job time: 1370 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:50 ; Search time 140.4 Seconds  
(without alignments)  
12.322 Million cell updates/sec

Title: US-09-339-922A-34

Perfect score: 53

Sequence: 1 GFTFSSYDMS 10

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	86.8	119	11 Q920E7	Q920E7 mus musculus
2	46	86.8	486	11 Q91Z07	Q91Z07 mus musculus
3	45	84.9	437	11 Q9R1A4	Q9R1A4 mus musculus
4	45	84.9	487	11 Q99KA4	Q99KA4 mus musculus
5	44	83.0	118	4 Q9UL91	Q9UL91 homo sapien
6	43	81.1	95	4 Q9ULB6	Q9ULB6 homo sapien
7	43	81.1	147	4 Q9V509	Q9V509 homo sapien
8	42	79.2	113	4 Q9UL90	Q9UL90 homo sapien
9	42	79.2	140	10 Q9ARP0	Q9ARP0 oryza sativ
10	41	77.4	116	4 Q9UL93	Q9UL93 homo sapien
11	38	71.7	112	4 Q9HCC1	Q9HCC1 homo sapien
12	38	71.7	412	10 Q9ZQR5	Q9ZQR5 arabidopsis
13	38	71.7	473	11 Q91Z05	Q91Z05 mus musculus
14	38	71.7	597	4 Q96BB9	Q96BB9 homo sapien
15	38	71.7	702	10 Q9LNL6	Q9LNL6 arabidopsis
16	38	71.7	2133	12 Q98203	Q98203 molluscum c

17	37	69.8	124	4 Q9UL92	Q9UL92 homo sapien
18	37	69.8	594	5 P91823	P91823 caenorhabdi
19	37	69.8	1436	5 Q9W159	Q9W159 drosophila
20	36	67.9	479	11 Q91WP5	Q91WP5 mus musculus
21	36	67.9	690	10 Q9LIB7	Q9LIB7 arabidopsis
22	36	67.9	690	10 Q940D0	Q940D0 arabidopsis
23	36	67.9	1383	5 Q91Z07	Q91Z07 caenorhabdi
24	35	66.0	112	4 Q9UGP3	Q9UGP3 homo sapien
25	35	66.0	128	3 Q94499	Q94499 schizosacch
26	35	66.0	159	4 Q96QSO	Q96QSO homo sapien
27	35	66.0	1121	2 Q9AKN9	Q9AKN9 rickettsia
28	35	66.0	1264	12 Q89230	Q89230 variola vir
29	35	66.0	1896	12 Q89096	Q89096 variola vir
30	35	66.0	1896	12 Q89117	Q89117 variola vir
31	35	66.0	1896	12 Q89192	Q89192 variola vir
32	35	66.0	1897	12 Q85406	Q85406 variola maj
33	35	66.0	1924	12 Q9JFS2	Q9JFS2 ectromelia
34	35	66.0	1933	12 Q72759	Q72759 cowpox viru
35	35	66.0	1949	12 Q9J5C1	Q9J5C1 fowlpox vir
36	34	64.2	109	11 Q9JL75	Q9JL75 mus musculus
37	34	64.2	341	4 Q9H795	Q9H795 homo sapien
38	34	64.2	379	10 Q9SSA7	Q9SSA7 arabidopsis
39	34	64.2	397	16 Q97GF8	Q97GF8 clostridium
40	34	64.2	504	2 Q9KZF1	Q9KZF1 streptomyce
41	34	64.2	520	16 Q9PMZ7	Q9PMZ7 campylobact
42	34	64.2	573	4 Q9NWM4	Q9NWM4 homo sapien
43	34	64.2	583	4 Q9H587	Q9H587 homo sapien
44	34	64.2	643	2 Q9KJI6	Q9KJI6 desulfovibr
45	34	64.2	690	2 Q9RBG8	Q9RBG8 aeromonas p

#### ALIGNMENTS

RESULT 1

Q920E7 PRELIMINARY; PRT; 119 AA.  
AC Q920E7  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE PTERIN-MIMICKING ANTI-IDIOPOPE HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF307937; AAL09421.1; -.  
FT NON\_TER 1 119  
FT SEQUENCE 119 AA; 13025 MW; F6E90404381CA7C CRC64;

Query Match 86.8%; Score 46; DB 11; Length 119;  
Best Local Similarity 90.0%; Pred. No. 0.36;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10

Db 26 GFTFSSYDMS 35

RESULT 2

Q91Z07 PRELIMINARY; PRT; 486 AA.  
ID Q91Z07  
AC Q91Z07  
DT 01-DEC-2001 (TREMBlrel. 19, Created)

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DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 52.7 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC010324; AAH0324.1; -.
KW Hypothetical protein.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match      86.8%; Score 46; DB 11; Length 486;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 45 GFTFSSYDMS 54

RESULT 3
Q9RIA4
ID Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152372; AAD40243.1; -.
DR HSSP: P01842; 7FAB.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 437
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match      84.9%; Score 45; DB 11; Length 437;
Best Local Similarity 90.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 25 GFTFSSYAMS 34

RESULT 4
Q99KA4
ID Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

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DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 52.6 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC004786; AAH04786.1; -.
DR HSSP: P01810; 2FBJ
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_Cl.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGCl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match      84.9%; Score 45; DB 11; Length 487;
Best Local Similarity 90.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10
Db 45 GFTFSSYAMS 54

RESULT 5
Q9UL91
ID Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035023; AAD56259.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match      83.0%; Score 44; DB 4; Length 118;
Best Local Similarity 80.0%; Pred. No. 0.84;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10

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Db 26 GFTFSSYMN 35  
||||||| I:

RESULT 6  
Q9ULB6 ID Q9ULB6 PRELIMINARY; PRT; 95 AA.  
AC Q9ULB6;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE IMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).  
GN VH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tange Y., Kayano H.;  
RT "Human VH gene sequence."  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB035268; BAA87067.1; -.  
DR HSP; P01772; 2FB4.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 1  
FT NON\_TER 95  
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 81.1%; Score 43; DB 4; Length 95;  
Best Local Similarity 90.0%; Pred. No. 1;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
||||||| I:  
Db 25 GFTFSSYWMS 34

RESULT 7  
Q9Y509 ID Q9Y509 PRELIMINARY; PRT; 147 AA.  
AC Q9Y509;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE VH3 PROTEIN (FRAGMENT).  
GN VH3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=96071149; PubMed=7475288;  
CAO J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,  
Lichtenstein A.K., Berenson J.R.;  
RT "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers."  
RL Leukemia 9:1948-1953(1995).  
DR EMBL; S80860; AAD14339.1; -.  
DR HSP; P01772; 2FB4.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 1  
FT NON\_TER 147  
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 81.1%; Score 43; DB 4; Length 147;  
Best Local Similarity 80.0%; Pred. No. 1.6;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
||||||| I:  
Db 26 GFTFSSYGMS 35

RESULT 8  
Q9UL90 ID Q9UL90 PRELIMINARY; PRT; 113 AA.  
AC Q9UL90;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
GN MYO.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98277139; PubMed=9614934;  
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035024; AAD56260.1; -.  
DR HSP; P01772; 2FB4.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 1  
FT NON\_TER 113  
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 79.2%; Score 42; DB 4; Length 113;  
Best Local Similarity 88.9%; Pred. No. 1.9;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9  
||||||| I:  
Db 26 GFTFSSYGM 34

RESULT 9  
Q9ARPO ID Q9ARPO PRELIMINARY; PRT; 140 AA.  
AC Q9ARPO;  
DT 01-JUN-2001 (TReMBLrel. 17, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE P0024G09.20 PROTEIN.  
GN P0024G09.20.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=CV. NIPPONBARE;  
Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0024G09."  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP003311; BAB40128.1; -.  
SQ SEQUENCE 140 AA; 15782 MW; 222CB6E0CA6FCBDD CRC64;

```

Query Match          79.2%; Score 42; DB 10; Length 140;
Best Local Similarity 77.6%; Pred. No. 2.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9
DB 131 GFTFSSYEL 139

RESULT 10
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match          77.4%; Score 41; DB 4; Length 116;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9
DB 25 GFTFSSYAM 33

RESULT 11
Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE SINGLE CHAIN FV (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme : Isolation from a
RT human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003599; Ig.

```

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DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24FLA45EC3B84788 CRC64;

Query Match          71.7%; Score 38; DB 4; Length 112;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
DB 26 GFTFDDYDMS 35

RESULT 12
Q9ZQR5 PRELIMINARY; PRT; 412 AA.
AC Q9ZQR5;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE AT2G14530 PROTEIN.
GN AT2G14530.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006067; AAD15463.1; -.
DR InterPro; IPR004253; DUF231.
DR Pfam; PF03005; DUF231; 1.
SQ SEQUENCE 412 AA; 46462 MW; 1155D765FAD34CCE CRC64;

Query Match          71.7%; Score 38; DB 10; Length 412;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10
DB 170 GFTFSQYNLT 179

RESULT 13
Q91Z05 PRELIMINARY; PRT; 473 AA.
ID Q91Z05
AC Q91Z05;

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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC010327; AAH10327.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 71.7%; Score 38; DB 11; Length 473;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFSYDM 9
DB 45 GFTFSYGM 53
|||||
45 GFTFSYGM 53

RESULT 14
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC015760; AAH15760.1; -.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 71.7%; Score 38; DB 4; Length 597;
Best Local Similarity 70.0%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFSYDMS 10
DB 45 GFTFSYAMN 54
|||||
45 GFTFSYAMN 54

RESULT 15
Q9LNL6 PRELIMINARY; PRT; 702 AA.
AC Q9LNL6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE FLK21.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,

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RA Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC Fl2K21 from chromosome
RT I.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBDJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBDJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBDJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AC023279; AAF9257.1; -.
SQ SEQUENCE 702 AA; 80578 MW; 425B0F22B76EC786 CRC64;

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Query Match 71.7%; Score 38; DB 10; Length 702;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GFTFSYD 8
DB 143 GFTYNSYD 150
|||||

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Search completed: August 19, 2002, 06:58:08
Job time: 1398 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:14:39 ; Search time 180.34 Seconds  
(without alignments)  
6.159 Million cell updates

Title: US-09-339-922A-34

Perfect score:

Sequence: 1 GTFSSYDMS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum D8 seg length: 0

Maximum DB seq length:	200000000
Maximum DB seq length:	200000000

Post-processing: Minimum Match 0%

100% Processing. Minimum Match 0%  
Maximum Match 100%

Maximum March 1998  
Listing first 45 summaries

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22:	/SIDSL1/cgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	53	100.0	10	19	AAW76007	LM609 grafted anti	
2	53	100.0	10	22	AAB61365	LM609 VH CDR1 pept	
3	53	100.0	117	19	AAG76001	Vitaxin antibody h	
4	53	100.0	117	22	AAG63587	A heavy chain vari	
5	53	100.0	117	22	AAB61359	Vitaxin heavy chai	
6	50	94.3	117	20	AAW86137	Protein sequence o	
7	50	94.3	128	19	AAW54000	Anti-CD4 antibody	
8	50	94.3	134	13	AAZ24713	Sequence encoded b	
9	50	94.3	466	13	AAZ24812	Sequence encoded b	
10	49	92.5	97	21	ABA40112	Anti-H1u12 antibod	
11	49	92.5	102	22	AB339276	peptide #6782 enco	

12	49	92.5	102	22	AAW59940	Human brain expres
13	49	92.5	102	22	AAW72535	Human bone marrow
14	49	92.5	102	22	AAW32779	Peptide #6816 enco
15	49	92.5	139	18	AAW21652	Humanised reshaped
16	48	90.6	10	19	AAW76015	LM609 grafted anti
17	48	90.6	10	22	AAW61373	Mutant VH CDRI pep
18	48	90.6	117	19	AAW76003	LM609 antibody hea
19	48	90.6	117	20	AAW706381	Murine monoclonal
20	48	90.6	117	22	AAW63589	A heavy chain vari
21	48	90.6	117	22	AAW61361	Antibody LM609 hea
22	48	90.6	130	20	AAW06379	Murine monoclonal
23	48	90.6	239	14	AAW34511	Fv(TU25). Homo sa
24	48	90.6	247	16	AAW11917	Murine MAb SK48-E2
25	47	88.7	10	19	AAW76016	LM609 grafted anti
26	47	88.7	10	22	AAW61374	Mutant VH CDRI pep
27	47	88.7	115	22	AAW69601	Huntingtin minimal
28	47	88.7	117	20	AAW86141	Protein sequence O
29	47	88.7	119	16	AAW11919	Humanised MAb SK48
30	47	88.7	123	19	AAW53998	Anti-CD4 antibody
31	47	88.7	239	22	AAW69603	Huntingtin intrabo
32	46	86.8	10	22	AAW07457	Synthetic peptide
33	46	86.8	87	22	AAW06990	Mouse germline hea
34	46	86.8	89	22	AAW06985	Mouse germline hea
35	46	86.8	97	21	AAW40089	Anti-hIL12 antibod
36	46	86.8	98	19	AAW59614	Anti-RSV F protein
37	46	86.8	98	21	AAW40113	Anti-hIL12 antibod
38	46	86.8	98	22	AAW06975	Mouse germline hea
39	46	86.8	98	22	AAW06976	Mouse germline hea
40	46	86.8	98	22	AAW06981	Mouse germline hea
41	46	86.8	98	22	AAW06982	Mouse germline hea
42	46	86.8	98	22	AAW48022	Heavy chain sequen
43	46	86.8	116	16	AAW48037	Human immunoglob
44	46	86.8	116	18	AAW13529	Anti-melanoma anti
45	46	86.8	116	22	AAW07483	Synthetic antibody

## ALIGNMENTS

RESULT 1

AAW76007  
ID AAW76007 standard; Protein: 10 AA.

AA AAW76007:

XX  
DT 02-NOV-1998 (first entry)XX  
DE LM609 grafted antibody V-H region CDR1 protein fragment #1.

xx Vitaxin; antibody; variable region; heavy chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;  
 KW complementarity determining region.

XX  
US Misc enXX  
DN  
W00933010-12XX  
PD 06-AUG-1998

XX  
DE 30-TAN-1000. 00000-11001000

XX  
 30-TAN-1997. 0711S-0791391XX  
DA (TYGV-) TYGVG TNCXX  
BT  
Class CM  
Hisco WD:

XX  
DR WPT: 1998-437A72/37

DR N-PSDB; AAV49844.  
YY

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
PT integrin - and related grafted antibodies based on murine monoclonal  
PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
PT angiogenesis or restenosis  
XX  
XX  
PS Disclosure; Page 40; 129pp; English.  
XX  
CC AA76007-W76040 are protein fragments of the grafted monoclonal antibody  
CC LM609 heavy and light chain variable region. LM609 and the antibody  
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to  
CC inhibit binding of alphavbeta3 to a ligand and thus block  
CC integrin-mediated signal transduction. This is useful in the treatment,  
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically  
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
CC antibodies contain non-murine framework regions so are suitable for use  
CC in humans. Enhanced types of LM609 have affinity more than 90 times  
CC greater than that of parent the parent antibody.  
XX  
XX Sequence 10 AA;  
  
Query Match 100.0%; Score 53; DB 19; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GFTFSSYDMS 10  
DB 1 gftfssyds 10  
|||||||  
  
RESULT 2  
AAB61365  
ID AAB61365 standard; peptide; 10 AA.  
XX  
AC AAB61365;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE LM609 VH CDR1 peptide.  
XX  
KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis.  
XX  
OS Unidentified.  
XX  
PN WO200078815-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 23-JUN-2000; 2000WO-US17454.  
XX  
PR 24-JUN-1999; 99US-0339922.  
XX  
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX  
PI Huse WD, Wu H;  
XX  
DR WPI; 2001-050110/06.  
XX  
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis.  
XX  
PS Claim 4; Page 39; 132pp; English.  
XX  
CC The present invention relates to enhanced LM609 grafted antibodies  
CC exhibiting selective binding affinity to alphavbeta3 integrin or  
CC their functional fragments. The antibodies or their functional  
CC fragments can be used in the diagnosis and treatment of  
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism), of  
CC disorders associated with inappropriate or inopportune invasion of  
CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
CC diseases (such as macular degeneration), restenosis and  
CC osteoporosis.  
XX  
XX Sequence 10 AA;  
  
Query Match 100.0%; Score 53; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GFTFSSYDMS 10  
DB 1 gftfssyds 10  
|||||||  
  
RESULT 3  
AAW76001  
ID AAW76001 standard; Protein; 117 AA.  
XX  
AC AAW76001;  
XX  
DT 02-NOV-1998 (first entry)  
XX  
DE Vitaxin antibody heavy chain variable region protein fragment.  
XX  
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis.  
XX  
OS Mus sp.  
XX  
PN WO9833919-A2.  
XX  
PD 06-AUG-1998.  
XX  
PF 30-JAN-1998; 98WO-US01826.  
XX  
PR 30-JAN-1997; 97US-0791391.  
XX  
PA (IXSY-) IXSYS INC.  
XX  
XX Glaser SM, Huse WD;  
XX  
XX WPI; 1998-437472/37.  
DR N-PSDB; AAV49820.  
XX  
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
PT integrin - and related grafted antibodies based on murine monoclonal  
PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
PT angiogenesis or restenosis  
XX  
XX Claim 1; Fig 1a; 129pp; English.  
XX  
XX This sequence represents a fragment of the vitaxin antibody variable  
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to  
CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3  
CC to a ligand and thus block integrin-mediated signal transduction. This is  
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated  
CC disease, specifically angiogenesis and restenosis (but also e.g.  
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,  
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,  
CC osteoporosis etc.). The antibodies contain non-murine framework regions  
CC so are suitable for use in humans. Enhanced types of LM609 have affinity  
CC more than 90 times greater than that of parent the parent antibody.  
XX  
XX Sequence 117 AA;  
XX



{

Query Match 100.0%; Score 53; DB 19; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 0.019; 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
 DB 26 gftfssyds 35  
 |||

RESULT 4  
 AAG63587  
 ID AAG63587 standard; Protein; 117 AA.  
 XX  
 AC AAG63587;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX  
 DE A heavy chain variable region of LM609 grafted antibody.  
 XX  
 KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 XX  
 PN US2001011125-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 30-JAN-1997; 97US-0790540.  
 XX  
 PR 30-JAN-1997; 97US-0790540.  
 XX  
 PA (HUSE/) HUSE W D.  
 XX  
 PI Huse WD;  
 XX  
 WPI; 2001-496171/54.  
 DR N-PSDB; AAH74623.  
 XX  
 PT New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer.  
 XX  
 PS Claim 1; Fig 1A; 25pp; English.  
 XX  
 CC The present sequence represents the heavy chain variable region of the  
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which  
 CC specifically recognises the integrin alphavbeta3, and inhibits its  
 CC functional activity. The LM609 grafted antibody has the  
 CC complementarity determining regions (CDRs) substituted into a non-murine  
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain  
 CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis  
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
 CC disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 CC an alphavbeta3-mediated disease.  
 XX  
 SQ Sequence 117 AA;

Query Match 100.0%; Score 53; DB 22; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
 DB 26 gftfssyds 35  
 |||

RESULT 6  
 AAW86137  
 ID AAW86137 standard; Protein; 117 AA.  
 XX  
 AC AAW86137;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Vitaxin heavy chain variable region protein.  
 XX  
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 WPI; 2001-050110/06.  
 XX  
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Fig 1; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 117 AA;

Query Match 100.0%; Score 53; DB 22; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
 DB 26 gftfssyds 35  
 |||

RESULT 6  
 AAW86137  
 ID AAW86137 standard; Protein; 117 AA.  
 XX  
 AC AAW86137;  
 XX

XY

Musculus.

KW XY

KW XY

```

FH FT      Key      Location/Qualifiers
FT FT      1..19
FT FT      /label= leader
FT FT      Region
FT FT      /label= Framework Region (FR) 1
FT FT      Region
FT FT      /label= Complementarity determining region(CDR)1
FT FT      Region
FT FT      /label= FR-2
FT FT      Region
FT FT      /label= CDR-2
FT FT      Region
FT FT      /label= FR-3
FT FT      Region
FT FT      /label= CDR-3
FT FT      Region
FT FT      /label= FR-4
FT FT      EP491351-A.
FT FT      24-JUN-1992.
FT FT      17-DEC-1991; 91EP-0121591.
FT FT      18-DEC-1990; 90JP-0413829.
FT FT      11-NOV-1991; 91JP-0294464.
FT FT      (TAKE ) TAKEDA CHEM IND LTD.
FT FT      Iwasa S, Taka H, Watanabe T, Tada H;
FT FT      WPI; 1992-209528/26.
FT FT      N-PSDB; AAQ25666.
FT FT      Chimeric monoclonal antibodies - contain anti-human fibrin
FT FT      antibody light and heavy chain variable and constant for treating
FT FT      thrombotic conditions e.g. myocardial infarction
FT FT      Example; Figure 4; 87pp; English.
FT FT      PCR primers 5'mvH and 3'mvH were used to produce a VH gene-contg.
FT FT      fragment of about 330bp. The fragment was isolated and subcloned in
FT FT      pUC119. The fragment was found to be a functional VH structural
FT FT      gene, referred to as VFH, comprising a VH gene belonging to the
FT FT      subgroup III (VHIII) and the DSP2 and JH4 genes. Northern blot
FT FT      analysis using the whole RNA of FIB1-11 cells confirmed that VFH
FT FT      was the gene expressed in FIB1-11 cells. The sequence is given in
FT FT      AAQ25666.
FT FT      SQ      Sequence      134 AA;
FT FT      Query Match      94.3%; Score 50; DB 13; Length 134;
FT FT      Best Local Similarity 90.0%; Pred. No. 0.077;
FT FT      Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
FT FT      Qy      1 GFTFSSYDMS 10
FT FT      | | | | |
FT FT      Db      45 gftfsnydms 54
FT FT      RESULT      9
FT FT      AAR24812
FT FT      ID      AAR24812 standard; Protein; 466 AA.
FT FT      XX
FT FT      AC      AAR24812;
FT FT      XX
FT FT      DT      28-DEC-1992 (first entry)
FT FT      XX
FT FT      DE      Sequence encoded by the chimeric H chain cDNA contained in pTB1373.
FT FT      XX      Chimeric monoclonal antibody; anti-fibrin antibody; primer;
FT FT      KW      antithrombotic agent; myocardial infarction therapy.

```

```

XX OS      Synthetic.
XX FT      Key      Location/Qualifiers
XX FT      13..19
XX FT      /label= Leader
XX FT      Region
XX FT      /label= VH
XX FT      Region
XX FT      /label= CH1
XX FT      Region
XX FT      /label= hinge
XX FT      Region
XX FT      /label= CH2
XX FT      Region
XX FT      /label= CH3
XX FT      Misc-difference 465
XX FT      /note= "translated stop codon"
XX FT      EP491351-A.
XX FT      24-JUN-1992.
XX FT      17-DEC-1991; 91EP-0121591.
XX FT      18-DEC-1990; 90JP-0413829.
XX FT      11-NOV-1991; 91JP-0294464.
XX FT      (TAKE ) TAKEDA CHEM IND LTD.
XX FT      Iwasa S, Taka H, Watanabe T, Tada H;
XX FT      WPI; 1992-209528/26.
XX FT      N-PSDB; AAQ25692.
XX FT      Chimeric monoclonal antibodies - contain anti-human fibrin
XX FT      antibody light and heavy chain variable and constant for treating
XX FT      thrombotic conditions e.g. myocardial infarction
XX FT      Example; Figure 11; 87pp; English.
XX FT      Plasmid pTB1373 contains the whole length of a mouse-human
XX FT      chimeric anti-human fibrin heavy chain cDNA open reading
XX FT      frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin
XX FT      chimeric Ab-producing transfectant FIB1-H01/X63 as a template
XX FT      to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
XX FT      a primer for first strand cDNA synthesis and the 5'C2H and 3'EH
XX FT      primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
XX FT      cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
XX FT      encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
XX FT      peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CLH
XX FT      respectively as a primer for first strand cDNA synthesis and the
XX FT      primer combination of 5'CLH and 3'C2H, of 5'CLH and 3'CLH and of
XX FT      5'SH and 3'EH respectively as primers for PCR. The amplified gene
XX FT      products were isolated and used to produce plasmids. After
XX FT      confirmation of the cDNA sequence of each plasmid, the cDNA
XX FT      encoding LH, VH, CH1 and CH2CH3 were joined together to give
XX FT      plasmid pTB1373 contg. the whole length chimeric H chain
XX FT      (LH, VH, CH1, CH2CH3), also abbreviated as IGH-FIB,
XX FT      SQ      Sequence      466 AA;

```

```

Query Match      94.3%; Score 50; DB 13; Length 466;
Best Local Similarity 90.0%; Pred. No. 0.29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GFTFSSYDMS 10
      | | | | |
Db      45 gftfsnydms 54
RESULT 10

```

AAB40112  
ID AAB40112 standard; Protein; 97 AA.  
XX  
AC AAB40112;  
XX  
DT 05-FEB-2001 (first entry)  
XX  
DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 638.  
XX  
KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
KW antisclerotic; neuroprotective; antipsoriatic; antidiabetic; cardiant;  
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
KW multiple sclerosis; rheumatoid arthritis.  
XX  
OS Homo sapiens.  
XX  
PN WO2000056772-A1.  
XX  
PD 28-SEP-2000.  
XX  
PF 24-MAR-2000; 2000WO-US07946.  
XX  
PR 25-MAR-1999; 99US-0126603.  
XX  
PA (BADI ) BASF AG.  
XX  
PB (GEM ) GENETICS INST INC.  
XX  
PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
PI Veldman GM, Venturini A, Warne NW, Wildom A, Elvin JG, Duncan AR;  
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
XX  
DR WPI; 2000-638250/61.  
XX  
PT New human antibody specific for human interleukin-12 (IL-12) used to  
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
PT disease and multiple sclerosis -  
XX  
PS Claim 75; Page 121; 377pp; English.  
XX  
CC This invention relates to a new human antibody specific for human  
CC interleukin-12 (IL-12). The invention also includes antigen binding  
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
CC anti-IL-12 antibody heavy and light chain complementarity determining  
CC region (CDR) amino acid sequences, and also includes variable region  
CC amino acid sequences. Other variable region amino acid sequences are  
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
CC given in AAB40064-B40067. Primers used in the identification and  
CC construction of the antibodies of the invention are given in  
CC AAC61062-C61071. The antibody of the invention is a neutralising  
CC antibody and has antirheumatic; antiarthritic; antisclerotic;  
CC antiinflammatory; neuroprotective; antipsoriatic; antidiabetic;  
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.  
CC The antibodies or antigen-binding fragments are useful in the treatment  
CC of disorders associated with detrimental release of human IL-12,  
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.  
CC They can also be used in the manufacture of a pharmaceutical composition  
CC to treat human IL-12 disorders.  
XX  
SQ Sequence 97 AA;

Query Match 92.5%; Score 49; DB 21; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.084;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9  
DB 26 gftfssydm 34

RESULT 11  
ABB39276  
ID ABB39276 standard; Peptide; 102 AA.  
XX  
AC ABB39276;  
XX  
DT 04-FEB-2002 (first entry)  
XX  
DE Peptide #6782 encoded by human foetal liver single exon probe.  
KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX  
OS Homo sapiens.  
XX  
PN WO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00669.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483447/52.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human fetal liver -  
XX  
PS Claim 27; SEQ ID NO 31911; 639pp + sequence listing; English.  
XX  
CC The invention relates to a single exon nucleic acid probe for  
CC measuring human gene expression in a sample derived from human foetal  
CC liver. The single exon nucleic acid probes may be used for predicting,  
CC measuring and displaying gene expression in samples derived from human  
CC fetal liver. The present sequence is a peptide encoded by a single exon  
CC nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 102 AA;

Query Match 92.5%; Score 49; DB 22; Length 102;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDM 9  
DB 17 gftfssydm 25

RESULT 12  
AAM59940  
ID AAM59940 standard; Protein; 102 AA.  
XX  
AC AAM59940;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32045.  
KW Human; brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
 KW epilepsy; cancer.

XX Homo sapiens.

XX WO200157275-A2.

PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00667.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human  
 PT brains -

XX Example 4; SEQ ID NO: 32045; 650pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is a protein encoded by one of  
 CC the probes of the invention.

XX Sequence 102 AA;

Query Match 92.5%; Score 49; DB 22; Length 102;

Best Local Similarity 100.0%; Pred. No. 0.089;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDM 9

Db 17 gftfssydm 25

RESULT 13

AAM72535

ID AAM72535 standard; Protein; 102 AA.

XX AC AAM72535;

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed probe encoded protein SEQ ID NO: 32841.

XX Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

XX WO200157276-A2.

PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00668.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human bone marrow -

XX Example 4; SEQ ID NO: 32841; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
 CC protein encoded by one of the probes of the invention.

XX Sequence 102 AA;

Query Match 92.5%; Score 49; DB 22; Length 102;

Best Local Similarity 100.0%; Pred. No. 0.089;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDM 9

Db 17 gftfssydm 25

RESULT 14

AAM32779

ID AAM32779 standard; Protein; 102 AA.

XX AC AAM32779;

XX 17-OCT-2001 (first entry)

XX Peptide #6816 encoded by probe for measuring placental gene expression.  
 DE Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder.  
 XX Homo sapiens.  
 OS WO200157272-A2.  
 PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00663.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-48897/53.

XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human placenta -

```

XX Claim 27; SEQ ID No 33048; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP:
CC see AA131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
XX Sequence 102 AA;
SQ
    Query Match          92.5%; Score 49; DB 22; Length 102;
    Best Local Similarity 100.0%; Pred. No. 0.089;
    Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 GFTFSSYDM 9
    Db 17 gftfssydm 25
    RESULT 15
    AAW21652
    ID AAW21652 standard; Protein; 139 AA.
    XX
    AC AAW21652;
    XX
    DT 03-JAN-1998 (first entry)
    XX
    DE Humanised reshaped Mab 15 heavy chain variable region.
    XX
    KW Humanised antibody; monoclonal antibody; Mab 15; tumour;
    KW lung cancer; therapy.
    XX
    OS Chimeric Mus musculus.
    OS Chimeric Homo sapiens.
    OS Chimeric synthetic.
    XX
    FH Key Location/Qualifiers
    FT Peptide 1..19
    FT /label= Sig_peptide
    FT Protein 20..139
    FT /label= Mat_protein
    FT Region 20..49
    FT /label= Framework-1
    FT Region 50..54
    FT /label= CDR1
    FT /note= "Complementarity determining region 1"
    FT Region 55..68
    FT /label= Framework-2
    FT Region 69..85
    FT /label= CDR2
    FT /note= "complementarity determining region 2"
    FT Region 86..117
    FT /label= Framework-3
    FT Region 118..128
    FT /label= CDR3
    FT /note= "complementarity determining region 3"
    FT Region 129..138
    FT /label= Framework-4
    XX
    PN EP781847-A1.
    XX
    PD 02-JUL-1997.
    XX
    PF 25-OCT-1996; 96EP-0117154.
    XX
    PR 06-NOV-1995; 95EP-0117407.
    XX
    PA (MÈRE ) MERCK PATENT GMBH.
    XX
    PI Bendig; M, Jones T, Saldana J;

```

```

XX WPI; 1997-334904/31.
DR N-PSDB; AAT72237.
XX
XX Humanised form of murine monoclonal antibody Mab 15 - useful for
XX treating lung cancer
XX
XX Claim 2; Fig 12; 71pp; English.
XX
XX This polypeptide comprises the heavy chain variable region VH
CC of humanised reshaped monoclonal antibody (Mab) 15 comprising
CC complementarity determining regions of murine Mab 15 (DSM ACC2117),
CC and reshaped human 30p1 framework regions. It is expressed by a
CC cDNA clone (see AAT72237) prepared using PCR mutagenesis methods. A
CC claimed process for preparation of humanised reshaped Mab 15
CC involves: cloning and sequencing murine Mab 15 VL and VH regions
CC (see AAW21653 and AAW21654); constructing, expressing and analysing
CC chimeric Mab 15 antibody (see AAW21655-56); modelling the structure
CC of murine Mab 15 variable regions; designing reshaped human Mab 15
CC variable regions; preparing an oligonucleotide sequence which codes
CC for the constant regions of the light and heavy chain of a human
CC immunoglobulin; and constructing, expressing and analysing the
CC complete reshaped human Mab 15. The humanised Mab can be used for
CC treating tumours, especially lung cancer, and for the manufacture
CC of a drug related to tumours, especially lung cancer.
XX
XX Sequence 139 AA;
SQ
    Query Match          92.5%; Score 49; DB 18; Length 139;
    Best Local Similarity 90.0%; Pred. No. 0.12;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    QY 1 GFTFSSYDMS 10
    Db 45 gftfssydm 54
    Search completed: August 19, 2002, 06:39:10
    Job time: 1471 sec

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GenCore version 4.5  
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# OM protein - protein search, using sw model

Run on: August 19, 2002, 06:14:39 ; Search time 61.75 seconds  
(without alignments)  
3.956 Million cell updates/sec

Title: US-09-339-922A-34

Perfect score: 53

Sequence: 1 GFTFSSYDMS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	94.3	128	1	US-08-478-039-73
2	50	94.3	128	1	US-08-478-039-102
3	50	94.3	128	1	US-08-476-349A-73
4	50	94.3	128	1	US-08-476-349A-102
5	48	90.6	239	2	US-07-956-399-4
6	48	90.6	247	5	PCT-US94-07659-2
7	47	88.7	123	1	US-08-478-039-71
8	47	88.7	123	1	US-08-478-039-104
9	47	88.7	123	1	US-08-476-349A-71
10	47	88.7	123	1	US-08-476-349A-104
11	47	88.7	123	1	US-08-665-202-31
12	46	86.8	98	2	US-08-545-809A-101
13	46	86.8	116	3	US-08-545-809A-101
14	46	86.8	116	4	US-08-983-607-36
15	46	86.8	122	1	US-08-276-852-80
16	46	86.8	122	1	US-08-899-575-80
17	46	86.8	122	1	US-08-899-575-80
18	46	86.8	122	5	PCT-US95-08743-80
19	46	86.8	123	2	US-08-665-202-30
20	46	86.8	239	2	US-08-553-497A-18
21	45	84.9	35	2	US-08-765-179B-1
22	45	84.9	98	2	US-08-428-197-48
23	45	84.9	98	5	PCT-US93-10555-48
24	45	84.9	102	2	US-08-273-146-65
25	45	84.9	110	1	US-08-211-202-117
26	45	84.9	113	3	US-08-974-899-6
27	45	84.9	116	2	US-08-428-197-2

28	45	84.9	116	5	PCT-US93-10555-2
29	45	84.9	117	3	US-08-545-809A-109
30	45	84.9	117	4	US-08-983-607-46
31	45	84.9	117	4	US-08-752-693A-3
32	45	84.9	117	4	US-08-752-693A-4
33	45	84.9	117	4	US-09-157-370-1
34	45	84.9	118	2	US-08-652-816A-12
35	45	84.9	118	4	US-08-487-761-15
36	45	84.9	118	5	PCT-US93-08435-10
37	45	84.9	120	4	US-09-025-769B-38
38	45	84.9	120	1	US-09-025-769B-63
39	45	84.9	121	1	US-08-339-582-2
40	45	84.9	122	2	US-07-934-373C-21
41	45	84.9	122	3	US-08-437-642B-21
42	45	84.9	122	5	PCT-US93-07832-21
43	45	84.9	122	5	PCT-US93-08435-12
44	45	84.9	122	5	PCT-US93-08435-14
45	45	84.9	122	5	PCT-US93-08435-43

## ALIGNMENTS

RESULT 1  
US-08-478-039-73  
; Sequence 73, Application US/08478039  
; Patent No. 5681722  
; GENERAL INFORMATION:  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Raab, Ronald W.  
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,039  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/379,072  
; FILING DATE: 25-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/912,292  
; FILING DATE: 10-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/856,281  
; FILING DATE: 23-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/735,064  
; FILING DATE: 25-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin Esq., Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-160  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Monkey  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: VH3 clone 3-40  
US-08-478-039-73

Query Match 94.3%; Score 50; DB 1; Length 128;  
Best Local Similarity 90.0%; Pred. No. 0.028;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTSSYDMS 10  
Db 26 GFTSSYDMN 35

RESULT 2  
US-08-478-039-102  
; Sequence 102, Application US/08478039  
; Patent No. 5681722  
; GENERAL INFORMATION:  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Raab, Ronald W.  
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,039  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/379,072  
; FILING DATE: 25-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/912,292  
; FILING DATE: 10-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/856,281  
; FILING DATE: 23-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/735,064  
; FILING DATE: 25-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin Esq., Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-160  
; TELEPHONE: 703-836-6620  
; INFORMATION FOR SEQ ID NO: 102:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Monkey  
; POSITION IN GENOME:

; CHROMOSOME/SEGMENT: #40  
US-08-478-039-102

Query Match 94.3%; Score 50; DB 1; Length 128;  
Best Local Similarity 90.0%; Pred. No. 0.028;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTSSYDMS 10  
Db 26 GFTSSYDMN 35

RESULT 3  
US-08-476-349A-73  
; Sequence 73, Application US/08476349A  
; Patent No. 5750105  
; GENERAL INFORMATION:  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Raab, Ronald W.  
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,349A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/379,072  
; FILING DATE: 25-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/912,292  
; FILING DATE: 10-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/856,281  
; FILING DATE: 23-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/735,064  
; FILING DATE: 25-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin Esq., Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-161  
; TELEPHONE: 703-836-6620  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Monkey  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: VH3 clone 3-40  
US-08-476-349A-73

Query Match

94.3%; Score 50; DB 1; Length 128;



Best Local Similarity 90.0%; Pred. No. 0.028;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10  
|||||

Db 26 GFTFSSYDMS 35

RESULT 4  
US-08-476-349A-102  
; Sequence 102, Application US/08476349A  
; Patent No. 5750105  
; GENERAL INFORMATION:  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Haana, Nabil  
; APPLICANT: Raab, Ronald W.  
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,349A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/379,072  
; FILING DATE: 25-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/912,292  
; FILING DATE: 10-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/856,281  
; FILING DATE: 23-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/735,064  
; FILING DATE: 25-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin Esq., Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-161  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 102:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Monkey  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: #40  
US-08-476-349A-102

Query Match 94.3%; Score 50; DB 1; Length 128;  
Best Local Similarity 90.0%; Pred. No. 0.028;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10  
|||||

Db 26 GFTFSSYDMS 35

RESULT 5  
US-07-956-399-4  
; Sequence 4, Application US/07956399  
; Patent No. 5876717  
; GENERAL INFORMATION:  
; APPLICANT: SHIMAMURA, TOSHIRO  
; APPLICANT: TAKI, SHINSUKE  
; APPLICANT: HAMURO, JUNJI  
; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY  
; TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBOLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
; ADDRESS: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/956,399  
; FILING DATE: 19921005  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Obolon, No. 5876717man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 10-586-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-956-399-4

Query Match 90.6%; Score 48; DB 2; Length 239;  
Best Local Similarity 90.0%; Pred. No. 0.13;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10  
|||||

Db 148 GFTFSSYDMS 157

RESULT 6  
PCT-US94-07659-2  
; Sequence 2, Application PC/TUS9407659  
; GENERAL INFORMATION:  
; APPLICANT: Young, Peter  
; APPLICANT: Gross, Mitchell  
; APPLICANT: Jonak, Zdenka L.  
; APPLICANT: Theisen, Timothy  
; APPLICANT: Hurie, Mark  
; APPLICANT: Jackson, Jeffrey R.  
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta  
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory  
; TITLE OF INVENTION: Disorders in Man  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corp.

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07659-6

Query Match 88.7% Score 47; DB 5; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 1; Indels 0

QY 1 GFTFSSYDMS 10
|||
Db 26 GFIFSSYDMS 35

RESULT 8
US-08-478-039-71
Sequence 71. Application US/08478039

```

GENERAL INFORMATION:  
APPLICANT: Newman, Roland A.  
APPLICANT: Hanna, Nabil  
APPLICANT: Raab, Ronald W.  
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STATE: VA  
 COUNTRY: USA  
 ZIP: 22313-1404  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/478,039  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/379,072  
 FILING DATE: 25-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/912,292  
 FILING DATE: 10-JUL-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/856,281  
 FILING DATE: 23-MAR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/735,064  
 FILING DATE: 25-JUL-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Teskin Esq., Robin L.  
 REGISTRATION NUMBER: 35,030  
 REFERENCE/DOCKET NUMBER: 012712-160  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021  
 INFORMATION FOR SEQ ID NO: 71:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 123 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Monkey  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: VH3 clone 3-34  
 US-08-478-039-71

Query Match 88.7%; Score 47; DB 1; Length 123;  
 Best Local Similarity 80.0%; Pred. No. 0.094;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10  
 Db 26 GFTFSTYDMT 35

## RESULT 9

US-08-478-039-104  
 ; Sequence 104, Application US/08478039  
 ; Patent No. 5681722  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Newman, Roland A.  
 ; APPLICANT: Hanna, Nabil  
 ; APPLICANT: Raab, Ronald W.  
 ; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
 ; NUMBER OF SEQUENCES: 114  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 ; STREET: 699 Prince St.  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22313-1404  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/478,039  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION NUMBER: US 08/379,072  
 ; FILING DATE: 25-JAN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/912,292  
 ; FILING DATE: 10-JUL-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/856,281  
 ; FILING DATE: 23-MAR-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/735,064  
 ; FILING DATE: 25-JUL-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Teskin Esq., Robin L.  
 ; REGISTRATION NUMBER: 35,030  
 ; REFERENCE/DOCKET NUMBER: 012712-160  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 703-836-6620  
 ; TELEFAX: 703-836-2021  
 ; INFORMATION FOR SEQ ID NO: 104:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 123 amino acids  
 ; TYPE: amino acid

STRANDEDNESS: not relevant  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Monkey  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: #34  
 US-08-478-039-104

Query Match 88.7%; Score 47; DB 1; Length 123;  
 Best Local Similarity 80.0%; Pred. No. 0.094;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10  
 Db 26 GFTFSTYDMT 35

## RESULT 10

US-08-476-349A-71  
 ; Sequence 71, Application US/08476349A  
 ; Patent No. 5750105  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Newman, Roland A.  
 ; APPLICANT: Hanna, Nabil  
 ; APPLICANT: Raab, Ronald W.  
 ; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
 ; NUMBER OF SEQUENCES: 114  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 ; STREET: 699 Prince St.  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22313-1404  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/476,349A  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/379,072  
 ; FILING DATE: 25-JAN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/912,292  
 ; FILING DATE: 10-JUL-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/856,281  
 ; FILING DATE: 23-MAR-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/735,064  
 ; FILING DATE: 25-JUL-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Teskin Esq., Robin L.  
 ; REGISTRATION NUMBER: 35,030  
 ; REFERENCE/DOCKET NUMBER: 012712-161  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 703-836-6620  
 ; TELEFAX: 703-836-2021  
 ; INFORMATION FOR SEQ ID NO: 71:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 123 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: not relevant  
 ; TOPOLOGY: not relevant  
 ; MOLECULE TYPE: peptide  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Monkey

; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: VH3 clone 3-34  
US-08-476-349A-71

Query Match 88.7%; Score 47; DB 1; Length 123;  
Best Local Similarity 80.0%; Pred. No. 0.094;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
Db 26 GFTFSTYDMT 35  
|||||:|:

RESULT 11  
US-08-476-349A-104  
; Sequence 104, Application US/08476349A  
; Patent No. 5750105  
; GENERAL INFORMATION:  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Raab, Ronald W.  
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,349A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/379,072  
FILING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/912,292  
FILING DATE: 10-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,281  
FILING DATE: 23-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/735,064  
FILING DATE: 25-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin Esq., Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-161  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Monkey  
POSITION IN GENOME:  
-CHROMOSOME/SEGMENT: #34  
US-08-476-349A-104

Query Match 88.7%; Score 47; DB 1; Length 123;  
Best Local Similarity 80.0%; Pred. No. 0.094;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
Db 26 GFTFSTYDMT 35  
|||||:|:

RESULT 12  
US-08-665-202-31  
; Sequence 31, Application US/08665202  
; Patent No. 5977322  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D.  
; APPLICANT: Schier, Robert  
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,202  
FILING DATE: 13-JUN-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061410  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-665-202-31

Query Match 86.8%; Score 46; DB 2; Length 98;  
Best Local Similarity 80.0%; Pred. No. 0.11;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFSSYDMS 10  
Db 26 GFTFSSYEMN 35  
|||||:|:

RESULT 13  
US-08-545-809A-101  
; Sequence 101, Application US/08545809A  
; Patent No. 6096878  
; GENERAL INFORMATION:  
; APPLICANT: Honjo, Tasuku

```

; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-101

Query Match      86.8%; Score 46; DB 3; Length 116;
Best Local Similarity 88.9%; Pred. No. 0.13;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTFSSYDM 9
Db      45 GFTFSNYDM 53

RESULT 14
US-08-983-607-36
; Sequence 36, Application US/089836507
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607

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; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: fuses5 fusion phage construct
; CLONE: V474
; FEATURE:
; NAME/KEY: heavy chain
US-08-983-607-36

Query Match      86.8%; Score 46; DB 4; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GFTFSSYDMS 10
Db      26 GFTFSSYDMS 35

RESULT 15
US-08-276-852-80
; Sequence 80, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCR1452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-80

Query Match 86.8%; Score 46; DB 1; Length 122;  
Best Local Similarity 80.0%; Pred. No. 0.14;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTFSSYDMS 10  
Db 23 GFTFSSYEMN 32

Search completed: August 19, 2002, 06:34:38  
Job time: 1199 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:03 ; Search time 78.53 seconds  
(without alignments)  
11.012 Million cell updates/sec

Title: US-09-339-922A-90

Perfect score: 51

Sequence: 1 QQSGSWPLT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR71:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	88.2	104	2 B43413	Ig kappa chain V r
2	45	88.2	138	2 A26471	Ig kappa chain pre
3	40	78.4	106	2 PL0267	Ig kappa chain V r
4	40	78.4	106	2 PC4282	Ig kappa chain (an
5	40	78.4	107	2 C45722	anti-glycoprotein
6	39	76.5	67	2 PH1081	Ig light chain V r
7	39	76.5	69	2 PH1080	Ig light chain V r
8	39	76.5	553	2 T15220	hypothetical prote
9	38	74.5	107	2 A45722	anti-glycoprotein
10	38	74.5	123	2 S35479	Ig kappa chain pre
11	38	74.5	506	2 AH3252	thymidylate kinase
12	37	72.5	102	2 S26346	Ig kappa chain V r
13	37	72.5	128	2 PN0445	Ig kappa chain pre
14	37	72.5	144	2 PL0106	Ig kappa chain pre
15	37	72.5	154	2 T17816	hypothetical prote
16	37	72.5	642	2 H69466	conserved hypothet
17	37	72.5	677	2 D97335	hypothetical prote
18	37	72.5	764	2 T48446	hypothetical prote
19	36	70.6	87	2 PH1082	Ig light chain V r
20	36	70.6	91	2 S37525	Ig kappa chain V r
21	36	70.6	108	2 C30502	Ig kappa chain V r
22	36	70.6	115	1 KVM5L7	Ig kappa chain pre
23	36	70.6	117	2 S40362	Ig kappa chain - h
24	36	70.6	169	2 D65126	probable general s
25	36	70.6	204	2 T32062	hypothetical prote
26	36	70.6	275	2 D70737	hypothetical prote
27	36	70.6	543	2 T06523	cytochrome P450 mo
28	36	70.6	1221	2 E83327	conserved hypothet
29	35	68.6	100	2 G81749	hypothetical prote

30 35 68.6 107 2 B45722 anti-glycoprotein  
31 35 68.6 146 2 AD0929 conserved hypothet  
32 35 68.6 181 2 A10861 syd protein [impor  
33 35 68.6 235 1 S0MS parotid secretory  
34 35 68.6 317 2 B82084 probable cobalamin  
35 35 68.6 365 1 SAVLWE large surface anti  
36 35 68.6 366 1 SAVLWD large surface anti  
37 35 68.6 366 1 SAVLWD large surface anti  
38 35 68.6 499 2 A27198 cellulase (EC 3.2.  
39 35 68.6 508 2 A26874 cellulase (EC 3.2.  
40 35 68.6 939 2 H71532 valine--trna ligas  
41 35 68.6 939 2 H81686 valyl-trna synthet  
42 35 68.6 940 2 F86502 alyl-trna syntheta  
43 35 68.6 940 2 B72120 valine--trna ligas  
44 34 66.7 91 2 S37511 Ig kappa chain V r  
45 34 66.7 96 2 JC5945 regulatory protein

#### ALIGNMENTS

##### RESULT 1

B43413  
Ig kappa chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: B43413  
R:Tomiyama, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; J. Biol. Chem. 267, 18085-18092, 1992  
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct speci  
A:Reference number: A43413; MUID:92388177  
A:Accession: B43413  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-104 <TOM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 45; DB 2; Length 104;  
Best Local Similarity 88.9%; Pred. No. 0.59; Mismatches 0; Indels 1; Gaps 0;  
Matches 8; Conservative 0;

Qy 1 QQSGSWPLT 9

Db 86 QQSNWPLT 94

##### RESULT 2

A26471  
Ig kappa chain precursor V region (MAK33) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 23-Jul-1999  
C:Accession: A26471  
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K. Gene 51, 13-19, 1987  
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat  
A:Reference number: A91572; MUID:87248058  
A:Accession: A26471  
A:Molecule type: mRNA  
A:Residues: 1-138 <BUG>  
A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 88.2%; Score 45; DB 2; Length 138;  
Best Local Similarity 88.9%; Pred. No. 0.79; Mismatches 0; Indels 1; Gaps 0;  
Matches 8; Conservative 0;

QY 1 QOQSGSWPLT 9  
 DB 109 QQSNWPLT 117

RESULT 3  
 PL0267  
 Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
 C:Accession: PL0267  
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
 J. Exp. Med. 171, 265-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A:Reference number: PL0231; MUID:90111618  
 A:Accession: PL0267  
 A:Molecule type: mRNA  
 A:Residues: 1-106 <SHL>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:1-23/Region: framework 1  
 F:16-90/Domain: immunoglobulin homology <IMM>  
 F:24-34/Region: complementarity-determining 1  
 F:35-49/Region: framework 2  
 F:50-56/Region: complementarity-determining 2  
 F:57-88/Region: framework 3  
 F:89-97/Region: complementarity-determining 3  
 F:98-106/Region: framework 4

Query Match 78.4%; Score 40; DB 2; Length 106;  
 Best Local Similarity 77.8%; Pred. No. 4.4;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9  
 DB 89 QQSNWPLT 97

RESULT 4  
 PC4282  
 Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 21-Jan-2000  
 C:Accession: PC4282; PC4284  
 R:Suzuki, H.; Takemura, H.; Sekine, Y.; Kashiwagi, H.  
 Biochem. Biophys. Res. Commun. 232, 101-106, 1997  
 A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltrating  
 A:Reference number: PC4279; MUID:97236289  
 A:Accession: PC4282  
 A:Molecule type: protein  
 A:Residues: 1-106 <SUZ>  
 A:Note: E-42  
 A:Accession: PC4284  
 A:Molecule type: protein  
 A:Residues: 1-106 <SU2>  
 A:Note: E-56  
 C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjogren's  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 40; DB 2; Length 106;  
 Best Local Similarity 77.8%; Pred. No. 4.4;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9  
 DB 87 QQRASWPLT 95

RESULT 5

C45722  
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: C45722  
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdaloovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va  
 J. Virol. 67, 489-496, 1993  
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on  
 A:Reference number: A45722; MUID:93100833  
 A:Accession: C45722  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-107 <STM>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:120591)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: glycoprotein  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 40; DB 2; Length 107;  
 Best Local Similarity 77.8%; Pred. No. 4.5;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9  
 DB 89 QQSHWPLT 97

RESULT 6  
 PH1081  
 Ig light chain V region (clone 165.6) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Jun-1996  
 C:Accession: PH1081  
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective  
 A:Reference number: PH0971; MUID:92381444  
 A:Accession: PH1081  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-67 <TIL>  
 A:Experimental source: B cell, strain [NZB x NZW]F1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin

Query Match 76.5%; Score 39; DB 2; Length 67;  
 Best Local Similarity 77.8%; Pred. No. 4.2;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9  
 DB 58 QQSNWPLT 66

RESULT 7  
 PH1080  
 Ig light chain V region (clone 165.60) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Jun-1996  
 C:Accession: PH1080  
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective  
 A:Reference number: PH0971; MUID:92381444  
 A:Accession: PH1080  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-69 <TIL>  
 A:Experimental source: B cell, strain [NZB x NZW]F1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin



Query Match 76.5%; Score 39; DB 2; Length 69;  
 Best Local Similarity 77.8%; Pred. No. 4.3;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
 ||| ||| |  
 Db 60 QQSNSWPQT 68

## RESULT 8

TI5220  
 hypothetical protein F57C9.8 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: TI5220  
 R:Geisler, C.; Kramer, J.; Gibson, A.  
 submitted to the EMBL Data Library, May 1997  
 A:Description: The sequence of C. elegans cosmid F57C9.  
 A:Reference number: Z18309  
 A:Accession: TI5220  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-553 <GET>  
 A:Cross-references: EMBL:AF003142; NID:g2088743; PID:g2088751; PIDN:AA854191.1; GSPDB:GN  
 A:Experimental source: strain Bristol N2; clone F57C9  
 C:Genetics:  
 A:Gene: CESP:F57C9.8  
 A:Map position: 1  
 A:Introns: 184/1; 233/3; 286/3; 496/1

Query Match 76.5%; Score 39; DB 2; Length 553;  
 Best Local Similarity 66.7%; Pred. No. 35;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
 |:||||| :  
 Db 373 QRSGSWPFS 381

## RESULT 9

A45722  
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (fra  
 C:Species: Mus musculus (house mouse)  
 C:Date: 03-Mar-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: A45722  
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu  
 J. Virol. 67, 489-496, 1993  
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu  
 A:Reference number: A45722; MUID:93100833  
 A:Accession: A45722  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <SIM>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:120589)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: glycoprotein  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 38; DB 2; Length 107;  
 Best Local Similarity 77.8%; Pred. No. 9.9;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
 ||| ||| |  
 Db 89 QQSNSWPHT 97

## RESULT 10

S35479

Ig kappa chain precursor V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
 C:Accession: S35479  
 R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.

Nucleic Acids Res. 20, 4099, 1992  
 A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from  
 A:Reference number: S35479; MUID:92375706

A:Accession: S35479  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA

A:Residues: 1-123 <TAK>

A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148

C:Genetics:

A:Map position: 6

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>

F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>

F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 38; DB 2; Length 123;  
 Best Local Similarity 77.8%; Pred. No. 11;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
 ||| ||| |  
 Db 101 QQSNSWPHT 109

## RESULT 11

AH3252  
 thymidylate kinase (EC 2.7.4.9) [imported] - Brucella melitensis (strain 16M)  
 C:Species: Brucella melitensis  
 C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
 C:Accession: AH3252  
 R:DelVecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Mujter, C.; Los, T.; Ivanov  
 ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit  
 A:Reference number: AD3252; PMID:11756688  
 A:Accession: AH3252  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-506 <KUR>  
 A:Cross-references: GB:AE008917; PIDN:AAL511187.1; PID:g17981871; GSPDB:GN00190

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI0005

A:Map position: 1

C:Keywords: phosphotransferase

Query Match 74.5%; Score 38; DB 2; Length 506;  
 Best Local Similarity 75.0%; Pred. No. 48;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QSGSWPLT 9  
 | | | ||| |  
 Db 135 QGGWPLT 142

## RESULT 12

S26346  
 Ig kappa chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
 C:Accession: S26346  
 R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protei  
 A:Reference number: S26309; MUID:91341421

A:Accession: S26346  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-102 <STA>  
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:g1334075  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 102;  
Best Local Similarity 66.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9  
|||:||||  
Db 87 QOQNTWPT 95

## RESULT 13

PN0445  
Ig kappa chain precursor V-I region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PN0445  
R:Kaluza, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.  
Gene 122, 321-328, 1992  
A:Title: A general method for chimeraization of monoclonal antibodies by inverse polymerase chain reaction  
A:Reference number: PN0444; MUID:93138402  
A:Accession: PN0445

A:Molecule type: mRNA  
A:Residues: 1-128 <KAL>  
A:Cross-references: GB:L02347

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-10/Domain: signal sequence #status predicted <SIG>  
F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>  
F:126-100/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 128;  
Best Local Similarity 66.7%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9  
|||:||||  
Db 99 QOQNTWPT 107

## RESULT 14

PL0106  
Ig kappa chain precursor V-J-C region (Ls1) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000  
C:Accession: PL0106  
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.  
J. Exp. Med. 169, 1631-1643, 1989  
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma secretory cell line to the immunoglobulin gene family  
A:Reference number: PL0106; MUID:89235583  
A:Accession: PL0106

A:Molecule type: mRNA  
A:Residues: 1-144 <SIL>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-115/Domain: V region <VRE>  
F:136-110/Domain: immunoglobulin homology <IMM>  
F:44-54/Region: complementarity-determining 1  
F:70-76/Region: complementarity-determining 2  
F:109-115/Region: complementarity-determining 3  
F:116-147/Domain: J region <JRG>  
F:128-144/Domain: C region (fragment) <CRE>

Query Match 72.5%; Score 37; DB 2; Length 144;  
Best Local Similarity 66.7%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9  
|||:||||  
Db 109 QOQNSWPLT 117

## RESULT 15

TL7816  
hypothetical protein a317L - Chlorella virus PBCV-1  
C:Species: Chlorella virus PBCV-1  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: TL7816  
R:Graves, M.V.; Van Etten, J.L.  
submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806  
A:Accession: TL7816  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-154 <GRA>  
A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96685.1  
A:Experimental source: specific host Chlorella strain NC64A  
C:Genetics:  
A:Note: a317L

Query Match 72.5%; Score 37; DB 2; Length 154;  
Best Local Similarity 75.0%; Pred. No. 21;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPL 8  
|||:||||  
Db 33 QOQSGSWPV 40

Search completed: August 19, 2002, 06:36:04  
Job time: 1285 sec

GenCore version 4.5  
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# OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:05 ; Search time 51.81 Seconds  
(without alignments)  
6.726 Million cell updates/sec

Title: US-09-339-922A-90

Perfect score: 51

Sequence: 1 QSGSWPLT 9

## Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	78.4	745	1 CUL2_HUMAN	Q13617 homo sapien
2	38	74.5	418	1 OR13_DROME	Q9VX10 drosophila
3	38	74.5	471	1 P2X2_HUMAN	Q9UB19 homo sapien
4	36	70.6	115	1 KV51_MOUSE	P01642 mus musculus
5	36	70.6	169	1 GSPH_ECOLI	P41443 escherichia
6	36	70.6	544	1 C821_PEA	Q43068 pisum sativ
7	35	68.6	235	1 PSP_MOUSE	P07743 mus musculus
8	35	68.6	365	1 VMSA_HPBDC	P30029 duck hepati
9	35	68.6	366	1 VMSA_HPBDB	P17194 duck hepati
10	35	68.6	366	1 VMSA_HPBDB	P17195 duck hepati
11	35	68.6	499	1 GUN1_BACSU	P07983 bacillus su
12	35	68.6	939	1 SYV_CHLMU	Q9PK91 chlamydia m
13	35	68.6	939	1 SYV_CHLTPN	O84304 chlamydia t
14	35	68.6	940	1 SYV_CHLTPN	Q92987 chlamydia p
15	34	66.7	92	1 CATPC_RHOOP	P95609 rhodococcus
16	34	66.7	96	1 CTCL1_ACILW	Q33947 acinetobact
17	34	66.7	146	1 YFCK_ECOLI	P77656 escherichia
18	34	66.7	470	1 IE63_HSVB	P28939 equine herp
19	34	66.7	470	1 IE63_HSVK	Q05906 equine herp
20	34	66.7	540	1 NUSA_MYCPN	P75591 mycoplasma
21	34	66.7	777	1 BISC_ECOLI	P20099 escherichia
22	34	66.7	1047	1 RIR1_CHLMU	Q9P193 chlamydia m
23	34	66.7	1456	1 RRPO_PVX	P09195 potato viru
24	34	66.7	1456	1 RRPO_PVXCP	P22591 potato viru
25	34	66.7	1456	1 RRPO_PVXHB	Q07630 potato viru
26	34	66.7	1456	1 RRPO_PVXX3	P17779 potato viru
27	34	66.7	2329	1 YS89_CAEEL	Q09624 caenorhabdi
28	33	64.7	226	1 NUKM_NEUCR	Q47950 neorospora
29	33	64.7	251	1 BIOC_ECOLI	P12999 escherichia
30	33	64.7	300	1 GP40_HUMAN	Q14842 homo sapien
31	33	64.7	432	1 NFPI_RAT	Q9EP86 rattus norv
32	33	64.7	468	1 NIEB_KLEPN	P10390 klebsiella
33	33	64.7	516	1 Y4NN_RHISN	P55585 rhizobium s

34	33	64.7	517	1 LAD1_HUMAN	O00515 homo sapien
35	33	64.7	796	1 PTRR_RAT	Q03348 rattus norv
36	33	64.7	802	1 PTRR_HUMAN	P18433 homo sapien
37	33	64.7	829	1 PTRR_MOUSE	P18052 mus musculu
38	33	64.7	3329	1 BRC2_MOUSE	P97929 mus musculu
39	33	64.7	3418	1 BRC2_HUMAN	P51587 homo sapien
40	32	62.7	302	1 CYSD_BUCAI	P57499 buchnera ap
41	32	62.7	302	1 CYSD_ECOLI	P21156 escherichia
42	32	62.7	336	1 CH12_ORYSA	P25765 oryza sativ
43	32	62.7	401	1 FXH1_MOUSE	O88621 mus musculu
44	32	62.7	402	1 OPDE_PSEAE	Q01602 pseudomonas
45	32	62.7	471	1 STCH_HUMAN	P48723 homo sapien

## ALIGNMENTS

```

RESULT_1
CUL2_HUMAN
ID CUL2_HUMAN STANDARD; PRT: 745 AA.
AC Q13617; O00200; Q9UNF9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cullin homolog 2 (CUL-2).
GN CUL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RP SEQUENCE FROM N.A., AND VARIANT SER-109.
RC TISSUE=Kidney;
RX MEDLINE=97225922; PubMed=9122164;
RA Pause A., Lee S., Worrel R., Chen D.Y.T., Burgess W.H.,
RA Linehan W.M., Klausner R.D.;
RT "The von Hippel-Lindau tumor-suppressor gene product forms a stable
RT complex with human CUL-2, a member of the Cdc53 family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:2156-2161(1997).
[2]
RN RP SEQUENCE FROM N.A., AND VARIANT SER-109.
RC TISSUE=Brain;
RX MEDLINE=99194561; PubMed=10092517;
RA Wada H., Yeh E.T.H., Kamitani T.;
RT "Identification of NEDD8-conjugation site in human cullin-2.";
RL Biochem. Biophys. Res. Commun. 257:100-105(1999).
[3]
RN RP SEQUENCE OF 95-745 FROM N.A.
RX MEDLINE=96279828; PubMed=8681378;
RA Kipreos E.T., Lander L.E., Wing J.P., He W.W., Hedgecock E.M.;
RT "cul-1 is required for cell cycle exit in C. elegans and identifies a
RT novel gene family.";
RL Cell 85:829-839(1996).
CC -!- FUNCTION: FORMS A STABLE COMPLEX WITH THE VHL TUMOR SUPPRESSOR.
CC -!- SIMILARITY: BELONGS TO THE CULLIN FAMILY.
CC -----
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CC -----
CC EMBL; U83410; AAC51190.1; -.
CC EMBL; AF126404; AAD23581.1; -.
CC EMBL; U58088; AAC50545.1; -.
CC MIM; 603135; -.
CC InterPro: IPR001373; Cullin.
CC Pfam; PF00886; Cullin; 1.
CC SMART; SM00182; CULLIN; 1.
CC PROSITE; PS01256; CULLIN_1; 1.
CC PROSITE; PS50069; CULLIN_2; 1.

```

KW Polymorphism. 689 NEDD8.  
 FT BINDING 689 N -> S.  
 FT VARIANT 109 /FTIG=VAR\_011374.  
 FT CONFLICT 95 SKGA -> IRHE (IN REF. 3).  
 FT CONFLICT 681 Q -> H (IN REF. 3).  
 SQ SEQUENCE 745 AA; 86983 MW; 30647248F671AB0E CRC64;

Query Match 78.4%; Score 40; DB 1; Length 745;  
 Best Local Similarity 75.0%; Pred. No. 11;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSGSWPLT 9  
 I:|||||  
 Db 513 QAGAMPLT 520

RESULT 2  
 OR13\_DROME

ID OR13\_DROME STANDARD; PRT; 418 AA.

AC Q9VXL0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Putative odorant receptor 13a.  
 GN OR13A OR G12697.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]

SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foaier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy L., Murphree L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).  
 RN [2]  
 RP CONCEPTUAL TRANSLATION.  
 RA Robertson H.M.;  
 RL Unpublished observations (MAY-2001).  
 CC -I- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT  
 CC RECEPTOR.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -I- SIMILARITY: BELONGS TO DROSOPHILA ODORANT RECEPTOR FAMILY OF G-  
 CC PROTEIN COUPLED RECEPTORS.  
 CC -I- CAUTION: REF.1 SEQUENCE DIFFERS AT SEVERAL POSITIONS FROM THAT  
 CC SHOWN DUE TO DIFFERENCES IN THE PREDICTION OF SPICE SITES.  
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 -----

CC EMBL; AE003500; AAF48549.1; ALT\_SEQ.  
 DR FlyBase; FBgn0030715; Or13a.  
 DR InterPro; IPR004117; 7tm\_6.  
 DR Pfam; PF02949; 7tm\_6; 1.  
 KW Hypothetical protein; Transmembrane; G-protein coupled receptor;  
 KW Gycoprotein; Olfaction; Multigene family.  
 FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 39 59 1 (POTENTIAL).  
 FT DOMAIN 60 70 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 71 91 2 (POTENTIAL).  
 FT DOMAIN 92 140 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 141 161 3 (POTENTIAL).  
 FT DOMAIN 162 195 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 196 216 4 (POTENTIAL).  
 FT DOMAIN 217 273 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 274 294 5 (POTENTIAL).  
 FT DOMAIN 295 299 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 300 320 6 (POTENTIAL).  
 FT DOMAIN 321 385 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 386 406 7 (POTENTIAL).  
 FT DOMAIN 407 418 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 418 AA; 48263 MW; 6E8EC466CF246F0E CRC64;

Query Match 74.5%; Score 38; DB 1; Length 418;  
 Best Local Similarity 85.7%; Pred. No. 14;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QSGSWPLT 9  
 Db 22 NGSWPLT 28

RESULT 3  
 P2X2\_HUMAN

ID P2X2\_HUMAN STANDARD; PRT; 471 AA.  
 AC Q9UBL9; Q9Y637; Q9Y638; Q9UHD5; Q9UHD6; Q9UHD7; Q9NR37; Q9NR38;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE P2X purinoceptor 2 (ATP receptor) (P2X2) (Purinergic receptor).  
 GN P2RX2 OR P2X2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).  
 RC TISSUE=pituitary;



DE transport protein hofH).  
GN HOFH OR HOPH OR B3329.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RN SEQUENCE OF 1-30 FROM N.A.  
RP STRAIN-K12;  
RC STRAIN-K12; PubMed=7896718;  
RX MEDLINE=95204361; PubMed=7896718;  
RA Stojiljkovic I., Schoenherr K., Kusters J.G.;  
RT "Identification of the hopG gene, a component of Escherichia coli  
RT K-12 type II export system, and its conservation among different  
RT pathogenic Escherichia coli and Shigella isolates.";  
RL J. Bacteriol. 177:1892-1895(1995)  
CC -!- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE  
CC EXPORT OF PROTEINS (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE PULH/OUTH/XPSH/XEHX/XCPU FAMILY.  
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DR EMBL; U18997; AAA58126.1; -.  
DR EMBL; AF000409; AAC76354.1; -.  
DR EMBL; U20786; AAA69032.1; -.  
DR EcoGene; EG12887; hofH.  
DR InterPro; IPR002416; Bac\_GSPH.  
DR PRINTS; PR00885; BCTERIALGSPH.  
DR PROSITE; PS00409; PROKAR\_NTER\_METHYL; 1.  
KW Transport; Methylation; Complete proteome.  
FT PROPEP 1 6 BY SIMILARITY.  
FT CHAIN 7 169 PUTATIVE GENERAL SECRETION PATHWAY  
FT MOD\_RES 7 7 PROTEIN H.  
FT METHYLATION (BY SIMILARITY).  
SQ SEQUENCE 169 AA; 18565 MW; D42B1127FBB81A09 CRC64;  
  
Query Match 70.6%; Score 36; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 SGSWPL 8  
Db 154 SGSWPL 159  
|||||  
RESULT 6  
ID C82L\_PEA STANDARD; PRT; 544 AA.  
AC Q43068;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Cytochrome P450 82A1 (EC 1.14.-.-) (CYPLXXII) (Fragment).  
DN CYP82A1 OR CYP82.  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RN SEQUENCE FROM N.A.  
RN TISSUE=Stem;  
RC MEDLINE=96417083; PubMed=8819874;  
RX Frank M.R., Deyneka J.M., Schuler M.A.;  
RT "Cloning of wound-induced cytochrome P450 monooxygenases expressed in  
RT pea.";  
RL Plant Physiol. 110:1035-1046(1996).  
RN [2]  
RN REVISTONS TO 47-48; 127; 198-199; 304; 311; 333-335 AND 454.  
RA Frank M.R.;  
RC Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- INDUCTION: By wounding.  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
CC -----  
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CC -----  
DR EMBL; U29333; AAC49188.2; -.  
DR InterPro; IPR001128; Cyt\_P450.  
DR Pfam; PF00067; p450; 1.  
DR PRINTS; PR00385; P450  
DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
KW Oxidoreductase; Monooxygenase; Membrane; Heme.  
FT NON\_TER 1 1  
FT BINDING 480 480 HEME (BY SIMILARITY).  
SQ SEQUENCE 544 AA; 62055 MW; DE006067C33DADE5 CRC64;  
  
Query Match 70.6%; Score 36; DB 1; Length 544;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 SGSWPL 8  
Db 39 SGSWPL 44  
|||||  
RESULT 7  
ID PSP\_MOUSE STANDARD; PRT; 235 AA.  
AC P07743;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Parotid secretory protein precursor (PSP).  
GN PSP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Parotid gland;  
RX MEDLINE=85215456; PubMed=2582349;  
RA Madsen H.O., Hjorth J.P.;  
RT "Molecular cloning of mouse PSP mRNA.";  
RL Nucleic Acids Res. 13:1-13(1985).  
RN [2]  
RN SEQUENCE OF 1-87 FROM N.A.  
RC STRAIN=C3H; TISSUE=Spleen;  
RX MEDLINE=87004556; PubMed=2428613;  
RA Poulsen K., Jakobsen B.K., Mikkelson B.M., Harnmark K.,  
RA Nielsen J.T., Hjorth J.P.;  
RT "Coordination of murine parotid secretory protein and salivary

RT amylose expression."  
 RL EMBO J. 5:1891-1896(1986).  
 CC -1- FUNCTION: PSP IS THE MOST ABUNDANT PROTEIN IN THE PAROTID GLAND.  
 CC ITS FUNCTION IS NOT KNOWN; HOWEVER, ITS PRODUCTION IS COORDINATED  
 CC WITH THAT OF SALIVARY AMYLASE.  
 CC -----  
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 CC -----  
 DR EMBL; X01697; CAA25846.1; -.  
 DR EMBL; M26807; AAA40009.1; -.  
 DR EMBL; M26806; AAA40009.1; JOINED.  
 DR PIR; A23031; SOMS.  
 DR MGD; MGI:97787; Psp.  
 KW Parotid gland; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 235  
 SQ SEQUENCE 235 AA; 24753 MW; 23311BAE15E2EF3 CRC64;  
 -----  
 Query Match 68.6%; Score 35; DB 1; Length 235;  
 Best Local Similarity 75.0%; Pred. No. 26;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 -----  
 QY 1 QQSGSWPL 8  
 DB 54 QQATSWPL 61  
 -----  
 RESULT 8  
 VMSA\_HPBDC STANDARD; PRT; 365 AA.  
 AC P30029;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Major surface antigen precursor.  
 GN S.  
 OS Duck hepatitis B virus (strain China) (DHBV).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.  
 OX NCBI\_TaxID=31510;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91045091; PubMed=2235506;  
 RA Tong S., Mattes F., Teubner K., Blum H.E.;  
 RT "Complete nucleotide sequence of a Chinese duck hepatitis B virus."  
 RL Nucleic Acids Res. 18:6139-6139(1990).  
 CC -----  
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 CC -----  
 DR EMBL; M21953; AAA45746.1; -.  
 DR PIR; S12842; SAVLWE.  
 DR InterPro; IPR000349; Hepadnavir\_surfac.  
 DR Pfam; PF00695; VMSA; 2.  
 KW Antigen.  
 FT PROPEP 1 198  
 FT CHAIN 199 365  
 FT CARBOHYD 297 297  
 SQ SEQUENCE 365 AA; 40511 MW; 67F3A4174CB7D884 CRC64;  
 -----  
 Query Match 68.6%; Score 35; DB 1; Length 365;

Best Local Similarity 71.4%; Pred. No. 40;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 -----  
 QY 1 QQSGSWP 7  
 DB 96 QQQGAWP 102  
 -----  
 RESULT 9  
 VMSA\_HPBDC STANDARD; PRT; 366 AA.  
 AC P17194;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Major surface antigen precursor.  
 GN S.  
 OS Duck hepatitis B virus (brown Shanghai duck isolate S5) (DHBV).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.  
 OX NCBI\_TaxID=10439;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90085807; PubMed=2596031;  
 RA Uchida M., Esumi M., Shikata T.;  
 RT "Molecular cloning and sequence analysis of duck hepatitis B virus  
 RL genomes of a new variant isolated from Shanghai ducks."  
 RL Virology 173:600-606(1989).  
 CC -----  
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 CC -----  
 DR EMBL; M32990; AAA45755.1; ALT\_INIT.  
 DR PIR; C33746; SAVLBD.  
 DR InterPro; IPR000349; Hepadnavir\_surfac.  
 DR Pfam; PF00695; VMSA; 2.  
 KW Antigen.  
 FT PROPEP 1 199  
 FT CHAIN 200 366  
 FT CARBOHYD 170 170  
 FT CARBOHYD 298 298  
 SQ SEQUENCE 366 AA; 40897 MW; 5B72879A182EFF38 CRC64;  
 -----  
 Query Match 68.6%; Score 35; DB 1; Length 366;  
 Best Local Similarity 71.4%; Pred. No. 40;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 -----  
 QY 1 QQSGSWP 7  
 DB 96 QQQGAWP 102  
 -----  
 RESULT 10  
 VMSA\_HPBDC STANDARD; PRT; 366 AA.  
 AC P17195;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Major surface antigen precursor.  
 GN S.  
 OS Duck hepatitis B virus (white Shanghai duck isolate S31) (DHBV).  
 OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.  
 OX NCBI\_TaxID=10440;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90085807; PubMed=2596031;  
 RA Uchida M., Esumi M., Shikata T.;

RT "Molecular cloning and sequence analysis of duck hepatitis B virus  
 RL genomes of a new variant isolated from Shanghai ducks.";  
 CC Virology 173:600-606(1989).  
 CC -----  
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 CC -----  
 DR EMBL; M22991; AAA45752.1; ALT\_INIT.  
 DR PIR; D33746; SAVLWD.  
 DR InterPro; IPR000349; Hepadnavir\_surfac.  
 DR Pfam; PF00695; VMSA; 2.  
 KW Antigen.  
 FT PROPEP 1 199  
 FT CHAIN 200 366 MAJOR SURFACE ANTIGEN.  
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 366 AA; 40858 MW; CF60E78B7B2FCD52 CRC64;  
 CC -----  
 Query Match 68.6%; Score 35; DB 1; Length 366;  
 Best Local Similarity 71.4%; Pred. No. 40;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QQSGSWP 7  
 II I I I I  
 Db 96 QQQGAWP 102  
 CC -----  
 RESULT 11  
 GUN1\_BACSU STANDARD; PRT; 499 AA.  
 ID GUN1\_BACSU  
 AC P07983;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)  
 DE (Cellulase).  
 GN BGLC OR GLB.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 CC Bacillus/Staphylococcus group; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=DLG;  
 RX MEDLINE=87194581; PubMed=3106328;  
 RA Robson L.M.; Chambliss G.H.;  
 RT "Endo-beta-1,4-glucanase gene of Bacillus subtilis DLG.";  
 RL J. Bacteriol. 169:2017-2025(1987).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic  
 CC linkages in cellulose.  
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL  
 CC HYDROLASES).  
 CC -----  
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 CC -----  
 DR EMBL; M16185; AAA22496.1; ALT\_INIT.  
 DR PIR; A26874; A26874.  
 DR HSP; O85465; 1A3H.  
 DR InterPro; IPR001956; CBD\_3.  
 DR InterPro; IPR001547; Glyco\_hydro\_F5.  
 DR Pfam; PF00942; CBD\_3; 1.

DR Pfam; PF00150; cellulase; 1.  
 DR ProDom; PD001947; CBD\_3; 1.  
 DR PROSITE; PS00659; GLYCOSYL\_HYDROL\_F5; 1.  
 KW Cellulose degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 499 ENDOGLUCANASE.  
 FT ACT\_SITE 169 169 PROTON DONOR (BY SIMILARITY).  
 FT ACT\_SITE 257 257 NUCLEOPHILE (BY SIMILARITY).  
 FT DOMAIN 350 499 CELLULOSE-BINDING (BY SIMILARITY).  
 SQ SEQUENCE 499 AA; 55187 MW; 339D04EE95A63EE1 CRC64;  
 CC -----  
 Query Match 68.6%; Score 35; DB 1; Length 499;  
 Best Local Similarity 62.5%; Pred. No. 54;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 QSGSWPLT 9  
 : : I I I I  
 Db 309 KTGGMPLT 316  
 CC -----  
 RESULT 12  
 SYV\_CHLMU STANDARD; PRT; 939 AA.  
 ID SYV\_CHLMU  
 AC Q9PK91;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Valyl-trna synthetase (EC 6.1.1.9) (Valine--trna ligase) (ValRS).  
 GN VALS OR TC0576.  
 OS Chlamydia muridarum.  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=83560;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MOPN / NIGG;  
 RX MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.;  
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
 RT pneumoniae AR39.";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-valine + trna(Val) = AMP + diphosphate  
 CC + L-valyl-trna(Val).  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AE002326; AAF39411.1; -.  
 DR HSP; P96142; IGAX.  
 DR TIGR; TC0576; -.  
 DR InterPro; IPR002300; trna-synt\_la.  
 DR InterPro; IPR001412; trna-synt\_i.  
 DR InterPro; IPR002303; trna-synt\_val.  
 DR Pfam; PF00133; trna-synt\_1; 1.  
 DR PRINTS; PR00986; TRNASYNTHVAL.  
 DR PROSITE; PS00178; AA\_TRNA\_LIGASE\_I; 1.  
 KW Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Complete proteome.  
 FT SITE 47 57 "HIGH" REGION.  
 FT SITE 564 568 "KMSKS" REGION.  
 FT BINDING 567 567 ATP (BY SIMILARITY).



SQ SEQUENCE 939 AA; 107121 MW; 1D141FA682187869 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 939;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SCSWPLT 9  
II IIII  
DB 460 SGLWPLT 466

## RESULT 13

```

SYV_CHLTR
ID SYV_CHLTR STANDARD; PRT; 939 AA.
AC OB4304;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VALRS).
GN VALS OR CT302.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/CX;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -|- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC + L-valyl-tRNA(Val).
CC -|- SUBUNIT: MONOMER (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AE001302; AAC67895.1; -.
DR HSSP; P96142; IGAX.
DR InterPro; IPR002300; tRNA-synt_la.
DR InterPro; IPR001412; tRNA-synt_I.
DR InterPro; IPR002303; tRNA-synt_val.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00986; TRNASYNTHVAL.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 47 57 "HIGH" REGION.
FT SITE 563 566 "KMSKS" REGION.
FT BINDING 566 ATP (BY SIMILARITY).
SQ SEQUENCE 939 AA; 107036 MW; CEB8449DC7BB9066 CRC64;

```

Query Match 68.6%; Score 35; DB 1; Length 939;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SCSWPLT 9  
II IIII  
DB 459 SGLWPLT 465

## RESULT 14

```

SYV_CHLPN
ID SYV_CHLPN STANDARD; PRT; 940 AA.
AC Q92987; Q9JQA5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VALRS).
GN VALS OR CPN0094 OR CP0680.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinm M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -|- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC + L-valyl-tRNA(Val).
CC -|- SUBUNIT: MONOMER (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AE001595; AAD18247.1; -.
DR EMBL; AE002226; AAF38490.1; -.
DR EMBL; AP002545; BAA98304.1; -.
DR HSSP; P96142; IGAX.
DR TIGR; CP0680; -.
DR InterPro; IPR002300; tRNA-synt_la.
DR InterPro; IPR001412; tRNA-synt_I.
DR InterPro; IPR002303; tRNA-synt_val.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00986; TRNASYNTHVAL.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 47 57 "HIGH" REGION.
FT SITE 564 568 "KMSKS" REGION.
FT BINDING 567 567 ATP (BY SIMILARITY).
SQ SEQUENCE 940 AA; 107111 MW; 28054683FB9D0404 CRC64;

```

Query Match 68.6%; Score 35; DB 1; Length 940;  
 Best Local Similarity 85.7%; Pred. NO. 1e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSGSWPLT 9  
 Db 460 SGLWPLT 466

```

RESULT 15
CATC_RHOOP STANDARD; PRT; 92 AA.
AC P95609;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Muconolactone delta-isomerase (EC 5.3.3.4) (Miae).
GN CATC.
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=37919;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=ICP;
RX MEDLINE=97144521; PubMed=8990288;
RA Eulberg D., Golovleva L.A., Schloemann M.;
RT "Characterization of catechol catabolic genes from Rhodococcus
RT erythropolis ICP";
RL J. Bacteriol. 179:370-381(1997).
CC -I- CATALYTIC ACTIVITY: 2,5-dihydro-5-oxofuran-2-acetate = 3,4-
CC dihydro-5-oxofuran-2-acetate.
CC -I- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-
CC AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
CC -I- SUBUNIT: HOMODECAMER (BY SIMILARITY).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X99622; CAA67935.1; -
DR InterPro; IPR003464; Miae.
DR Pfam; PF02426; Miae; 1.
KW Aromatic hydrocarbons catabolism; Isomerase.
FT INIT_MET 0
SQ SEQUENCE 92 AA; 10780 MW; 9CCE5A17DED4B153 CRC64;

```

Query Match 66.7%; Score 34; DB 1; Length 92;  
 Best Local Similarity 71.4%; Pred. NO. 16;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7  
 Db 35 QRSWKWP 41

Search completed: August 19, 2002, 06:59:07  
 Job time: 1372 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:08 ; Search time 140.4 seconds  
(without alignments)  
11.089 Million cell updates/sec

Title: US-09-339-922A-90

Perfect score: 51

Sequence: 1 QOSGSWPLT 9

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	80.4	153	Q9YH52	Q9YH52 gallus gall
2	40	78.4	706	Q9D4H8	Q9D4H8 mus musculus
3	40	78.4	1194	Q9VSI2	Q9VSI2 drosophila
4	39	76.5	553	Q01825	Q01825 caenorhabdi
5	39	76.5	793	Q01443	Q01443 caenorhabdi
6	37	72.5	154	Q84631	Q84631 paramecium
7	37	72.5	612	Q041S9	Q041S9 oryza sativ
8	37	72.5	642	Q28537	Q28537 archaeoglob
9	37	72.5	677	Q97DD2	Q97DD2 clostridium
10	37	72.5	737	Q9U9P1	Q9U9P1 drosophila
11	37	72.5	764	Q01LZ75	Q01LZ75 arabidopsis
12	37	72.5	781	Q9VRA2	Q9VRA2 drosophila
13	37	72.5	1346	Q98IR5	Q98IR5 rhizobium 1
14	36	70.6	204	Q95X90	Q95X90 caenorhabdi
15	36	70.6	275	Q50711	Q50711 mycobacteri
16	36	70.6	396	Q9RDF1	Q9RDF1 streptomyce

Q9fvk6 pisum sativ  
Q9vhu1 drosophila  
Q9sgw2 arabidopsis  
Q9iou2 pseudomonas  
Q9u5d6 plautia sta  
Q9pl14 chlamydia m  
Q9ukb9 homo sapien  
Q9d734 mus musculu  
Q9kpi7 vibrio chol  
Q97852 duck hepati  
Q91hp5 duck hepati  
Q97885 duck hepati  
Q66405 duck hepati  
Q66404 duck hepati  
Q9r904 brachyspira  
Q9r905 brachyspira  
Q9r908 treponema h  
Q9zhj1 brachyspira  
Q9r902 brachyspira  
Q9zhj3 brachyspira  
Q9zh16 brachyspira  
Q9r907 treponema h  
Q9zh17 serpulina s  
Q9r906 brachyspira  
Q9zh18 brachyspira  
Q9r903 brachyspira  
Q9zhj2 brachyspira  
Q9zhj0 brachyspira  
Q9zh19 brachyspira

36 70.6 540 10 Q9FVK6  
36 70.6 613 5 Q9VHU1  
36 70.6 847 10 Q9SGW2  
36 70.6 1221 15 Q9IOU2  
36 70.6 1903 5 Q9U5D6  
36 70.6 100 16 Q9PLT4  
35 68.6 123 4 Q9UKB9  
35 68.6 235 11 Q9D734  
35 68.6 317 15 Q9KPI7  
35 68.6 327 12 Q67852  
35 68.6 329 12 Q91HP5  
35 68.6 330 12 Q72885  
35 68.6 330 12 Q66405  
35 68.6 366 12 Q66404  
35 68.6 407 2 Q9R904  
35 68.6 413 2 Q9R905  
35 68.6 415 2 Q9R908  
35 68.6 415 2 Q9ZHJ1  
35 68.6 415 2 Q9R902  
35 68.6 416 2 Q9ZHJ3  
35 68.6 418 2 Q9ZH16  
35 68.6 420 2 Q9R907  
35 68.6 420 2 Q9ZH17  
35 68.6 421 2 Q9R906  
35 68.6 421 2 Q9ZH18  
35 68.6 422 2 Q9R903  
35 68.6 423 2 Q9ZHJ2  
35 68.6 423 2 Q9ZHJ0  
35 68.6 424 2 Q9ZH19

#### ALIGNMENTS

RESULT 1

Q9YH52 PRELIMINARY; PRT; 153 AA.

AC Q9YH52;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
DE HYPOTHETICAL 17.4 KDA PROTEIN.

OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;

RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-H.B19;

RX MEDLINE=90077532; PubMed=2592020;

RA Kaufman J., Salomonsen J., Skjold K.;

RT "B-C DNA clones have multiple small repeats and hybridize to both

RL chicken MHC regions.";

RL Immunogenetics 30:440-451(1989).

DR EMBL; M27666; AAA69840.1; -

KW Hypothetical protein.

SQ SEQUENCE 153 AA; 17404 MW; 6D344F572FA7EE48 CRC64;

Query Match 80.4%; Score 41; DB 13; Length 153;  
Best Local Similarity 87.5%; Pred. No. 6.8;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QOSGSWPLT 9

Db 65 QSGHWPLT 72

RESULT 2

Q9D4H8 PRELIMINARY; PRT; 706 AA.

ID Q9D4H8

AC Q9D4H8;

DT 01-JUN-2001 (TremBLrel. 17, Created)  
 DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)  
 DE 4932411N15RIK PROTEIN.  
 GN 4932411N15RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gijobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,  
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Yawshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK016520; BAB30283.1; -;  
 DR MGD; MGI:1922970; 4932411N15RIK.  
 DR InterPro; IPR001373; Cullin.  
 DR Pfam; PF00888; Cullin; 2.  
 DR SMART; SM00182; CULLIN; 1.  
 DR PROSITE; PS01256; CULLIN; 1; 1.  
 DR PROSITE; PS50069; CULLIN; 2; 1.  
 SQ SEQUENCE 706 AA; 82298 MW; CBB796B20CA6E2B4 CRC64;

Query Match 78.4%; Score 40; DB 11; Length 706;  
 Best Local Similarity 75.0%; Pred. No. 48;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 QSGSWPLT 9  
 Db 513 QAGAWPLT 520  
 ||:||||  
 RESULT 3  
 Q9VSI2 PRELIMINARY; PRT; 1194 AA.  
 ID Q9VSI2;  
 AC Q9VSI2;  
 DT 01-MAY-2000 (TremBLrel. 13, Created)  
 DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)  
 DE CG7112 PROTEIN.  
 GN CG7112.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=107311132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Efankoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003555; AAF50437.1; -;  
 DR FlyBase; FBgn0035879; CG7112.  
 DR InterPro; IPR000050; PID\_domain.  
 DR InterPro; IPR000195; RabGAP\_TBC.  
 DR Pfam; PF00566; TBC; 1.  
 DR SMART; SM00462; PTB; 1.  
 DR SMART; SM00164; TBC; 1.  
 SQ SEQUENCE 1194 AA; 133393 MW; E0E3DB547B4924E0 CRC64;

Query Match 78.4%; Score 40; DB 5; Length 1194;  
 Best Local Similarity 77.8%; Pred. No. 81;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 QSGSWPLT 9  
 Db 461 QQSSSWPYT 469  
 ||| ||| |  
 RESULT 4  
 O01825  
 ID O01825 PRELIMINARY; PRT; 553 AA.  
 AC O01825;  
 DT 01-JUL-1997 (TremBLrel. 04, Created)  
 DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)  
 DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL 60.8 KDA PROTEIN.  
 GN F57C9.8.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for

RT Investigating biology. The C. elegans Sequencing Consortium. ";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RT "Direct Submission. ";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF003142; AAB54191.1; -;  
 DR HSSP; P27986; IPBW.  
 DR InterPro; IPR000198; RhoGAP.  
 DR Pfam; PF00620; RhoGAP; 1.  
 DR SMART; SM00324; RhoGAP; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 553 AA; 60849 MW; A50EDF9C2F560139 CRC64;

Query Match 76.5%; Score 39; DB 5; Length 553;  
 Best Local Similarity 66.7%; Pred. No. 56;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QSGSWPLT 9  
 I:|||||  
 Db 373 QSGSWPFS 381  
 RESULT 5  
 ID O01443 PRELIMINARY; PRT; 793 AA.  
 AC O01443;  
 DT 01-JUL-1997 (TReMBLrel. 04, Created)  
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL 87.6 KDA PROTEIN.  
 GN C01F4.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 investigating biology. The C. elegans Sequencing Consortium. ";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Wamsley P., Geisel C.;  
 RT "The sequence of C. elegans cosmid C01F4. ";  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RT "Direct Submission. ";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U97192; AAB52435.2; -;  
 DR InterPro; IPR000198; RhoGAP.  
 DR Pfam; PF00620; RhoGAP; 1.  
 DR SMART; SM00324; RhoGAP; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 793 AA; 87620 MW; 9BF89AEA54DAEA04 CRC64;

Query Match 76.5%; Score 39; DB 5; Length 793;  
 Best Local Similarity 66.7%; Pred. No. 80;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QSGSWPLT 9  
 I:|||||  
 Db 613 QSGSWPFS 621

RESULT 6  
 ID Q84631 PRELIMINARY; PRT; 154 AA.  
 AC Q84631;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE A317L PROTEIN.  
 DE A317L.  
 OS Paramacium bursaria chlorella virus 1 (PBCV-1).  
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.  
 OC NCBI\_TaxID=10506;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96187795; PubMed=8614977;  
 RA Lu Z., Li Y., Que O., Kutish G.F., Rock D.L., Van Etten J.L.;  
 RT "Analysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map  
 positions 88 to 182. ";  
 RL Virology 216:102-123(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20013326; PubMed=10544099;  
 RA Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,  
 RA Lisec A.D., Nickerson K.W., Van Etten J.L.;  
 RT "Chlorella virus PBCV-1 encodes a functional homosperridine  
 RT synthase. ";  
 RL Virology 263:254-262(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20478054; PubMed=11021991;  
 RA Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;  
 RT "Characterization of a beta-1,3-glucanase encoded by chlorella virus  
 PBCV-1. ";  
 RL Virology 276:27-36(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Van Etten J.L.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Van Etten J.L.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Van Etten J.L.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Graves M.V., Van Etten J.L.;  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RA Graves M.V., Van Etten J.L.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RA Gurnon J.R., Graves M.V., Van Etten J.L.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U42580; AAC9685.1; -;  
 SQ SEQUENCE 154 AA; 18564 MW; 7B45EE2E7F518E15 CRC64;

Query Match 72.5%; Score 37; DB 12; Length 154;  
 Best Local Similarity 75.0%; Pred. No. 35;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPL 8  
| | | | |  
DB 33 QTSQSWPV 40

RESULT 7  
Q941S9 PRELIMINARY; PRT; 612 AA.  
AC Q941S9;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE PUTATIVE HOMEODOMAIN PROTEIN.  
GN P0005H10.19.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPPONBARE;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
clone:P0005H10.";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP004127; BAB64282.1; -  
KW Homeobox; DNA-binding; Nuclear protein.  
SQ SEQUENCE 612 AA; 65175 MW; A5B7AA5281CD28E4 CRC64;

Query Match 72.5%; Score 37; DB 10; Length 612;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7  
| | | | |  
DB 93 QQHGSWP 99

RESULT 8  
O28537 PRELIMINARY; PRT; 642 AA.  
ID O28537  
AC O28537;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
DE CONSERVED HYPOTHETICAL PROTEIN.  
GN AFI737.  
OS Archaeoglobus fulgidus.  
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;  
OC Archaeoglobus.  
OX NCBI\_TaxID=2234;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
RX MEDLINE=98049343; PubMed=9389475;  
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,  
RA Fleischmann R.D., Dougherty B.J., Lee N.H., Sutton G.G., Gill S.,  
RA Kirkness E.F., Doughty K., McKenney K., Adams M.D., Loftus B.,  
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,  
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
RA Venter J.C.;  
RT "The complete genome sequence of the hyperthermophilic, sulphate-  
reducing archaeon Archaeoglobus fulgidus.";  
RL Nature 390:364-370(1997).

DR EMBL; AE000983; AAB89512.1; -  
DR TIGR; AFI737; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 642 AA; 74057 MW; 3E80BA624D747B5 CRC64;

Query Match 72.5%; Score 37; DB 17; Length 642;  
Best Local Similarity 85.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSGSWPLT 9  
| | | | |  
DB 101 SSGWPLT 107

RESULT 9  
Q97DD2 PRELIMINARY; PRT; 677 AA.  
ID Q97DD2;  
AC Q97DD2;  
DT 01-OCT-2001 (TREMBlrel. 18, Created)  
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
DE HIGHLY CONSERVED PROTEIN CONTAINING A DOMAIN RELATED TO CELLULOSE  
DE CATALYTIC DOMAIN AND A THIOREDOXIN DOMAIN.  
GN CAC3346.  
OS Clostridium acetobutylicum.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1488;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
RX MEDLINE=21359325; PubMed=11466286;  
RA Neelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,  
RA Tatusov R.L., Sabache F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
RA Bennett G.N., Koonin E.V., Smith D.R.;  
RT "Genome sequence and comparative analysis of the solvent-producing  
bacterium Clostridium acetobutylicum.";  
RL J. Bacteriol. 183:4823-4838(2001).  
DR EMBL; AE007851; AAK81471.1; -  
KW Complete proteome.  
SQ SEQUENCE 677 AA; 78241 MW; F8ED0443466830F3 CRC64;

Query Match 72.5%; Score 37; DB 16; Length 677;  
Best Local Similarity 85.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SSGSWPLT 9  
| | | | |  
DB 108 SSGWPLT 114

RESULT 10  
Q9U9P1 PRELIMINARY; PRT; 737 AA.  
ID Q9U9P1  
AC Q9U9P1;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE MAROON-LIKE PROTEIN.  
GN MAL OR CG1692.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CANTON S;  
RA Primus J., Arcangeli L., Finnerty V.;  
RT "The maroon-like gene in Drosophila encodes a putative sulfatase.";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF162681; AAD50777.1; -;  
 DR FlyBase: FBgn0002641; mal  
 SQ SEQUENCE 737 AA; 83139 MW; 76DFEE077E3F06D4 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 737;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GSWPLT 9

Db 533 GSWPLT 538

RESULT 11

ID Q9LZ75 PRELIMINARY; PRT; 764 AA.

AC Q9LZ75;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE HYPOTHEtical 86.3 KDA PROTEIN.

GN T32M21.100.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Bevan M., Terry N., Ardiles W., Buysshaert C., Dasseville R.,

RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,

RA Villarroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,

RA Rudd S., Lemcke K., Mayer K.F.X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL162875; CAB85556.1; -;

KW Hypothetical protein.

SQ SEQUENCE 764 AA; 86299 MW; AFE0E482FF091CB8 CRC64;

Query Match 72.5%; Score 37; DB 10; Length 764;

Best Local Similarity 62.5%; Pred. No. 1.7e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSGSWPLT 9

Db 112 ESGAWPVT 119

RESULT 12

Q9VRA2

ID Q9VRA2 PRELIMINARY; PRT; 781 AA.

AC Q9VRA2;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE MAL PROTEIN.

GN MAL OR CG1692.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=BERKELEY;

RC MEDLINE=20196006; PubMed=10731132;

RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 Beson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 de Pablos B., Delcher A., Deng X., Mays A.D., Dew I., Dietz S.M.,  
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

DR EMBL: AE003571; AAF50901.1; -;

DR FlyBase: FBgn0002641; mal.

SQ SEQUENCE 781 AA; 88103 MW; D2B2D5F52FDDF712 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 781;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GSWPLT 9

Db 533 GSWPLT 538

RESULT 13

Q98IR5

ID Q98IR5 PRELIMINARY; PRT; 1346 AA.

AC Q98IR5;

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)

DE MLL2286

GN MLL2286.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI\_TaxID=381;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MAFF303099;

RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

RA Takeuchi C., Yamada M., Tabata S.;

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RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RL Mesorhizobium loti.",
DR EMBL; AP002999; BAB49451.1; -.
DR InterPro; IPR003975; Shal_channel.
DR PRINTS; PR01497; SHALCHANNEL.
KW Complete proteome.
SQ SEQUENCE 1346 AA; 148727 MW; 7D1288A3FC26E879 CRC64;

Query Match 72.5%; Score 37; DB 16; Length 1346;
Best Local Similarity 75.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSGSWPLT 9
I:|||||
Db 204 QTGSWPKT 211

RESULT 14
Q95X90 PRELIMINARY; PRT; 204 AA.
AC Q95X90;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE HYPOTHETICAL 22.8 KDA PROTEIN.
GN D2062.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_taxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Tin-Wollam A., Wohldmann P.;
RT "The sequence of C. elegans cosmid D2062.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston K.;
RT "Direct Submission.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016664; AAK72083.1; -.
KW Hypothetical protein.
SQ SEQUENCE 204 AA; 22758 MW; 27753F06500B35C8 CRC64;

Query Match 70.6%; Score 36; DB 5; Length 204;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSGSWPL 8
I|||I|
Db 107 QSGCWPL 113

RESULT 15
Q50711 PRELIMINARY; PRT; 275 AA.
AC Q50711;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

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DE HYPOTHETICAL 28.7 KDA PROTEIN CY78.14.
GN RV3415C OR MTCY78.14.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
RL Nature 393:537-544(1998).
CC -!- SIMILARITY: STRONG. TO M.LEPRAE B229_C1_175 AND B1620_C3_232.
DR EMBL; 277165; CAB01008.1; -.
DR Tuberculiist; RV3415c; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 275 AA; 28659 MW; 47634BCA57C3CB3E CRC64;

Query Match 70.6%; Score 36; DB 16; Length 275;
Best Local Similarity 85.7%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QSGSWPL 8
I|||||
Db 22 QPGSWPL 28

Search completed: August 19, 2002, 06:58:10
Job time: 1400 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:39:10 ; Search time 180.34 seconds

(without alignments)

5.543 Million cell updates/sec

Title: US-09-339-922A-90

Perfect score: 51

Sequence: 1 QQSGSWPLT 9

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Total number of hits satisfying chosen parameters: 747574

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	51	100.0	9	19	AAW76035
2	51	100.0	9	22	AA861393
3	45	88.2	9	14	AAK37604
4	45	88.2	9	19	AAW76036
5	45	88.2	9	22	AA861394
6	45	88.2	107	14	AAK37612
7	45	88.2	107	14	AAK37610
8	44	86.3	9	19	AAW76013
9	44	86.3	9	22	AA861371
10	44	86.3	107	19	AAW76006
11	44	86.3	107	19	AAW76002

12	44	86.3	107	19	AAW76004	LM609 antibody lig
13	44	86.3	107	22	AA861388	A light chain vari
14	44	86.3	107	22	AA861390	A light chain vari
15	44	86.3	107	22	AA861360	Vitaxin light chai
16	44	86.3	107	22	AA861362	Antibody LM609 lig
17	44	86.3	107	22	AA861364	Light chain variab
18	42	82.4	9	21	AA810015	H. pylori beta-ure
19	42	82.4	9	22	AA86063	H. pylori beta-ure
20	42	82.4	9	22	AA86095	H. pylori beta-ure
21	42	82.4	107	21	AA810023	H. pylori beta-ure
22	42	82.4	107	22	AA86071	H. pylori beta-ure
23	42	82.4	107	22	AA86109	H. pylori beta-ure
24	42	82.4	127	21	AA832405	Mouse anti-verotox
25	42	82.4	127	21	AA832407	Mouse anti-verotox
26	41	80.4	105	20	AA87456	JK gene product.
27	41	80.4	105	20	AA87458	Humanised anti-alp
28	41	80.4	107	20	AA84098	Humanised anti-alp
29	41	80.4	108	20	AA84094	Murine vitronectin
30	41	80.4	112	20	AA84100	Vitronectin alpha-
31	40	78.4	107	14	AA83601	HYH light chain.
32	40	78.4	107	19	AAW58482	Murine HYH antibod
33	40	78.4	108	12	AA815438	Light chain variab
34	40	78.4	109	15	AA852033	Light chain variab
35	40	78.4	143	18	AAW19580	Mouse anti-idiotyp
36	40	78.4	240	12	AA815443	Single chain Fv fr
37	40	78.4	1194	22	AA862985	Drosophila melanog
38	39	76.5	9	19	AAW41180	Monoclonal antibod
39	39	76.5	9	20	AA826992	CDR3 domain reshap
40	39	76.5	106	19	AAW71241	Light chain variab
41	39	76.5	107	15	AA850190	Light chain variab
42	39	76.5	107	18	AAW28531	Humanised cA2 ligh
43	39	76.5	107	19	AAW40820	Light chain variab
44	39	76.5	107	20	AAW26979	Light chain variab
45	39	76.5	107	20	AAW23243	Light chain variab

#### ALIGNMENTS

RESULT 1

AAW76035  
ID AAW76035 standard; Protein; 9 AA.

XX

AC AAW76035;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-L region CDR3 protein fragment #4.

XX

Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
LM609; inhibitor; integrin-mediated signal transduction; treatment;  
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
macular degeneration; osteoporosis; primer; V-L region; CDR;  
complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

XX

PD 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI; 1998-437472/37.

XX

DR N-PSDB; AAV49872.

XX

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
PT integrin - and related grafted antibodies based on murine monoclonal  
PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
PT angiogenesis or restenosis  
XX  
PS Claim 62; Page 44; 129pp; English.  
XX  
CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody  
CC LM609 heavy and light chain variable region. LM609 and the antibody  
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to  
CC inhibit binding of alphavbeta3 to a ligand and thus block  
CC integrin-mediated signal transduction. This is useful in the treatment,  
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically  
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
CC antibodies contain non-murine framework regions so are suitable for use  
CC in humans. Enhanced types of LM609 have affinity more than 90 times  
CC greater than that of parent the parent antibody.  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
|||||||  
Db 1 qqsgswplt 9

RESULT 2  
AAB61393  
ID AAB61393 standard; peptide; 9 AA.  
AC AAB61393;  
XX  
XX 03-APR-2001 (first entry)  
XX  
XX Mutant VL CDR3 peptide #3.  
XX  
XX LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis.  
XX  
XX Unidentified.  
XX  
XX WO200078815-A1.  
XX  
XX 28-DEC-2000.  
XX  
XX 23-JUN-2000; 2000WO-US17454.  
XX  
XX 24-JUN-1999; 99US-0339922.  
XX  
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX  
XX Huse WD, Wu H;  
XX  
XX WPI; 2001-050110/06.  
XX

Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis -  
XX  
XX Claim 4; Page 41; 132pp; English.  
XX  
XX The present invention relates to enhanced LM609 grafted antibodies  
CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
CC their functional fragments. The antibodies or their functional  
CC fragments can be used in the diagnosis and treatment of  
CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),  
CC disorders associated with inappropriate or inopportune invasion of  
CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
CC diseases (such as macular degeneration), restenosis and  
CC osteoporosis.  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
|||||||  
Db 1 qqsgswplt 9

RESULT 3  
AAR37604  
ID AAR37604 standard; peptide; 9 AA.  
XX  
AC AAR37604;  
XX  
XX 13-OCT-1993 (first entry)  
XX  
XX hIL2R Ab L chain V region CDR3.  
XX

Complementarity-determining region; CDR; humanised; antibody; hIL2R;  
KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;  
KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;  
KW region; PCR; framework; plasmid.  
XX  
XX Mus musculus.  
XX  
XX WO9311238-A.  
XX  
XX 10-JUN-1993.  
XX  
XX 03-DEC-1992; 92WO-JP01583.  
XX  
XX 06-DEC-1991; 91JP-0323319.  
XX

(BIOT ) BIOTEST PHARMA GMBH.  
PA (INNO-) INNOTHERAPIE LAB.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
XX  
XX Gomi H, Nakatani T, Noguchi H, Wijdenes J;  
XX  
XX WPI; 1993-197057/24.  
XX  
XX Humanised antibody comprising - CDR region of mouse MAB B-B10  
PT specific for IL-2 receptor useful for treating carcinoma  
PT expressing IL-2 receptor  
XX  
XX Claim 1; Page 43; 62pp; English.

The sequences given in AAR37599-604 represent the complementarity-  
determining regions (CDRs) of a humanised antibody (Ab) which binds  
specifically to human interleukin (IL)-2 receptor (hIL2R). These  
CDRs were derived from the murine anti-human IL-2 receptor monoclonal  
Ab (WAB) B-B10 (see also AAQ43242-43). This MAB is antagonistic to the  
binding of IL-2 to the IL-2 receptor on human T-cells. It also  
inhibits the human mixed lymphocyte reaction. The cDNA encoding the  
variable (V) region of the B-B10 Ab was cloned by PCR and sequenced  
CC (see also AAQ43226-32 and AAQ43233-36). A human Ab with high levels of  
CC amino acid sequence homology to the murine sequence was selected and  
CC the framework of this Ab was bound with the B-B10 V region CDR and a  
CC part of the framework to design several kinds of the humanised B-B10 V  
CC region (see also AAQ43244-45). The DNA sequence coding this humanised  
CC B-B10 was synthesised and a plasmid expressing humanised B-B10 was  
CC constructed.

XX SQ Sequence 9 AA;  
 Query Match 88.2%; Score 45; DB 14; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 6.4e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGSWPLT 9  
 Db 1 qsgswpqt 9  
 IIIIIII I  
 1 qsgswpqt 9

RESULT 5  
 AAB61394  
 ID AAB61394 standard; peptide; 9 AA.  
 XX AC AAB61394;  
 XX 03-APR-2001 (first entry)  
 DT Mutant VL CDR3 peptide #4.  
 DE LM609; grafted antibody; alphaVbeta<sub>3</sub> integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 XX OS Unidentified.  
 XX WO200078815-A1.  
 XX 28-DEC-2000.  
 XX 23-JUN-2000; 2000WO-US17454.  
 XX 24-JUN-1999; 99US-0339922.  
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX Huse WD, Wu H;  
 XX WPI; 2001-050110/06.  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta<sub>3</sub> integrin, useful in the diagnosis and treatment of  
 PT osteoporosis -  
 XX Disclosure; Page 41; 132pp; English.  
 XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX SQ Sequence 9 AA;  
 Query Match 88.2%; Score 45; DB 22; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 6.4e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGSWPLT 9  
 Db 1 qsgswpqt 9  
 IIIIIII I  
 1 qsgswpqt 9

RESULT 6  
 AAR37612  
 ID AAR37612 standard; Protein; 107 AA.  
 XX AC AAR37612;  
 XX 13-OCT-1993 (first entry)  
 DT

XX SQ Sequence 9 AA;  
 Query Match 88.2%; Score 45; DB 19; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 6.4e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGSWPLT 9  
 Db 1 qsgswpqt 9  
 IIIIIII I  
 1 qsgswpqt 9

RESULT 4  
 AAW76036  
 ID AAW76036 standard; Protein; 9 AA.  
 XX AC AAW76036;  
 XX 02-NOV-1998 (first entry)  
 DT LM609 grafted antibody V-L region CDR3 protein fragment #5.  
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;  
 KW complementarity determining region.  
 XX Mus sp.  
 XX WO9833919-A2.  
 XX 06-AUG-1998.  
 XX 30-JAN-1998; 98WO-US01826.  
 XX 30-JAN-1997; 97US-0791391.  
 XX (IXSY-) IXSYS INC.  
 XX Glaser SM, Huse WD;  
 XX WPI; 1998-437472/37.  
 XX N-PSDB; AAV49873.  
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta<sub>3</sub>  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX Claim 62; Page 44; 129pp; English.  
 XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody  
 CC LM609 heavy and light chain variable region. LM609 and the antibody  
 CC vitaxin bind selectively to integrin alphaVbeta<sub>3</sub> and can be used to  
 CC inhibit binding of alphaVbeta<sub>3</sub> to a ligand and thus block  
 CC integrin-mediated signal transduction. This is useful in the treatment,  
 CC prevention and diagnosis of alphaVbeta<sub>3</sub>-mediated disease, specifically  
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
 CC antibodies contain non-murine framework regions so are suitable for use  
 CC in humans. Enhanced types of LM609 have affinity more than 90 times  
 CC greater than that of parent the parent antibody.  
 XX SQ Sequence 9 AA;

XX DE hIL2R Ab L chain V region.  
 XX KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;  
 XX KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;  
 KW KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;  
 KW KW region; PCR; framework; plasmid; heavy; H; light; L.  
 XX OS Mus musculus/Homo sapiens.  
 XX XX WO9311238-A.  
 XX PN 10-JUN-1993.  
 XX PD 03-DEC-1992; 92WO-JP01583.  
 XX PF 06-DEC-1991; 91JP-0323319.  
 XX PR (BIOT) BIOTEST PHARMA GMBH.  
 XX PA (INNO-) INNOTHERAPIE LAB.  
 XX PA (SUMU) SUMITOMO PHARM CO LTD.  
 XX PI Gomi H, Nakatani T, Noguchi H, Wijdenes J;  
 XX WPI: 1993-197057/24.  
 XX DR N-PSDB; AAQ43245.  
 XX XX Humanised antibody comprising - CDR region of mouse MAB B-B10  
 PT specific for IL-2 receptor useful for treating carcinoma  
 PT expressing IL-2 receptor  
 XX Claim 2: Fig 5: 62pp; English.  
 XX The sequences given in AAR37611-12 represent the heavy (H) and light (L)  
 CC chain variable (V) regions of a humanised antibody (Ab) which binds  
 CC specifically to human interleukin (IL)-2 receptor (hIL2R). The  
 CC complementarity-determining regions (CDRs) of these V regions were  
 CC derived from the murine anti-human IL-2 receptor monoclonal Ab (MAB)  
 CC B-B10 (see also AAR37599-04). This MAB is antagonistic to the binding  
 CC of IL-2 to the IL-2 receptor on human T-cells. It also inhibits  
 CC the human mixed lymphocyte reaction. The cDNA encoding the variable  
 CC (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also  
 CC AAQ3226-32 and AAQ43233-36). A human Ab with high levels of amino acid  
 CC sequence homology to the murine sequence was selected and the  
 CC framework of this Ab was bound with the B-B10 V region CDR and a  
 CC part of the framework to design several kinds of the humanised B-B10  
 CC V region. The DNA sequence coding this humanised B-B10 was  
 CC synthesised and a plasmid expressing humanised B-B10 was constructed.  
 XX SQ Sequence 107 AA;

Query Match 88.2%; Score 45; DB 14; Length 107;  
 Best Local Similarity 88.9%; Pred. No. 1.1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9  
 ||| |||||  
 Db 89 qqssswpl 97

RESULT 7  
 AAR37610  
 ID AAR37610 standard; Protein; 107 AA.  
 XX AAR37610;  
 AC AAR37610;  
 XX 13-OCT-1993 (first entry)  
 DT B-B10 MAB L chain V region.  
 XX KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;  
 KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;

KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;  
 KW region; PCR; framework; plasmid; heavy; H; light; L.  
 XX Mus musculus.  
 OS WO9311238-A.  
 PN 10-JUN-1993.  
 PD 03-DEC-1992; 92WO-JP01583.  
 XX PF 06-DEC-1991; 91JP-0323319.  
 XX PR (BIOT) BIOTEST PHARMA GMBH.  
 XX PA (INNO-) INNOTHERAPIE LAB.  
 XX PA (SUMU) SUMITOMO PHARM CO LTD.  
 XX PI Gomi H, Nakatani T, Noguchi H, Wijdenes J;  
 XX WPI: 1993-197057/24.  
 XX DR N-PSDB; AAQ43243.  
 XX XX Humanised antibody comprising - CDR region of mouse MAB B-B10  
 PT specific for IL-2 receptor useful for treating carcinoma  
 PT expressing IL-2 receptor  
 XX Disclosure: Fig 2: 62pp; English.  
 XX The sequences given in AAR37609-10 represent the heavy (H) and light (L)  
 CC chain variable (V) regions of the murine anti-human IL-2 receptor  
 CC monoclonal antibody (MAB) B-B10, respectively. This MAB was used in  
 CC the construction of a humanised antibody (Ab) which binds specifically  
 CC to human interleukin (IL)-2 receptor (hIL2R). The complementarity-  
 CC determining regions (CDRs) for the hIL2R MAB were derived from B-B10  
 CC (see also AAR37599-04). The hIL2R MAB is antagonistic to the binding  
 CC of IL-2 to the IL-2 receptor on human T-cells. It also inhibits  
 CC the human mixed lymphocyte reaction. The cDNA encoding the variable  
 CC (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also  
 CC AAQ43226-32 and AAQ43233-36). A human Ab with high levels of amino acid  
 CC sequence homology to the murine sequence was selected and the  
 CC framework of this Ab was bound with the B-B10 V region CDR and a  
 CC part of the framework to design several kinds of the humanised B-B10  
 CC V region. The DNA sequence coding this humanised B-B10 was  
 CC synthesised and a plasmid expressing humanised B-B10 was constructed.  
 XX SQ Sequence 107 AA;

Query Match 88.2%; Score 45; DB 14; Length 107;  
 Best Local Similarity 88.9%; Pred. No. 1.1;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9  
 ||| |||||  
 Db 89 qqssswpl 97

RESULT 8  
 AAR76013  
 ID AAR76013 standard; Protein; 9 AA.  
 XX AAR76013;  
 AC AAR76013;  
 XX 02-NOV-1998 (first entry)  
 DT LM609 grafted antibody V-L region CDR3 protein fragment #1.  
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;  
 KW complementarity determining region.

XX OS Mus sp.  
 XX PN WO9833919-A2.  
 XX PD 06-AUG-1998.  
 XX PF 30-JAN-1998; 98WO-US01826.  
 XX PR 30-JAN-1997; 97US-0791391.  
 XX PA (IXSY-) IXSYS INC.  
 XX PI Glaser SM, Huse WD;  
 XX WPI: 1998-437472/37.  
 DR N-PSDB; AAV49850.  
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX Disclosure: Page 40; 129pp; English.  
 XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody  
 CC LM609 heavy and light chain variable region. LM609 and the antibody  
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to  
 CC inhibit binding of alphavbeta3 to a ligand and thus block  
 CC integration-mediated signal transduction. This is useful in the treatment,  
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically  
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
 CC antibodies contain non-murine framework regions so are suitable for use  
 CC in humans. Enhanced types of LM609 have affinity more than 90 times  
 CC greater than that of parent the parent antibody.  
 XX Sequence 9 AA;  
 SQ

Query Match 86.3%; Score 44; DB 19; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 6.4e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
 Db 1 qqsgswpht 9  
 ||||| |

RESULT 9  
 AAB61371  
 ID AAB61371 standard; peptide; 9 AA.  
 AC AAB61371;  
 XX 03-APR-2001 (first entry)  
 DT LM609 VL CDR3 peptide.  
 DE LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 KW Unidentified.  
 XX WO200078815-A1.  
 XX 28-DEC-2000.  
 PN 23-JUN-2000; 2000WO-US17454.  
 PD 24-JUN-1999; 99US-0339922.  
 XX

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX Huse WD, Wu H;  
 XX WPI: 2001-050110/06.  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX Disclosure: Page 39; 132pp; English.  
 XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC alphaBeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX Sequence 9 AA;  
 SQ

Query Match 86.3%; Score 44; DB 22; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 6.4e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
 Db 1 qqsgswpht 9  
 ||||| |

RESULT 10  
 AAW76006  
 ID AAW76006 standard; Protein; 107 AA.  
 XX AAW76006;  
 AC 02-NOV-1998 (first entry)  
 DT LM609 grafted antibody light chain variable region protein fragment.  
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis.  
 XX Mus sp.  
 XX Key Location/Qualifiers  
 FT Misc-difference 49  
 FT /label= Arg, Met  
 XX WO9833919-A2.  
 XX 06-AUG-1998.  
 XX 30-JAN-1998; 98WO-US01826.  
 XX 30-JAN-1997; 97US-0791391.  
 XX (IXSY-) IXSYS INC.  
 XX Glaser SM, Huse WD;  
 XX WPI: 1998-437472/37.  
 DR N-PSDB; AAV49843.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3  
PT integrin - and related grafted antibodies based on murine monoclonal  
PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
PT angiogenesis or restenosis  
XX  
XX Claim 19; Fig 7; 129pp; English.  
XX  
CC This sequence represents a LM609 grafted antibody variable light chain  
CC region. LM609 and the antibody vitaxin bind selectively to integrin  
CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand  
CC and thus block integrin-mediated signal transduction. This is useful in  
CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
CC etc.). The antibodies contain non-murine framework regions so are  
CC suitable for use in humans. Enhanced types of LM609 have affinity more  
CC than 90 times greater than that of parent the parent antibody.  
XX  
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;  
Best Local Similarity 88.9%; Pred. No. 1.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9  
|||||||  
DB 89 qsgsgswpht 97

## RESULT 11

AAW76002  
ID AAW76002 standard; Protein; 107 AA.

AC AAW76002;

DT 02-NOV-1998 (first entry)

DE Vitaxin antibody light chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis.

XX Mus sp.

PN WO9833919-A2.

XX 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAW49821.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3  
PT integrin - and related grafted antibodies based on murine monoclonal  
PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
PT angiogenesis or restenosis  
XX  
XX Claim 1; Fig 1b; 129pp; English.

PS This sequence represents the vitaxin antibody variable light chain  
XX  
CC This sequence represents the vitaxin antibody variable light chain

CC region. Vitaxin and the antibody LM609 bind selectively to integrin  
CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a  
CC ligand and thus block integrin-mediated signal transduction. This is  
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated  
CC disease, specifically angiogenesis and restenosis (but also e.g.  
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,  
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,  
CC osteoporosis etc.). The antibodies contain non-murine framework regions  
CC so are suitable for use in humans. Enhanced types of LM609 have affinity  
CC more than 90 times greater than that of parent the parent antibody.  
XX  
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;  
Best Local Similarity 88.9%; Pred. No. 1.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9  
|||||||  
DB 89 qsgsgswpht 97

## RESULT 12

AAW76004  
ID AAW76004 standard; Protein; 107 AA.

AC AAW76004;

DT 02-NOV-1998 (first entry)

DE LM609 antibody light chain variable region protein fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis.

XX Mus sp.

PN WO9833919-A2.

XX 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01826.

PR 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAW76004.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3  
PT integrin - and related grafted antibodies based on murine monoclonal  
PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
PT angiogenesis or restenosis  
XX  
XX Claim 46; Fig 2b; 129pp; English.

PS This sequence represents the LM609 antibody variable light chain region.

XX LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3  
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
CC block integrin-mediated signal transduction. This is useful in the  
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
CC etc.). The antibodies contain non-murine framework regions so are  
CC suitable for use in humans. Enhanced types of LM609 have affinity more

CC than 90 times greater than that of parent the parent antibody.

XX  
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 19; Length 107;  
Best Local Similarity 88.9%; Pred. No. 1.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
| | | | | | | |  
Db 89 qsgsgswpht 97

#### RESULT 13

AAG63588  
ID AAG63588 standard; Protein: 107 AA.

XX AC AAG63588;

XX DT 15-OCT-2001 (first entry)

XX DE A light chain variable region of LM609 grafted antibody.

XX KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
XX KW Chronic articular rheumatism; psoriasis; diabetic retinopathy;  
XX KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
XX KW cancer.

XX OS Synthetic.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX FT Misc-difference 49

XX FT /note= "unspecified residue encoded by MKK"

XX PN US2001011125-A1.

XX PD 02-AUG-2001.

XX PF 30-JAN-1997; 97US-0790540.

XX PR 30-JAN-1997; 97US-0790540.

XX PA (HUSE/) HUSE W D.

XX PI Huse WD;

XX DR WPI; 2001-496171/54.

XX DR N-PSDB; AAH74624.

XX New LM609 grafted antibody exhibiting selective binding affinity to  
XX alphavbeta3, comprising at least one LM609 grafted heavy and light  
XX chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
XX disorders or cancer

XX PS Claim 1; Fig 1B; 25pp; English.

XX The present sequence represents the light chain variable region of the  
XX grafted monoclonal antibody LM609. LM609 is a murine antibody which  
XX specifically recognises the integrin alphavbeta3, and inhibits its  
XX functional activity. The LM609 grafted antibody has the  
XX complementary determining regions (CDRs) substituted into a non-murine  
XX framework. Nucleic acids encoding LM609 grafted heavy and light chain  
XX polypeptides and fragments are useful in diagnostic and therapeutic  
XX purposes, such as in the production of LM609 grafted antibodies and  
XX fragments having binding specificity and inhibitory activity against  
XX the integrin alphavbeta3. The antibody can be used for the diagnosis  
XX or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
XX disorders, chronic articular rheumatism, psoriasis, disorders  
XX as diabetic retinopathy, neovascular glaucoma and capillary  
XX proliferation in atherosclerotic plaques, or cancers), and to inhibit

CC binding activity of alphavbeta3 that are necessary for progression of  
CC an alphavbeta3-mediated disease.

XX  
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 22; Length 107;  
Best Local Similarity 88.9%; Pred. No. 1.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
| | | | | | | |  
Db 89 qsgsgswpht 97

#### RESULT 14

AAG63590  
ID AAG63590 standard; Protein: 107 AA.

XX AC AAG63590;

XX DT 15-OCT-2001 (first entry)

XX DE A light chain variable region of LM609 antibody.

XX KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
XX KW Chronic articular rheumatism; psoriasis; diabetic retinopathy;  
XX KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
XX KW cancer.

XX OS Mus sp.

XX PN US2001011125-A1.

XX PD 02-AUG-2001.

XX PF 30-JAN-1997; 97US-0790540.

XX PR 30-JAN-1997; 97US-0790540.

XX PA (HUSE/) HUSE W D.

XX PI Huse WD;

XX DR WPI; 2001-496171/54.

XX DR N-PSDB; AAH74626.

XX New LM609 grafted antibody exhibiting selective binding affinity to  
XX alphavbeta3, comprising at least one LM609 grafted heavy and light  
XX chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
XX disorders or cancer

XX PS Disclosure; Fig 2B; 25pp; English.

XX The present sequence represents the light chain variable region of the  
XX monoclonal antibody LM609. LM609 is a murine antibody which specifically  
XX recognises the integrin alphavbeta3, and inhibits its functional activity.  
XX The specification describes a LM609 grafted antibody which has the  
XX complementarity determining regions (CDRs) substituted into a non-murine  
XX framework. Nucleic acids encoding LM609 grafted heavy and light chain  
XX polypeptides and fragments are useful in diagnostic and therapeutic  
XX purposes, such as in the production of LM609 grafted antibodies and  
XX fragments having binding specificity and inhibitory activity against  
XX the integrin alphavbeta3. The antibody can be used for the diagnosis  
XX or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
XX disorders, chronic articular rheumatism, psoriasis, disorders  
XX associated with inappropriate or inopportune invasion of vessels such  
XX as diabetic retinopathy, neovascular glaucoma and capillary  
XX proliferation in atherosclerotic plaques, or cancers), and to inhibit  
XX binding activity of alphavbeta3 that are necessary for progression of  
XX an alphavbeta3-mediated disease.

XX SQ Sequence 107 AA;

Job time: 1472 sec

Query Match 86.3%; Score 44; DB 22; Length 107;  
Best Local Similarity 88.9%; Pred. No. 1.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
|||||||  
Db 89 qqsgswpht 97

RESULT 15  
AAB61360  
ID AAB61360 standard; protein; 107 AA.  
XX  
AC AAB61360;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE Vitaxin light chain variable region protein.  
XX  
KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis.  
XX  
OS Unidentified.  
XX  
PN WO200078815-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 23-JUN-2000; 2000WO-US17454.  
XX  
PR 24-JUN-1999; 99US-0339922.  
XX  
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX  
PI Huse WD, Wu H;  
XX  
DR WPI; 2001-050110/06.  
XX  
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis -  
XX  
PS Disclosure; Fig 1; 132pp; English.  
XX

CC The present invention relates to enhanced LM609 grafted antibodies  
CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
CC their functional fragments. The antibodies or their functional  
CC fragments can be used in the diagnosis and treatment of  
CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
CC diseases (such as psoriasis and chronic articular rheumatism),  
CC disorders associated with inappropriate or inopportune invasion of  
CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
CC diseases (such as macular degeneration), restenosis and  
CC osteoporosis.  
XX  
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 22; Length 107;  
Best Local Similarity 88.9%; Pred. No. 1.6;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
|||||||  
Db 89 qqsgswpht 97

Search completed: August 19, 2002, 06:39:11



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:38 ; Search time 61.75 Seconds  
(without alignments)  
3.560 Million cell updates/sec

Title: US-09-339-922A-90

Perfect score: 51

Sequence: 1 QOSGSWPLT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	88.2	9	2	US-08-232-081B-6
2	45	88.2	103	1	US-08-436-453-21
3	45	88.2	107	2	US-08-232-081B-9
4	45	88.2	107	2	US-08-232-081B-40
5	45	88.2	127	1	US-08-436-463-18
6	40	78.4	33	4	US-08-525-539A-12
7	40	78.4	107	1	US-08-436-463-20
8	40	78.4	107	1	US-08-107-659D-1
9	40	78.4	107	1	US-08-472-788A-1
10	40	78.4	107	2	US-08-477-531B-1
11	40	78.4	107	2	US-08-082-842A-1
12	40	78.4	109	1	US-07-942-245-4
13	40	78.4	143	2	US-08-653-402B-8
14	39	76.5	9	2	US-08-476-176B-55
15	39	76.5	9	3	US-08-127-721A-55
16	39	76.5	9	3	US-08-485-246A-55
17	39	76.5	13	1	US-08-221-580-7
18	39	76.5	13	5	PCT-US95-04018-69
19	39	76.5	106	2	US-08-800-198-4
20	39	76.5	106	3	US-09-296-595-4
21	39	76.5	107	1	US-08-192-102-3
22	39	76.5	107	1	US-08-324-799-3
23	39	76.5	107	2	US-08-192-861A-3
24	39	76.5	107	2	US-08-476-176B-4
25	39	76.5	107	3	US-08-127-721A-4
26	39	76.5	107	3	US-08-485-246A-4
27	39	76.5	107	4	US-09-133-119-3

28	39	76.5	107	4	US-08-192-093A-3	Sequence 3, Appli
29	39	76.5	127	2	US-08-476-176B-6	Sequence 6, Appli
30	39	76.5	127	2	US-08-476-176B-8	Sequence 8, Appli
31	39	76.5	127	2	US-08-476-176B-10	Sequence 10, Appli
32	39	76.5	127	3	US-08-127-721A-6	Sequence 6, Appli
33	39	76.5	127	3	US-08-127-721A-8	Sequence 8, Appli
34	39	76.5	127	3	US-08-127-721A-10	Sequence 10, Appli
35	39	76.5	127	3	US-08-485-246A-6	Sequence 6, Appli
36	39	76.5	127	3	US-08-485-246A-8	Sequence 8, Appli
37	39	76.5	127	3	US-08-485-246A-10	Sequence 10, Appli
38	39	76.5	240	2	US-08-800-198-8	Sequence 8, Appli
39	39	76.5	240	3	US-09-296-595-8	Sequence 8, Appli
40	38	74.5	100	1	US-08-436-463-19	Sequence 19, Appli
41	38	74.5	107	1	US-07-634-278-62	Sequence 62, Appli
42	38	74.5	107	1	US-07-634-278-63	Sequence 63, Appli
43	38	74.5	107	1	US-07-634-278-87	Sequence 87, Appli
44	38	74.5	107	1	US-08-477-728-62	Sequence 62, Appli
45	38	74.5	107	1	US-08-477-728-63	Sequence 63, Appli

ALIGNMENTS

RESULT 1  
US-08-232-081B-6  
; Sequence 6, Application US/08232081B  
; Patent No. 5886152  
; GENERAL INFORMATION:  
; APPLICANT: NAKATANI, TOMOYUKI  
; APPLICANT: GOMI, HIDEYUKI  
; APPLICANT: WIJENES, JOHN  
; APPLICANT: NOGUCHI, HIROSHI  
; TITLE OF INVENTION: HUMANIZED B-B10  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/232,081B  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SVENSSON, LEONARD R  
; REGISTRATION NUMBER: 30,330  
; REFERENCE/DOCKET NUMBER: 20-3484  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-232-081B-6

Query Match 88.2%; Score 45; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.7e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSGSWPLT 9  
||| |||||

Db 1 QOSSSWPLT 9

## RESULT 2

US-08-436-463-21  
; Sequence 21, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoto  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROMDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,463  
; FILING DATE: 26-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 341255/1992  
; FILING DATE: 28-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: KIMACHI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 103 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-436-463-21

Query Match 88.2%; Score 45; DB 1; Length 103;  
Best Local Similarity 88.9%; Pred. No. 0.48;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSGSWPLT 9

Db 86 QOSSSWPLT 94

## RESULT 3

US-08-232-081B-9  
; Sequence 9, Application US/08232081B  
; Patent No. 5886152  
; GENERAL INFORMATION:  
; APPLICANT: NAKATANI, TOMOYUKI  
; APPLICANT: GOMI, HIDEYUKI  
; APPLICANT: WIJDENES, JOHN  
; APPLICANT: NOGUCHI, HIROSHI  
; TITLE OF INVENTION: HUMANIZED B-B10  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH

; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,081B  
; FILING DATE:  
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:  
; NAME: SVENSSON, LEONARD R  
; REGISTRATION NUMBER: 30,330  
; REFERENCE/DOCKET NUMBER: 20-3484  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-232-081B-9

Query Match 88.2%; Score 45; DB 2; Length 107;  
Best Local Similarity 88.9%; Pred. No. 0.5;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSGSWPLT 9

Db 89 QOSSSWPLT 97

## RESULT 4

US-08-232-081B-40  
; Sequence 40, Application US/08232081B  
; Patent No. 5886152  
; GENERAL INFORMATION:  
; APPLICANT: NAKATANI, TOMOYUKI  
; APPLICANT: GOMI, HIDEYUKI  
; APPLICANT: WIJDENES, JOHN  
; APPLICANT: NOGUCHI, HIROSHI  
; TITLE OF INVENTION: HUMANIZED B-B10  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,081B  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SVENSSON, LEONARD R  
; REGISTRATION NUMBER: 30,330  
; REFERENCE/DOCKET NUMBER: 20-3484  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000

```

; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-232-081B-40

Query Match      88.2%; Score 45; DB 2; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQSSSWPLT 97

RESULT 5
US-08-436-463-18
; Sequence 18, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-463-18

Query Match      88.2%; Score 45; DB 1; Length 127;
Best Local Similarity 88.9%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 89 QQSSSWPLT 97

US-08-525-539A-12
; Sequence 12, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: M63 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-12

Query Match      78.4%; Score 40; DB 4; Length 33;
Best Local Similarity 77.8%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
Db 21 QQSSSWPYT 29

US-08-436-463-20
; Sequence 20, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
```

; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,463  
; FILING DATE: 26-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 341255/1992  
; FILING DATE: 28-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: KIMACHI-1  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-436-463-20

Query Match 78.4%; Score 40; DB 1; Length 107;  
Best Local Similarity 77.8%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
Db 89 QQSNWPYT 97

RESULT 8  
US-08-107-669D-1  
; Sequence 1, Application US/08107669D  
; Patent No. 5766886  
; GENERAL INFORMATION:  
; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
; STREET: 1100 New York Ave., N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States of America  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/107,669D  
; FILING DATE: 13-AUG-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/10906  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/808,464  
; FILING DATE: 13-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michele A. Cimbala

; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202/371-2600  
; TELEFAX: 202/371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-107-669D-1

Query Match 78.4%; Score 40; DB 1; Length 107;  
Best Local Similarity 77.8%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9  
Db 89 QQSNWPYT 97

RESULT 9  
US-08-472-788A-1  
; Sequence 1, Application US/08472788A  
; Patent No. 5770196  
; GENERAL INFORMATION:  
; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Modified Antibody Variable Domains  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
; STREET: 1100 New York Ave., N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,788A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/082,842  
; FILING DATE: 23-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/10906  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/808,464  
; FILING DATE: 13-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cimbala, Michele A.  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 0610.1000003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202/371-2600  
; TELEFAX: 202/371-2540  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-472-788A-1

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Query Match          78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
    ||| ||| |
Db 89 QQSNSWPYT 97

RESULT 10
US-08-477-531B-1
; Sequence 1, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-531B-1

Query Match          78.4%; Score 40; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
    ||| ||| |
Db 89 QQSNSWPYT 97

RESULT 11
US-08-082-842A-1
; Sequence 1, Application US/08082842A
; Patent No. 5865619
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.

```

```

; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,842A
; FILING DATE: 23-JUN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-082-842A-1

Query Match          78.4%; Score 40; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
    ||| ||| |
Db 89 QQSNSWPYT 97

RESULT 12
US-07-942-245-4
; Sequence 4, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation

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; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-4

Query Match 78.4%; Score 40; DB 1; Length 109;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 89 QQNSNWPYT 97

RESULT 13
US-08-653-402B-8
; Sequence 8, Application US/08653402B
; Patent No. 5969107
; GENERAL INFORMATION:
; APPLICANT: CARCELLER, Ana
; APPLICANT: ROSELL, Elisabet
; APPLICANT: GOMEZ, Alicia
; APPLICANT: ADEN, Jaume
; APPLICANT: PIULATS, Jaume
; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an
; TITLE OF INVENTION: immune response against epidermal growth factor receptor.
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,402B
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95107967.2
; FILING DATE: 26-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: MERCK 1781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-653-402B-8

Query Match 78.4%; Score 40; DB 2; Length 143;
Best Local Similarity 77.8%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 109 QQNSNWPYT 117

RESULT 14
US-08-476-176B-55
; Sequence 55, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-476-176B-55

Query Match 76.5%; Score 39; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 1 QQSDSNWPTT 9

RESULT 15
US-08-127-721A-55
; Sequence 55, Application US/08127721A
; Patent No. 6066718

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GENERAL INFORMATION:  
APPLICANT: Hardman, No. 6066718man  
APPLICANT: Kolbinger, Frank  
APPLICANT: Saldanha, Jose  
TITLE OF INVENTION: Reshaped monoclonal antibodies against an  
TITLE OF INVENTION: Immunoglobulin isotype  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6066718artis Patent and Trademark Department  
STREET: 59 Route 10  
CITY: East Hanover  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07936-1080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/127,721A  
FILING DATE: 27-SEPTEMBER-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/952,802  
FILING DATE: 25-SEPTEMBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6066718ak, Henry P.  
REGISTRATION NUMBER: 33,200  
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-127-721A-55

Query Match 76.58; Score 39; DB 3; Length 9;  
Best Local Similarity 77.88; Pred. No. 1.7e+05;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QQSGSWPLT 9  
Db 1 QQSDSWPTT 9

Search completed: August 19, 2002, 06:34:39  
Job time: 1200 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:04 ; Search time 78.53 Seconds  
(without alignments)  
20.801 Million cell updates/sec

Title: US-09-339-922A-102

Perfect score: 88

Sequence: 1 KVSSGGSTYYLDTVQG 17

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	80.7	113	2 S26468	Ig heavy chain V r
2	71	80.7	117	1 HVMS34	Ig heavy chain pre
3	68	77.3	117	1 HVMS84	Ig heavy chain pre
4	67	76.1	108	2 PLO248	Ig heavy chain V r
5	67	76.1	111	2 PH1007	Ig heavy chain V r
6	67	76.1	118	2 S00700	Ig heavy chain V r
7	64	72.7	118	2 PH1006	Ig heavy chain V r
8	64	72.7	118	2 S20841	Ig heavy chain V r
9	64	72.7	138	2 S09258	Ig heavy chain V r
10	62	70.5	113	2 S02717	Ig heavy chain V r
11	62	70.5	115	2 PH1538	Ig H chain V regio
12	62	70.5	117	1 HVMSRF	Ig heavy chain pre
13	62	70.5	119	2 PH1548	Ig H chain V regio
14	62	70.5	119	2 PH1549	Ig H chain V regio
15	60	68.2	83	2 S21593	Ig heavy chain V r
16	60	68.2	111	2 S51211	Ig heavy chain V r
17	60	68.2	145	2 I47203	Ig heavy chain var
18	59	67.0	90	2 S24248	Ig heavy chain V r
19	59	67.0	98	2 S26889	Ig heavy chain V r
20	59	67.0	99	2 S24259	Ig heavy chain V r
21	59	67.0	100	2 S24258	Ig heavy chain V r
22	59	67.0	101	2 S24257	Ig heavy chain V r
23	59	67.0	102	2 S24260	Ig heavy chain V r
24	59	67.0	104	2 S24255	Ig heavy chain V r
25	59	67.0	105	2 S24249	Ig heavy chain V r
26	59	67.0	106	2 S24256	Ig heavy chain V r
27	59	67.0	108	2 PH1648	Ig heavy chain V r
28	59	67.0	109	2 PH1649	Ig heavy chain V r
29	59	67.0	109	2 S24254	Ig heavy chain V r

#### ALIGNMENTS

##### RESULT 1

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J. submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <NAV>

A:Cross-references: EMBL:X59107; NID:g51944; PTDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 71; DB 2; Length 113;  
Best Local Similarity 81.2%; Pred. No. 0.00054;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17

DB 47 ISSGGSTYYPTVKG 62

##### RESULT 2

HVMS34

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 31-Mar-1997

C:Accession: JT0502

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0502

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted



Query Match 80.7%; Score 71; DB 1; Length 117;  
 Best Local Similarity 81.2%; Pred. No. 0.00056;  
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 70 ISSGGGTTYPDVKG 85

RESULT 3

HVMS84

Ig heavy chain precursor V region (5-84) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 31-Mar-1997

C:Accession: J0505

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: J0501; MUID:89279149

A:Accession: J0505

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAN>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 77.3%; Score 68; DB 1; Length 117;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 70 ISNGGGTTYPDVKG 85

RESULT 4

PL0248

Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

C:Accession: PL0248

R:Shlomchik, M.; Maccelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618

A:Accession: PL0248

A:Molecule type: mRNA

A:Residues: 1-108 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-24/Region: framework 1

F:9-92/Domain: immunoglobulin homology <IMM>

F:25-29/Region: complementarity-determining 1

F:30-43/Region: framework 2

F:44-60/Region: complementarity-determining 2

F:61-92/Region: framework 3

F:93-99/Region: complementarity-determining 3

F:100-108/Region: framework 4

Query Match

Best Local Similarity 76.1%; Score 67; DB 2; Length 108;

Matches: 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 70 ISSGGGTTYPDVKG 85

Db 45 ISSGGGTTYPDVKG 60

RESULT 5

PH1007

Ig heavy chain V region (clone 163-cl) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH1007

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1007

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-111 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 76.1%; Score 67; DB 2; Length 111;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

Db 51 ISSGGGTTYPDVKG 66

RESULT 6

S00700

Ig heavy chain V region - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 23-Jul-1999

C:Accession: S00700

R:Yamawaki-Kataoka, Y.; Honjo, T.

Nucleic Acids Res. 15, 5888, 1987

A:Title: Nucleotide sequences of variable region segments of the immunoglobulin heavy

A:Reference number: S00700; MUID:87289054

A:Accession: S00700

A:Molecule type: DNA

A:Residues: 1-118 <YAM>

A:Cross-references: EMBL:Y00380; NID:g64810; PIDN:CAA68452.1; PID:g64811

A:Note: the sequence was determined from the germline gene

C:Genetics:

A:Introns: 15/3

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 76.1%; Score 67; DB 2; Length 118;

Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KVSSGGGTTYLDTVQG 17

Db 69 RISDGGGTTYADSVKG 85

RESULT 7

PH1006

Ig heavy chain V region (clone 202.33) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH1006

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1006

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-108 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 64; DB 2; Length 108;

Best Local Similarity 68.8%; Pred. No. 0.0065;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

DB 46 ISGGGNTYPTVKG 61

RESULT 8

S20641

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C:Accession: S20641

R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.

submitted to the EMBL Data Library, February 1992

A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react

A:Reference number: S20639

A:Accession: S20641

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-118 <LOS>

A:Cross-references: EMBL:X65003; NID:g52602; PIDN:CAA46136.1; PID:g52603

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 64; DB 2; Length 118;

Best Local Similarity 68.8%; Pred. No. 0.0071;

Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

DB 51 ISGGGNTYPTVKG 66

RESULT 9

S09258

Ig heavy chain V region precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 23-Jul-1999

C:Accession: S09258

R:Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A:Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK

A:Reference number: S09258; MUID:90245594

A:Accession: S09258

A:Molecule type: DNA

A:Residues: 1-138 <HAM>

A:Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 64; DB 2; Length 138;

Best Local Similarity 68.8%; Pred. No. 0.0084;

Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

DB 70 ISGGGNTYPTSVKG 85

RESULT 10

S02717

Ig heavy chain V region (clone pH62) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000

C:Accession: S02717

R:Sollazzo, M.; Hasemann, C.A.; Meek, K.D.; Glotz, D.; Capra, J.D.; Zanetti, M.

submitted to the EMBL Data Library, February 1989

A:Reference number: S02717

A:Accession: S02717

A:Molecule type: DNA

A:Residues: 1-113 <SOL>

A:Cross-references: EMBL:Y00744; NID:g52472; PIDN:CAA68713.1; PID:gl334095

A:Note: this sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 62; DB 2; Length 113;

Best Local Similarity 68.8%; Pred. No. 0.014;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

DB 51 INSGGTTYPTVKG 66

RESULT 11

PH1538

Ig H chain V region (clone 13G12) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jan-2000

C:Accession: PH1538

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to Cryptococcus neoforma

A:Reference number: PH1528; MUID:93210465

A:Accession: PH1538

A:Molecule type: mRNA

A:Residues: 1-115 <MKR>

A:Note: the stop codons X appear in residues 82, 85 and 106

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:14-99/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 62; DB 2; Length 115;

Best Local Similarity 68.8%; Pred. No. 0.014;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17

DB 50 INSGGTTYPTVKG 65

RESULT 12

HMSRF

Ig heavy chain precursor V region (RF) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 31-Mar-1997

C:Accession: JT0503

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0503

A:Status: translation not shown

A:Molecule type: mRNA  
A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; hybridoma; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (RF) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 70.5%; Score 62; DB 1; Length 117;

Best Local Similarity 68.8%; Pred. No. 0.014;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17

::: ||||| |||:|

Db 70 INSGGSTYYPDVTYKG 85

RESULT 13

PH1548

Ig H chain V region (clone 12F4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 17-Mar-1999

C:Accession: PH1548

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans

A:Reference number: PH1528; MUID:93210465

A:Accession: PH1548

A:Molecule type: mRNA

A:Residues: 1-119 <MUK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 62; DB 2; Length 119;

Best Local Similarity 68.8%; Pred. No. 0.015;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17

::: ||||| |||:|

Db 51 INSGGSTYYPDVTYKG 66

RESULT 14

PH1549

Ig H chain V region (clone 13F1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 17-Mar-1999

C:Accession: PH1549

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans

A:Reference number: PH1528; MUID:93210465

A:Accession: PH1549

A:Molecule type: mRNA

A:Residues: 1-119 <MUK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 62; DB 2; Length 119;

Best Local Similarity 68.8%; Pred. No. 0.015;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17

::: ||||| |||:|

Db 51 INSGGSTYYPDVTYKG 66

RESULT 15

S21593

Ig heavy chain V region (10C5) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C:Accession: S21593

R:Kaartinen, M.

submitted to the EMBL Data Library, May 1992

A:Reference number: S21591

A:Accession: S21593

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-83 <KAA>

A:Cross-references: EMBL:X66457; NID:g51598; PIDN:CAA47072.1; PID:g51599

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 68.2%; Score 60; DB 2; Length 83;

Best Local Similarity 68.8%; Pred. No. 0.021;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17

::: ||||| |||:|

Db 21 ITSGGSTYYSDTVKG 36

Search completed: August 19, 2002, 06:36:04

Job time: 1285 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:07 ; Search time 51.81 Seconds  
(without alignments)  
12.705 Million cell updates/sec

Title: US-09-339-922a-102

Perfect score: 88

Sequence: 1 KVSSGGSTYYLDTVQG 17

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	80.7	117	1 HV55_MOUSE	P18526 mus musculus
2	68	77.3	117	1 HV54_MOUSE	P18525 mus musculus
3	62	70.5	117	1 HV53_MOUSE	P18524 mus musculus
4	56	63.6	117	1 HV3C_HUMAN	P01764 homo sapien
5	54	61.4	97	1 HV56_MOUSE	P18527 mus musculus
6	53	60.2	119	1 HV3L_HUMAN	P01773 homo sapien
7	52	59.1	116	1 HV05_CARAU	P19181 carassius a
8	51	58.0	98	1 HV57_MOUSE	P18528 mus musculus
9	51	58.0	117	1 HV58_MOUSE	P18529 mus musculus
10	49	55.7	115	1 HV3F_HUMAN	P01767 homo sapien
11	47	53.4	136	1 HV16_MOUSE	P01783 mus musculus
12	45	51.1	117	1 HV02_CANFA	P01785 canis fami
13	45	51.1	814	1 DMSA_ECOLI	P18775 escherichia
14	44	50.0	503	1 CP7A_RAT	P18125 rattus norv
15	43	48.9	340	1 THPS_SULAC	P17118 sulfolobus
16	43	48.9	516	1 T2D5_YEAST	P53040 saccharomyc
17	43	48.9	2300	1 CXAA_NEUCR	Q01631 neurospora
18	42	47.7	117	1 HV59_MOUSE	P18530 mus musculus
19	42	47.7	480	1 6PGD_CHLTR	O84066 chlamydia t
20	42	47.7	807	1 YNPF_ECOLI	P77783 escherichia
21	41.5	47.2	114	1 HV3B_HUMAN	P01763 homo sapien
22	41.5	47.2	122	1 HV3A_HUMAN	P01762 homo sapien
23	41	46.6	442	1 CELF_BACSU	P46320 bacillus su
24	41	46.6	449	1 TBA2_SCHPO	P04689 schizosacch
25	41	46.6	468	1 6PG2_BACSU	P80859 bacillus su
26	41	46.6	652	1 ABG5_MOUSE	Q99pe8 mus musculus
27	41	46.6	652	1 ABG5_MOUSE	Q99pe8 mus musculus
28	40	45.5	72	1 NIPT_AZOVI	P09427 azotobacter
29	40	45.5	120	1 HV3U_HUMAN	P01782 homo sapien
30	40	45.5	383	1 MANA_STRLI	P51529 streptomyce
31	40	45.5	412	1 Y157_YEAST	Q12358 saccharomyc
32	40	45.5	462	1 DRTS_PARTE	Q27828 paramemomyc
33	40	45.5	652	1 T3MO_SALTY	P40814 salmonella

## ALIGNMENTS

### RESULT 1

HV55\_MOUSE  
ID HV55\_MOUSE STANDARD; PRT; 117 AA.  
AC P18526;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 345 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/CJ;  
RX MEDLINE=89279149; PubMed=2499654;  
RA Levy N.S., Mallpiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during  
the primary immune response.";  
RL J. Exp. Med. 169:2007-2019(1989).  
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.  
DR PIR; JT0502; HVMS34.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 80.7%; Score 71; DB 1; Length 117;  
Best Local Similarity 81.2%; Pred. No. 0.00012;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17  
Db 70 ISSGGSTYYPDVTKG 85

### RESULT 2

HV54\_MOUSE  
ID HV54\_MOUSE STANDARD; PRT; 117 AA.  
AC P18525;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 5-84 precursor.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 [1]  
 FT SEQUENCE FROM N.A.  
 RP STRAIN=BALB/CJ;  
 RC MEDLINE=89279149; PubMed=2499654;  
 RX Levy N.S., Malpiero U.V., Lebecqz S.G., Gearhart P.J.;  
 RA "Early onset of somatic mutation in immunoglobulin VH genes during  
 RT the primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.  
 DR PIR: J0505; HVMS84.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 77.3%; Score 68; DB 1; Length 117;  
 Best Local Similarity 75.0%; Pred. No. 0.00036;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTYLDTVOG 17  
 :||| ||||| |||:  
 Db 70 ISGGGTYPDIVK 85

RESULT 3  
 HV53\_MOUSE ID HV53\_MOUSE STANDARD; PRT; 117 AA.  
 AC P18524;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region RF precursor.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 [1]  
 FT SEQUENCE FROM N.A.  
 RP STRAIN=BALB/CJ;  
 RC MEDLINE=89279149; PubMed=2499654;  
 RX Levy N.S., Malpiero U.V., Lebecqz S.G., Gearhart P.J.;  
 RA "Early onset of somatic mutation in immunoglobulin VH genes during  
 RT the primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.  
 DR PIR: J0505; HVMSRF.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Hybridoma; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 70.5%; Score 62; DB 1; Length 117;  
 Best Local Similarity 68.8%; Pred. No. 0.0033;  
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTYLDTVOG 17  
 :||| ||||| |||:  
 Db 70 ISGGGTYPDIVK 85

RESULT 4  
 HV3C\_HUMAN ID HV3C\_HUMAN STANDARD; PRT; 117 AA.  
 AC P01764;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-III region VH26 precursor.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81101090; PubMed=6450418;  
 RA Matthyssens G., Rabbitts T.H.;  
 RT "Structure and multiplicity of genes for the human immunoglobulin  
 RT heavy chain variable region.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; J00236; AAA53516.1; -;  
 DR EMBL; M35415; AAA58735.1; -;  
 DR PIR: A02047; H3HU26.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 63.6%; Score 56; DB 1; Length 117;  
 Best Local Similarity 62.5%; Pred. No. 0.03;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTYLDTVOG 17  
 :||| ||||| |||:  
 Db 70 ISGGGTYGDSVK 85

RESULT 5  
 HV56\_MOUSE ID HV56\_MOUSE STANDARD; PRT; 97 AA.  
 AC P18527;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

```

DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J0504; HWS94.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 61.4%; Score 54; DB 1; Length 97;
Best Local Similarity 71.4%; Pred. No. 0.052; 2; Mismatches 2; Indels 0; Gaps 0;
Matches 10; Conservative 2;

QY 4 SGGSTYYLDTVQG 17
I | | | | | | | | | |
DB 52 SSGGSTYYPDSVKG 65

RESULT 6
HV3L_HUMAN STANDARD; PRT; 119 AA.
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
RT IgA1 protease, digestion, Fab and Fc fragments, and the complete
RT amino acid sequence of the alpha 1 heavy chain."
RL J. Biol. Chem. 254:2865-2874(1979).
DR PIR; A02056; ALHUBR.
DR HSSP; P01772; ZIG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Glycoprotein.
FT MOD_RES 1
FT DISULFID 22 96 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 28 28
FT NON_TER 119
FT SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 60.2%; Score 53; DB 1; Length 119;
Best Local Similarity 56.2%; Pred. No. 0.094;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17

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DB 51 ISYGGSBYYADSVRG 66
I | | | | | | | | | |

RESULT 7
HV05_CARAU STANDARD; PRT; 116 AA.
ID HV05_CARAU
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR; B28966; B28966.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 41 114 BY SIMILARITY.
FT NON_TER 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 59.1%; Score 52; DB 1; Length 116;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGSTYYLDTVQG 17
I | | | | | | | | | |
DB 73 GGSTYYADSVKG 84

RESULT 8
HV57_MOUSE STANDARD; PRT; 98 AA.
ID HV57_MOUSE
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.

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```
DR PIR; JT0501; HVMS96.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 58.0%; Score 51; DB 1; Length 98;
Best Local Similarity 56.2%; Pred. No. 0.16;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGGSTYYLDTVOG 17
   :||| ||| :|||
Db 51 ISDGGSTYYTPDSVKG 66

RESULT 9
ID HV58_MOUSE STANDARD; PRT; 117 AA.
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0506; HVMS57.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 58.0%; Score 51; DB 1; Length 117;
Best Local Similarity 52.5%; Pred. No. 0.19;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGSTYYLDTVOG 17
   :||| ||| :|||
Db 70 ISSGGLTYTPDSVKG 85

RESULT 10
ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0506; HVMS57.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 58.0%; Score 51; DB 1; Length 117;
Best Local Similarity 52.5%; Pred. No. 0.19;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGSTYYLDTVOG 17
   :||| ||| :|||
Db 70 ISSGGLTYTPDSVKG 85

RESULT 10
ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0506; HVMS57.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 55.7%; Score 49; DB 1; Length 115;
Best Local Similarity 66.7%; Pred. No. 0.4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGSYYLDTVOG 17
   ||||| :|||
Db 54 GGTYYADSVKRG 65

RESULT 11
ID HV16_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain V region MOPC 21 precursor (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
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CC -----
CC EMBL; J00522; AAD15290.1; -.
CC PIR; A02066; GIMS21.
CC HSSP; P01772; 2FB4.
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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IG; 1.
KW Immunoglobulin V region: Signal.
FT NON_TER 1 1
FT SIGNAL <1 16
FT CHAIN 17 136
FT CHAIN 115 119
FT DOMAIN 120 136
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90
FT CONFLICT 115 115
FT CONFLICT 120 120
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 53.4%; Score 47; DB 1; Length 136;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17
Db 67 ISSGSSTLHYADTVKG 82

RESULT 12
HV02_CANFA STANDARD; PRT; 117 AA.
AC P01785;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MOO.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
[1]
RP SEQUENCE OF 1-112.
RX MEDLINE-77242268; PubMed=407924;
RA Wasserman R.L., Capra J.D.;
RT "Primary structure of the variable regions of two canine
immunoglobulin heavy chains."
RL Biochemistry 16:3160-3168(1977).
[2]
RP SEQUENCE OF 113-117.
RX MEDLINE-80077682; PubMed=117299;
RA McCumber L.J., Capra J.D.;
RT "The complete amino-acid sequence of a canine mu chain."
RL Mol. Immunol. 16:565-570(1979).
[3]
CC 1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IG; 1.
KW Immunoglobulin V region.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12703 MW; FCE07309E0A84B35 CRC64;

Query Match 51.1%; Score 45; DB 1; Length 117;
Best Local Similarity 57.1%; Pred. No. 1.8;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 SGGSTYYLDTVQG 17
Db 52 SSSGQTYADAVKG 65

RESULT 13
DMSA_ECOLI STANDARD; PRT; 814 AA.
AC P18775;
DT 01-NOV-1990 (Rel. 16, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Anaerobic dimethyl sulfoxide reductase chain A precursor (EC 1.8.99.-)
DE (DMSO reductase).
GN DMSA OR B0894.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
[1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 46-51.
RC STRAIN=K12 / C600;
RX MEDLINE-89096500; PubMed=3062312;
RA Bilous P.T., Cole S.T., Anderson W.F., Weiner J.H.;
RT "Nucleotide sequence of the dmsABC operon encoding the anaerobic
dimethylsulphoxide reductase of Escherichia coli."
RL Mol. Microbiol. 2:785-795(1988).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE-97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE-97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemura K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horluchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map."
RL DNA Res. 3:137-155(1996).
[4]
RP MUTAGENESIS.
RX MEDLINE-94171715; PubMed=8125918;
RA Trieber C.A., Rothery R.A., Weiner J.H.;
RT "Multiple pathways of electron transfer in dimethyl sulfoxide
reductase of Escherichia coli."
RL J. Biol. Chem. 269:7103-7109(1994).
CC 1- FUNCTION: TERMINAL REDUCTASE DURING ANAEROBIC GROWTH ON
VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS. ALLOWS E.COLI TO GROW
ANAEROBICALLY ON ME(2)SO AS RESPIRATORY OXIDANT.
CC 1- CATALYTIC ACTIVITY: REDUCES VARIOUS N-OXIDE AND SULFOXIDE
COMPOUNDS INCLUDING TRIMETHYLAMINE N-OXIDE.
CC 1- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN); MAY BIND A 4FE-4S CLUSTER.
CC 1- SUBUNIT: HOMODIMER. THE COMPLEX CONSIST OF THREE SUBUNITS: DMSA,
THE REDUCTASE; DMSB, AN ELECTRON TRANSFER PROTEIN, AND DMSC,
A MEMBRANE ANCHOR PROTEIN.
CC 1- SUBCELLULAR LOCATION: CYTOSOL; CYTOSOLIC FACE OF THE MEMBRANE.
CC 1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
OXIDOREDUCTASE FAMILY.
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DR EMBL: J03412: AAA83843.1; ALT_INIT.
DR EMBL: AR000191: AAC73980.1; ALT_INIT.
DR EMBL: D90727: BAA35626.1; ALT_INIT.
DR PIR: S03785; S03785.
DR HSP: Q57366; IEU1.
DR EcoGene: EG10232; dmsA.
DR InterPro: IPR001467; Molybdopterin.
DR Pfam: PF00384; molybdopterin; 1.
DR Pfam: PF01588; Molybd-binding; 1.
DR PROSITE: PS00551; MOLYBDOPTERIN_PROK_1; 1.
DR PROSITE: PS00490; MOLYBDOPTERIN_PROK_2; 1.
DR PROSITE: PS00932; MOLYBDOPTERIN_PROK_3; 1.
DR Oxidoreductase: Signal; Molybdenum; 4Fe-4S; Iron-sulfur;
KW Complete proteome.
FT SIGNAL 1 45
FT CHAIN 46 814 ANAEROBIC DIMETHYL SULFOXIDE REDUCTASE
FT CHAIN A.
FT METAL 63 63 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 67 67 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 71 71 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 104 104 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 814 AA; 90398 MW; B97C830ABAC7C32C CRC64;

Query Match 51.1%; Score 45; DB 1; Length 814;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SGGSGTYILD 13
Db 248 SGGGVTVYLE 257

RESULT 14
CP7A_RAT
ID CP7A_RAT STANDARD; PRT; 503 AA.
AC P18125; P51543;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome P450 7A1 (Cholesterol 7-alpha-monooxygenase) (CYPVII)
DE (EC 1.14.13.17) (Cholesterol 7-alpha-hydroxylase).
GN CYP7A1 OR CYP7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE-90307735; PubMed=1694852;
RA Li Y.C., Wang D.P., Chiang J.Y.L.;
RT "Regulation of cholesterol 7 alpha-hydroxylase in the liver. Cloning,
RT sequencing, and regulation of cholesterol 7 alpha-hydroxylase mRNA.";
RL J. Biol. Chem. 265:12012-12019(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE-90243699; PubMed=2335522;
RA Jelinek D.F., Andersson S., Slaughter C.A., Russell D.W.;
RT "Cloning and regulation of cholesterol 7 alpha-hydroxylase, the rate-
RT limiting enzyme in bile acid biosynthesis.";
RL J. Biol. Chem. 265:8190-8197(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-90033362; PubMed=2806567;
RA Noshiro M., Nishimoto M., Morohashi K., Okuda K.;
RT "Molecular cloning of cDNA for cholesterol 7 alpha-hydroxylase from
RT rat liver microsomes. Nucleotide sequence and expression.";
RL FEBS Lett. 257:97-100(1989).
RN [4]
RP SEQUENCE FROM N.A.
TX TISSUE=Liver;

```

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RX MEDLINE-90277612; PubMed=1693613;
RA Noshiro M., Nishimoto M., Okuda K.;
RT "Rat liver cholesterol 7 alpha-hydroxylase. Pretranslational
RT regulation for circadian rhythm.";
RL J. Biol. Chem. 265:10036-10041(1990).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-91177904; PubMed=2007596;
RA Nishimoto M., Gotoh O., Okuda K., Noshiro M.;
RT "Structural analysis of the gene encoding rat cholesterol alpha-
RT hydroxylase, the key enzyme for bile acid biosynthesis.";
RL J. Biol. Chem. 266:6467-6471(1991).
RN [6]
RP SEQUENCE OF 1-325 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE-94292507; PubMed=8021257;
RA Chiang J.Y., Stroup D.;
RT "Identification and characterization of a putative bile acid-
RT responsive element in cholesterol 7 alpha-hydroxylase gene promoter.";
RL J. Biol. Chem. 269:17502-17507(1994).
RN [7]
RP SEQUENCE OF 1-27 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE-91084435; PubMed=2261433;
RA Jelinek D.F., Russell D.W.;
RT "Structure of the rat gene encoding cholesterol 7 alpha-hydroxylase.";
RL Biochemistry 29:7781-7785(1990).
RN [8]
RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE-93041942; PubMed=1420318;
RA Chiang J.Y., Yang T.P., Wang D.P.;
RT "Cloning and 5'-flanking sequence of a rat cholesterol 7 alpha-
RT hydroxylase gene.";
RL Biochim. Biophys. Acta 1132:337-339(1992).
CC -!- CATALYTIC ACTIVITY: Cholesterol + NADPH + O(2) = 7-alpha-
CC hydroxycholesterol + NADP(+) + H(2)O.
CC -!- ENZYME REGULATION: INHIBITION OF ACTIVITY BY BILE ACID FEEDBACK.
CC -!- PATHWAY: FIRST AND RATE-LIMITING STEP IN THE CONVERSION OF
CC CHOLESTEROL TO BILE ACIDS.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- TISSUE SPECIFICITY: LIVER.
CC -!- INDUCTION: BY CHOLESTYRAMINE AND CHOLESTEROL.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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DR EMBL: J05509; AAA40839.1; -
DR EMBL: J02926; AAA40923.1; -
DR EMBL: J05430; AAA41041.1; -
DR EMBL: J05460; AAA03649.1; -
DR EMBL: M59189; AAA41042.1; -
DR EMBL: M59184; AAA41042.1; JOINED.
DR EMBL: M59185; AAA41042.1; JOINED.
DR EMBL: M59186; AAA41042.1; JOINED.
DR EMBL: M59187; AAA41042.1; JOINED.
DR EMBL: M59188; AAA41042.1; JOINED.
DR EMBL: U01962; AAA21144.2; -
DR EMBL: X17595; CAB57878.1; -
DR EMBL: Z14108; CAA78481.1; -
DR PIR: A35376; A35376.
DR InterPro: IPR001128; Cyt_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum; Cholesterol metabolism; NADP.
TX BINDING 444 444 HEME (BY SIMILARITY).
FT

```

FT CONFLICT 371 371 T -> S (IN REF. 5).  
SQ SEQUENCE 503 AA; 56882 MW; EA825AA6E74BF5F6 CRC64;

Query Match 50.0%; Score 44; DB 1; Length 503;  
Best Local Similarity 69.2%; Pred. No. 13;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 SGGGTTYLDTVQ 16  
| ||| ||| ||  
Db 327 SGGGATYLDQVQ 339

## RESULT 15

THPS\_SULAC  
ID THPS\_SULAC STANDARD; PRT; 340 AA.  
AC P17118;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Thermopsin precursor (EC 3.4.23.42).  
OS Sulfolobus acidocaldarius.  
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.  
OX NCBI\_TaxID=2285;  
RN [1]  
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 42-76.  
RX MEDLINE=90110209; PubMed=2104843;  
RA Lin X.-L.; Tang J.;  
RT "Purification, characterization, and gene cloning of thermopsin, a  
thermostable acid protease from Sulfolobus acidocaldarius.";  
RL J. Biol. Chem. 265:1490-1495(1990).  
CC -1- FUNCTION: MAY REPRESENT A NEW CLASS OF ACID PROTEASES. IT DIGEST  
PROTEINS AND PEPTIDES IN ACIDIC SOLUTION, AND IS THERMOSTABLE. IT  
HAS MAXIMAL PROTEOLYTIC ACTIVITY AT PH 2 AND 90 DEGREES CELSIUS.  
CC -1- CATALYTIC ACTIVITY: Specificity similar to pepsin A, prefers bulky  
hydrophobic side-chains on either side of the scissile bond.  
CC -1- SUBCELLULAR LOCATION: MAY BE LINKED TO CELLS BY COVALENT LINKAGES  
THROUGH SOME SIDE CHAINS.  
CC -1- MISCELLANEOUS: THERMOP SIN HAS PERHAPS A DIFFERENT TYPE OF ACTIVE  
SITE THAN OTHER ASPARTIC PROTEASES.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A5.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; J05184; AAA72221.1; -.  
DR PIR; A35009; A35009.  
DR MEROPS; A05.001; -.  
KW Hydrolase; Aspartyl  
FT SIGNAL 1 28  
FT PROPEP 29 41  
FT CHAIN 42 340  
FT CARBOHYD 31 31 N-LINKED (POTENTIAL).  
FT CARBOHYD 65 65 N-LINKED (PROBABLE).  
FT CARBOHYD 69 69 N-LINKED (PROBABLE).  
FT CARBOHYD 85 85 N-LINKED (POTENTIAL).  
FT CARBOHYD 117 117 N-LINKED (POTENTIAL).  
FT CARBOHYD 148 148 N-LINKED (POTENTIAL).  
FT CARBOHYD 197 197 N-LINKED (POTENTIAL).  
FT CARBOHYD 277 277 N-LINKED (POTENTIAL).  
FT CARBOHYD 287 287 N-LINKED (POTENTIAL).  
FT CARBOHYD 327 327 N-LINKED (POTENTIAL).  
FT CARBOHYD 334 334 N-LINKED (POTENTIAL).  
SQ SEQUENCE 340 AA; 37262 MW; E2758C0BC287FCE1 CRC64;

Query Match 48.9%; Score 43; DB 1; Length 340;  
Best Local Similarity 63.6%; Pred. No. 12;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
OY 3 SGGGTTYLD 13  
|:|||||:|  
Db 169 SAGGGQTFYD 179

Search completed: August 19, 2002, 06:59:08  
Job time: 1373 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:10 ; Search time 140.4 Seconds  
(without alignments)  
20.947 Million cell updates/sec

**Title:** US-09-339-922A-102  
**Perfect score:** 88  
**Sequence:** 1 KVSSGGGGSTYYLPTVOG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 5622222

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```
Database :
SPTRWBL_19.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	59	67.0	597	4	Q96B99	Q96bb9 homo sapien
2	58	65.9	121	4	Q9UL71	Q9ul71 homo sapien
3	57	64.8	479	11	Q91WP5	Q91wp5 mus musculus
4	55	62.5	119	11	Q92QE7	Q92qe7 mus musculus
5	51	58.0	118	4	Q9UL72	Q9ul72 homo sapien
6	51	58.0	211	11	Q9DBR6	Q9dbr6 mus musculus
7	50	56.8	487	11	Q99KA4	Q99ka4 mus musculus
8	47	53.4	211	4	Q9BQA2	Q9bqa2 homo sapien
9	47	53.4	473	11	Q91Z05	Q91z05 mus musculus
10	47	53.4	486	11	Q91Z07	Q91z07 mus musculus
11	47	53.4	545	4	Q96SL2	Q96sl2 homo sapien
12	47	53.4	798	2	Q9RKF0	Q9rkf0 streptomyce
13	47	53.4	1176	4	Q96Q05	Q96q05 homo sapien
14	46	52.3	473	11	Q96DL4	Q96dl4 mus musculus
15	45	51.1	129	2	O60111	O60111 versinia ps
16	45	51.1	162	10	Q9FY12	Q9fy12 arabidopsis

## ALIGNMENTS

```

RESULT 1
Q96BB9
ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AANH5760.1; -.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 67.0%; Score 59; DB 4; Length 597;
Best Local Similarity 62.5%; Pred. No. 0.34;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGGSTYYLDTVQG 17
Db :| ||||| | :|
70 ISGSGGGSTYYADSVKG 85

RESULT 2
Q9UL71
ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION

```

```
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2FBA.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 65.9%; Score 58; DB 4; Length 121;
Best Local Similarity 62.5%; Pred. No. 0.086;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17
Db 51 ISGGGGTTYADSVKG 66

RESULT 3
Q91WP5 PRELIMINARY; PRT; 479 AA.
AC Q91WP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 51.6 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013656; AAH13656.1; -.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 64.8%; Score 57; DB 11; Length 479;
Best Local Similarity 56.2%; Pred. No. 0.56;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17
Db 70 INSGNGTYSDTMKG 85

RESULT 4
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PTERIN-MIMICKING ANTI-IDIOPOPE HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307937; AAL09421.1; -.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match 62.5%; Score 55; DB 11; Length 119;
Best Local Similarity 62.5%; Pred. No. 0.26;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17
Db 51 ISGGGGTTYPDVSKG 66

RESULT 5
Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035042; AAD56278.1; -.
DR HSSP; P01772; 2FBA.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 58.0%; Score 51; DB 4; Length 118;
Best Local Similarity 56.2%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17
Db 50 VTYSGGSSYYADSVKG 65

RESULT 6
Q9D8R6 PRELIMINARY; PRT; 211 AA.
AC Q9D8R6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
```

DE 181004A24RIK PROTEIN.  
GN 181004A24RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyo-oka K., Wang K.H., Welz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL: AK007766; BAB25242.1; -;  
DR MGD: MGI:1923760; 181004A24RIK.  
SQ SEQUENCE 211 AA; 23482 MW; 018A9D083CACBBDB8 CRC64;

Query Match 58.0%; Score 51; DB 11; Length 211;  
Best Local Similarity 66.7%; Pred. No. 2.1;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTYLDTVQ 16  
: | | | | | | | | | |  
DB 144 ISFVGSSTFYLDVQ 158

RESULT 7  
Q99KA4 PRELIMINARY; PRT; 487 AA.  
AC Q99KA4;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 52.6 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC004786; AAH04786.1; -;  
DR HSSP: P01810; 2FBJ.  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR003597; Ig-cl.  
DR InterPro: IPR003600; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig; 4.  
DR SMART: SM00409; IG; 3.  
DR SMART: SM00407; IGC1; 3.  
DR SMART: SM00406; IGV; 1.  
DR SMART: SM00410; IG\_like; 1.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.

KW Hypothetical protein.  
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;  
Query Match 56.8%; Score 50; DB 11; Length 487;  
Best Local Similarity 56.2%; Pred. No. 7.6;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 2 VSSGGGTYLDTVQ 17  
: | | | | | | | | | |  
DB 70 ISDGGSTYYPDNVKG 85  
RESULT 8  
Q9BQA2 PRELIMINARY; PRT; 211 AA.  
AC Q9BQA2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE UNKNOWN (PROTEIN FOR MGC:4769) (SIMILAR TO RIKEN CDNA 181004A24A2  
DE GENE).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LUNG CARCINOMA;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LUNG CARCINOMA;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC006206; AAH06206.1; -;  
DR EMBL: BC003650; AAH03650.1; -;  
SQ SEQUENCE 211 AA; 23486 MW; 3CB581BC07F42018 CRC64;

Query Match 53.4%; Score 47; DB 4; Length 211;  
Best Local Similarity 66.7%; Pred. No. 9.3;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGGTYLDTVQ 16  
: | | | | | | | | | |  
DB 144 VSFVGSSTFYLDVQ 158

RESULT 9  
Q91Z05 PRELIMINARY; PRT; 473 AA.  
AC Q91Z05;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 51.9 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC010327; AAH10327.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 53.4%; Score 47; DB 11; Length 473;  
Best Local Similarity 50.0%; Pred. No. 23;



QY 2 VSSGGSTYVLDTVQ 16  
 ||| ||| ||| |||  
 Db 1109 VSVGSSTFYLDVAQ 1123

## RESULT 14

Q9D8L4 PRELIMINARY; PRT: 473 AA.  
 AC Q9D8L4;  
 DT 01-JUN-2001 (TREMREL. 17, Created)  
 DT 01-JUN-2001 (TREMREL. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
 DE 1810060009RIK PROTEIN.  
 GN IGH-1 OR 1810060009RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;  
 RX MEDLINE=21085660; Pubmed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombaeerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK007918; BAB25349.1; -.  
 DR HSSP; P01842; 7FAB.  
 DR MGD; MGI:96443; Igh-1.  
 DR InterPro; IPR003599; Igh.  
 DR InterPro; IPR003597; Igh-cl.  
 DR InterPro; IPR003600; Igh-like.  
 DR InterPro; IPR003006; Igh\_MHC.  
 DR InterPro; IPR003596; Igh\_v.  
 DR Pfam; PF00047; Igh; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00410; IG-like; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN1.  
 SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 52.3%; Score 46; DB 11; Length 473;  
 Best Local Similarity 47.1%; Pred. No. 33;  
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 KVSSGGSTYVLDTVQ 17  
 |:| ||||| :|  
 Db 69 KIGPGSGSTYINERFKG 85

## RESULT 15

Q60111 PRELIMINARY; PRT: 129 AA.  
 ID Q60111  
 AC Q60111;

DT 01-NOV-1996 (TREMREL. 01, Created)  
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
 DE 6-PHOSPHOGLUCONATE DEHYDROGENASE (EC 1.1.1.44) (FRAGMENT).  
 GN GND.  
 OS Yersinia pseudotuberculosis.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Yersinia.  
 OX NCBI\_TaxID=633;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GROUP V;  
 RA Thanapailai G., Lan R., Reeves P.R.;  
 RA "Molecular evolution in the gnd locus of Salmonella enterica.";  
 RL Mol. Biol. Evol. 0:0-0(1994).  
 DR EMBL; U14633; AAAS8595.1; -.  
 DR HSSP; P00349; 2PGD.  
 DR InterPro; IPR001744; 6PGD.  
 DR Pfam; PF00393; 6PGD; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 1  
 FT NON\_TER 129 129  
 SQ SEQUENCE 129 AA; 13859 MW; 8856FC8ECF4F570 CRC64;  
 Query Match 51.1%; Score 45; DB 2; Length 129;  
 Best Local Similarity 63.6%; Pred. No. 11;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 GGSTYYLDTVQ 16  
 ||:|||||:  
 Db 95 GGTTYKDTIR 105  
 Search completed: August 19, 2002, 06:58:12  
 Job time: 1402 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run On: August 19, 2002, 06:39:11 ; Search time 180.34 Seconds  
(without alignments)  
10.471 Million cell updates/sec

Title: US-09-339-922A-102

Perfect score: 88

Sequence: 1 KVSXGGSTYLDIVQG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

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- 19: /SIDS1/gcgdata/hold-geneseq/geneq-emb1/AA1998.DAT.\*
- 20: /SIDS1/gcgdata/hold-geneseq/geneq-emb1/AA1999.DAT.\*
- 21: /SIDS1/gcgdata/hold-geneseq/geneq-emb1/AA2000.DAT.\*
- 22: /SIDS1/gcgdata/hold-geneseq/geneq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	17	22 AAB61399	Enhanced 6H6LH hea
2	88	100.0	117	19 AAW76001	Vitaxin antibody h
3	88	100.0	117	19 AAW76003	LM609 antibody hea
4	88	100.0	117	20 AAY06381	Murine monoclonal
5	88	100.0	117	22 AAG53587	A heavy chain vari
6	88	100.0	117	22 AAG63589	A heavy chain vari
7	88	100.0	117	22 AAB61359	Vitaxin heavy chai
8	88	100.0	117	22 AAB61361	Antibody LM609 hea
9	88	100.0	130	20 AAY06379	Murine monoclonal
10	81	92.0	17	22 AAB61400	Enhanced LM609 VH
11	68	77.3	87	22 AAE06990	Mouse germline hea

12	68	77.3	98	22	AAE06978	Mouse germline hea
13	68	77.3	120	17	AAW00240	EGF receptor chime
14	68	77.3	123	19	AAW66099	anti-CD22 monoclon
15	67	76.1	119	16	AAW11919	Humanised MAB SK48
16	67	76.1	125	22	AAB48937	Anti-TrkA murine m
17	67	76.1	247	16	AAW11917	Murine MAB SK48-E2
18	67	76.1	295	22	AAB48934	Anti-TrkA single c
19	66	75.0	159	22	AAU14226	Human novel protel
20	65	73.9	125	20	AAV39817	Llama antibody VHH
21	64	72.7	98	22	AAE06981	Mouse germline hea
22	64	72.7	119	19	AAW69322	15D3 antibody hea
23	64	72.7	119	20	AAV32832	15D3 VH chain prot
24	64	72.7	119	20	AAW73503	Antibody 15D3 hea
25	64	72.7	138	13	AAW20064	MRK16-H chain. Ch
26	64	72.7	139	18	AAW21652	Humanised reshaped
27	64	72.7	139	18	AAW21656	Chimeric MAB 15 PC
28	64	72.7	140	18	AAW21654	Mouse MAB 15 heavy
29	63	71.6	98	21	AAB40094	Anti-hil12 antibod
30	63	71.6	98	21	AAB40095	Anti-hil12 antibod
31	63	71.6	98	21	AAB40107	Anti-hil12 antibod
32	63	71.6	98	21	AAB40108	Anti-hil12 antibod
33	63	71.6	118	18	AAW19877	CEA-specific antib
34	63	71.6	120	17	AAW88510	Vhu for antibody
35	63	71.6	132	22	AAU00576	VH ligand-binding
36	63	71.6	132	22	AAU00580	Modified VH ligand
37	63	71.6	132	22	AAU00581	Modified VH ligand
38	63	71.6	132	22	AAU00582	Modified VH ligand
39	63	71.6	132	22	AAU00583	Modified VH ligand
40	63	71.6	132	22	AAU00584	Modified VH ligand
41	62	70.5	110	18	AAW06207	Rat antibody heavy
42	62	70.5	117	19	AAW48865	Murine monoclonal
43	62	70.5	117	19	AAW48866	Chimeric humanized
44	62	70.5	117	20	AAW86135	Protein sequence o
45	62	70.5	117	20	AAW86137	Protein sequence o

ALIGNMENTS

RESULT 1

AAE061399	
ID AAB61399 standard; peptide; 17 AA.	
AC AAB61399;	
XX 03-APR-2001 (first entry)	
DT Enhanced 6H6LH heavy chain CDR2.	
DE LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;	
KW Inflammatory; cancer; retina; restenosis; osteoporosis.	
XX Unidentified.	
XX WO200078815-A1.	
XX 28-DEC-2000.	
XX 23-JUN-2000; 2000WO-US17454.	
XX 24-JUN-1999; 99US-0339922.	
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.	
XX Huse WD, Wu H;	
XX WPI; 2001-050110/06.	
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity	
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of	
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and	
PT osteoporosis -	
XX	



PS Claim 4; Page 46; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX Sequence 17 AA;

SQ

Query Match 100.0%; Score 88; DB 22; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.6e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSSGGSTYYLDTVQG 17

Db 1 kvssgggstyyldtvqg 17

IIIIIIIIIIIIIIIIII

RESULT 2

AAW76001

ID AAW76001 standard; Protein; 117 AA.

XX

AC AAW76001;

XX

DT 02-NOV-1998 (first entry)

XX

DE Vitaxin antibody heavy chain variable region protein fragment.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI: 1998-437472/37.

DR N-PSDB; AAV49820.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Claim 1; Fig 1a; 129pp; English.

XX

CC This sequence represents a fragment of the vitaxin antibody variable

CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to

CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3

CC to a ligand and thus block integrin-mediated signal transduction. This is

CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.

CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,

CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,

CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity

CC more than 90 times greater than that of parent the parent antibody.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 88; DB 19; Length 117;

Best Local Similarity 100.0%; Pred. No. 3.1e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSSGGSTYYLDTVQG 17

Db 50 kvssgggstyyldtvqg 66

IIIIIIIIIIIIIIIIII

RESULT 3

AAW76003

ID AAW76003 standard; Protein; 117 AA.

XX

AC AAW76003;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 antibody heavy chain variable region protein fragment.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI: 1998-437472/37.

DR N-PSDB; AAV49822.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Claim 43; Fig 2a; 129pp; English.

XX

CC This sequence represents the LM609 antibody variable heavy chain region.

CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3

CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus

CC block integrin-mediated signal transduction. This is useful in the

CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,

CC specifically angiogenesis and restenosis (but also e.g. (non-)immune

CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,

CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis

CC etc.). The antibodies contain non-murine framework regions so are

CC suitable for use in humans. Enhanced types of LM609 have affinity more

CC than 90 times greater than that of parent the parent antibody.

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 88; DB 19; Length 117;

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Best Local Similarity 100.0%; Pred. NO. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSSGGSTYYLDTVQG 17
Db 50 kvssggsgstyldtvqg 66

RESULT 4
ID AAY06381 standard; Protein; 117 AA.
AC AAY06381;
XX
XX
DT 06-SEP-1999 (first entry)
DE Murine monoclonal antibody LM609 VH region.
XX
XX
KW Humanised antibody; antibody humanisation; antibody engineering;
KW LM609; monoclonal antibody; complementarity determining region;
KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;
KW cancer; therapy; diagnosis.
XX
XX
OS Mus musculus.
XX
XX WO9929888-A1.
XX
XX PD 17-JUN-1999.
XX
XX PF 04-DEC-1998; 98WO-US25828.
XX
XX PR 05-DEC-1997; 97US-0986016.
XX
XX PA (SCRI ) SCRIPPS RES INST.
XX
XX PI Barbas CF, Rader C;
XX
XX DR WPI; 1999-394979/33.
XX
XX PT Production of humanized mouse monoclonal antibodies
XX
XX PS Disclosure; Page 52-53; 55pp; English.
XX
XX This sequence represents the heavy chain variable region of murine
CC monoclonal antibody LM609. LM609 is directed to integrin
CC alpha-v beta-3. It selectively promotes apoptosis of vascular
CC cells that have been stimulated to undergo angiogenesis, making it
CC a tool for cancer diagnosis and therapy. The invention provides
CC humanised antibodies, especially humanised LM609. In such humanized
CC antibodies, a light chain CDR from a mouse antibody such as LM609 is
CC grafted onto a human light chain, and a heavy chain CDR from a mouse
CC antibody is grafted onto a human antibody heavy chain to produce
CC libraries from which a humanised murine antibody having the desired
CC specificity is selected. By preserving the original CDR sequences
CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the
CC humanisation strategy ensures epitope conservation.
XX
XX Sequence 117 AA;

Query Match 100.0%; Score 88; DB 20; Length 117;
Best Local Similarity 100.0%; Pred. NO. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSSGGSTYYLDTVQG 17
Db 50 kvssggsgstyldtvqg 66

RESULT 5
ID AAG63587 standard; Protein; 117 AA.
XX

```

```

AC AAG63587;
XX
XX 15-OCT-2001 (first entry)
XX
XX A heavy chain variable region of LM609 grafted antibody.
XX
XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
XX chronic articular rheumatism; psoriasis; diabetic retinopathy;
XX neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
XX cancer.
XX
XX Synthetic.
XX OS Mus sp.
XX
XX PN US2001011125-A1.
XX
XX PD 02-AUG-2001.
XX
XX PF 30-JAN-1997; 97US-0790540.
XX
XX PR 30-JAN-1997; 97US-0790540.
XX
XX PA (HUSE/) HUSE W D.
XX
XX PI Huse WD;
XX
XX DR WPI; 2001-496171/54.
XX
XX DR N-PSDB; AAH74623.
XX
XX PT New LM609 grafted antibody exhibiting selective binding affinity to
XX alphavbeta3, comprising at least one LM609 grafted heavy and light
XX chain polypeptide, useful for diagnosing and treating e.g. inflammatory
XX disorders or cancer
XX
XX PS Claim 1; Fig 1A; 25pp; English.
XX
XX CC The present sequence represents the heavy chain variable region of the
XX grafted monoclonal antibody LM609. LM609 is a murine antibody which
XX specifically recognises the integrin alphavbeta3, and inhibits its
XX functional activity. The LM609 grafted antibody has the
XX complementarity determining regions (CDRs) substituted into a non-murine
XX framework. Nucleic acids encoding LM609 grafted heavy and light chain
XX polypeptides and fragments are useful in diagnostic and therapeutic
XX purposes, such as in the production of LM609 grafted antibodies and
XX fragments having binding specificity and inhibitory activity against
XX the integrin alphavbeta3. The antibody can be used for the diagnosis
XX or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
XX disorders, chronic articular rheumatism, psoriasis, disorders
XX associated with inappropriate or inopportune invasion of vessels such
XX as diabetic retinopathy, neovascular glaucoma and capillary
XX proliferation in atherosclerotic plaques, or cancers), and to inhibit
XX binding activity of alphavbeta3 that are necessary for progression of
XX an alphavbeta3-mediated disease.
XX
XX SQ Sequence 117 AA;

Query Match 100.0%; Score 88; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSSGGSTYYLDTVQG 17
Db 50 kvssggsgstyldtvqg 66

RESULT 6
AAG63589
ID AAG63589 standard; Protein; 117 AA.
XX
XX AAG63589;
XX
XX 15-OCT-2001 (first entry)
XX

```

```

XX DE A heavy chain variable region of LM609 antibody.
XX KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
XX KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
XX KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
XX KW cancer.
XX OS Mus sp.
XX PN US2001011125-A1.
XX PD 02-AUG-2001.
XX PF 30-JAN-1997; 97US-0790540.
XX PR 30-JAN-1997; 97US-0790540.
XX PA (HUSE/) HUSE W D.
XX PI Huse WD;
XX DR WPI; 2001-496171/54.
XX DR N-PSDB; AAH74625.
XX PT New LM609 grafted antibody exhibiting selective binding affinity to
XX PT alphavbeta3, comprising at least one LM609 grafted heavy and light
XX PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
XX PT disorders or cancer.
XX PS Disclosure; Fig 2A; 25pp; English.
XX CC The present sequence represents the heavy chain variable region of the
XX CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
XX CC recognises the integrin alphavbeta3, and inhibits its functional activity.
XX CC The specification describes a LM609 grafted antibody which has the
XX CC complementarity determining regions (CDRs) substituted into a non-murine
XX CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
XX CC polypeptides and fragments are useful in diagnostic and therapeutic
XX CC purposes, such as in the production of LM609 grafted antibodies and
XX CC fragments having binding specificity and inhibitory activity against
XX CC the integrin alphavbeta3. The antibody can be used for the diagnosis
XX CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
XX CC disorders, chronic articular rheumatism, psoriasis, disorders
XX CC associated with inappropriate or inopportune invasion of vessels such
XX CC as diabetic retinopathy, neovascular glaucoma and capillary
XX CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
XX CC binding activity of alphavbeta3 that are necessary for progression of
XX CC an alphavbeta3-mediated disease.
XX SQ Sequence 117 AA;

Query Match 100.0%; Score 88; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSXGGSGSTYYLDTVQG 17
Db 50 kvssggsgstyldtvqg 66
|||||

RESULT 7
AAB61359
ID AAB61359 standard; protein; 117 AA.
XX AC AAB61359;
XX DT 03-APR-2001 (first entry)
XX DE Antigen heavy chain variable region protein.
XX KW Vltaxin heavy chain variable region protein.
XX DE LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
XX KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

inflammatory; cancer; retina; restenosis; osteoporosis.
Unidentified.
WO200078815-A1.
28-DEC-2000.
23-JUN-2000; 2000WO-US17454.
24-JUN-1999; 99US-0339922.
(MOLE-) APPLIED MOLECULAR EVOLUTION.
Huse WD, Wu H;
WPI; 2001-050110/06.
Enhanced LM609 grafted antibodies exhibiting selective binding affinity
to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
osteoporosis -
Disclosure; Fig 1; 132pp; English.
The present invention relates to enhanced LM609 grafted antibodies
exhibiting selective binding affinity to alphavbeta3 integrin or
their functional fragments. The antibodies or their functional
fragments can be used in the diagnosis and treatment of
alphavbeta3-mediated diseases such as angiogenesis, inflammatory
diseases (such as psoriasis and chronic articular rheumatism),
disorders associated with inappropriate or inopportune invasion of
vessels (such as diabetic retinopathy, neovascular glaucoma and
cancer disorders such as tumours and Kaposi's sarcoma), retinal
diseases (such as macular degeneration), restenosis and
osteoporosis.
XX SQ Sequence 117 AA;

Query Match 100.0%; Score 88; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSXGGSGSTYYLDTVQG 17
Db 50 kvssggsgstyldtvqg 66
|||||

RESULT 8
AAB61361
ID AAB61361 standard; protein; 117 AA.
XX AC AAB61361;
XX DT 03-APR-2001 (first entry)
XX DE Antibody LM609 heavy chain variable region protein.
XX KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

```

XX Huse WD, Wu H;  
 XX WPI; 2001-050110/06.  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX Disclosure; Fig 2; 132pp; English.  
 XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX Sequence 117 AA;  
 SQ

Query Match 100.0%; Score 88; DB 22; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSSGGSTYYLDTVQG 17  
 Db | | | | | | | | | | | | | | | | | | | |  
 50 kvssgggstyyldtvqg 66

RESULT 9  
 AAY06379  
 ID AAY06379 standard; Protein; 130 AA.  
 XX  
 AC AAY06379;  
 XX  
 DT 06-SEP-1999 (first entry)  
 XX  
 DE Murine monoclonal antibody LM609 V kappa.  
 XX  
 KW Humanised antibody; antibody humanisation; antibody engineering;  
 KW LM609; monoclonal antibody; complementarity determining region;  
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;  
 KW cancer; therapy; diagnosis.  
 XX  
 OS Mus musculus.  
 XX

Key Location/Qualifiers  
 FH Peptide 1..2  
 FT /note= "vector-encoded residues"  
 FT Region 28..32  
 FT /note= "CDR1"  
 FT Region 47..63  
 FT /note= "CDR2"  
 FT Region 96..103  
 FT /note= "CDR3"  
 XX  
 PN WO9929888-A1.  
 XX  
 XX 17-JUN-1999.  
 XX  
 XX 04-DEC-1998; 98WO-US25828.  
 XX  
 XX 05-DEC-1997; 97US-0986016.  
 XX  
 XX (SCRI) SCRIPPS RES INST.  
 XX

PI Barbas CF, Rader C;  
 DR WPI; 1999-394979/33.  
 XX  
 PT Production of humanized mouse monoclonal antibodies  
 PS Disclosure; Page 49-50; 55pp; English.  
 XX  
 CC This sequence represents the light chain V kappa region of murine  
 CC monoclonal antibody LM609. LM609 is directed to integrin  
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular  
 CC cells that have been stimulated to undergo angiogenesis, making it  
 CC a tool for cancer diagnosis and therapy. The invention provides  
 CC humanised antibodies, especially humanised LM609. In such humanized  
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is  
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse  
 CC antibody is grafted onto a human antibody heavy chain to produce  
 CC libraries from which a humanised murine antibody having the desired  
 CC specificity is selected. By preserving the original CDR sequences  
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the  
 CC humanisation strategy ensures epitope conservation.  
 XX Sequence 130 AA;  
 SQ

Query Match 100.0%; Score 88; DB 20; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSSGGSTYYLDTVQG 17  
 Db | | | | | | | | | | | | | | | | | | | |  
 47 kvssgggstyyldtvqg 63

RESULT 10  
 AAB61400  
 ID AAB61400 standard; peptide; 17 AA.  
 XX  
 AC AAB61400;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Enhanced LM609 VH CDR2 peptide.  
 XX  
 KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 XX 28-DEC-2000.  
 XX  
 XX 23-JUN-2000; 2000WO-US17454.  
 XX  
 XX 24-JUN-1999; 99US-0339922.  
 XX  
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 XX Huse WD, Wu H;  
 XX  
 XX WPI; 2001-050110/06.  
 XX  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX Claim 1; Page 45; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 17 AA;

Query Match 92.0%; Score 81; DB 22; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 4.5e-06;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSGGSTYYLDTVQG 17  
 DB 1 kvssgggstyydpdvvg 17  

RESULT 11  
 AAE06990  
 ID AAE06990 standard; Protein; 87 AA.  
 XX  
 AC AAE06990;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Mouse germline heavy chain variable (VH) region, VH7183.13.  
 XX  
 KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;  
 KW AIDS; inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; VH; heavy chain variable region.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200157226-A1.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 02-FEB-2001; 2001WO-US03537.  
 XX  
 PR 03-FEB-2000; 2000US-0497625.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;  
 XX  
 DR WPI; 2001-488888/53.  
 XX  
 PS Humanized immunoglobulin for treating a CC-chemokine receptor  
 PT 2-mediated disorder in a patient, comprises a binding specificity for  
 PT CCR2, and a non-human antigen binding region and human immunoglobulin  
 PT -  
 XX  
 PS Disclosure; Page 159; 183pp; English.  
 XX  
 CC The patent discloses a humanised antibody or its antigen-binding  
 CC fragment, having binding specificity for CC-chemokine receptor 2  
 CC (CCR2), comprising an antigen binding region of non-human origin  
 CC and at least a portion of an immunoglobulin of human origin. The  
 CC humanised antibodies are useful for inhibiting the interaction of  
 CC a cell expressing CCR2. They are useful for inhibiting or treating  
 CC HIV infection. The proteins of the invention are useful for inhibiting  
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as  
 CC inflammatory disorder, autoimmune disorders such as rheumatoid

CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,  
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,  
 CC and in the manufacture of a medicament for treating CCR-2 mediated  
 CC disease. They are also useful for treating allergy, anaphylaxis,  
 CC malignancy, chronic and acute inflammation, histamine and IgE-  
 CC mediated allergic reaction, shock, stenosis, allograft rejection,  
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired  
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular  
 CC intervention, including angioplasty and/or stent placement in a mammal.  
 CC Humanised antibodies are also useful for inhibiting narrowing of the  
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of  
 CC a vessel in a mammal, preferably associated with vascular intervention.  
 CC The present sequence is mouse germline heavy chain variable (VH)  
 CC region, VH7183.13.  
 XX  
 SQ Sequence 87 AA;

Query Match 77.3%; Score 68; DB 22; Length 87;  
 Best Local Similarity 75.0%; Pred. No. 0.0029;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17  
 DB 40 isngggstyydpdvkg 55  
 :||:|||||  
 |||:|

RESULT 12  
 AAE06978  
 ID AAE06978 standard; Protein; 98 AA.  
 XX  
 AC AAE06978;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Mouse germline heavy chain variable (VH) region, V(H) 50.1.  
 XX  
 KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;  
 KW AIDS; inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; VH; heavy chain variable region.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200157226-A1.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 02-FEB-2001; 2001WO-US03537.  
 XX  
 PR 03-FEB-2000; 2000US-0497625.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;  
 XX  
 DR WPI; 2001-488888/53.  
 XX  
 PS Humanized immunoglobulin for treating a CC-chemokine receptor  
 PT 2-mediated disorder in a patient, comprises a binding specificity for  
 PT CCR2, and a non-human antigen binding region and human immunoglobulin  
 PT -  
 XX  
 PS Disclosure; Page 154-155; 183pp; English.  
 XX  
 CC The patent discloses a humanised antibody or its antigen-binding  
 CC fragment, having binding specificity for CC-chemokine receptor 2  
 CC (CCR2), comprising an antigen binding region of non-human origin

CC and at least a portion of an immunoglobulin of human origin. The  
 CC humanised antibodies are useful for inhibiting the interaction of  
 CC a cell expressing CCR2. They are useful for inhibiting or treating  
 CC HIV infection. The proteins of the invention are useful for inhibiting  
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as  
 CC inflammatory disorder, autoimmune disorders such as rheumatoid  
 CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,  
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,  
 CC and in the manufacture of a medicament for treating CCR2 mediated  
 CC disease. They are also useful for treating allergy, anaphylaxis,  
 CC malignancy, chronic and acute inflammation, histamine and IgE-  
 CC mediated allergic reaction, shock, stenosis, allograft rejection,  
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired  
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular  
 CC intervention, including angioplasty and/or stent placement in a mammal.  
 CC Humanised antibodies are also useful for inhibiting narrowing of the  
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of  
 CC a vessel in a mammal, preferably associated with vascular intervention.  
 CC The present sequence is mouse germline heavy chain variable (VH)  
 CC region, V(H)50.1.  
 XX  
 SQ Sequence 98 AA;

Query Match 77.3%; Score 68; DB 22; Length 98;  
 Best Local Similarity 75.0%; Pred. No. 0.0033;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTYLDTVQG 17  
 :|:||||| | | | |  
 Db 51 lsngggstyypdvkg 66

RESULT 13  
 AAW00240  
 ID AAW00240 standard; Protein; 120 AA.

XX AC AAW00240;

DT 22-NOV-1996 (first entry)

XX EGF receptor chimeric MAb chMint5 VH chain.

KW Mouse-human chimeric antibody; monoclonal antibody; chMint5;  
 KW Epidermal growth factor receptor; EGF-R; diagnosis; therapy;  
 KW Immunotoxin; immunocytokine; tumour; cancer.

XX OS Mus musculus.

XX FH Key Location/Qualifiers  
 XX Region 31..35  
 FT /label= CDR1  
 FT Region 51..66  
 FT /label= CDR2  
 FT Region 99..109  
 FT /label= CDR3

XX PN WO9627010-A1.

XX PD 06-SEP-1996.

XX PF 01-MAR-1996; 96WO-EP00805.

XX PR 01-MAR-1995; 95IT-OFI0036.

XX PA (ITU-Y-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.

XX PI Anastasi AM, Colnaghi MI, De Santis R, Di Massimo AM;  
 XX PI Ferrer Marsal C, Mele A;

XX DR WPI; 1996-412776/41.

XX DR N-PSDB; AAT33445.

XX

PT Murine/human chimeric monoclonal antibody, chMint5 specific for  
 PT EGF-R - shows a lower immunogenicity when administered to humans  
 XX  
 PS Claim 7; Page 15; 28pp; English.

CC The amino acid sequence (AAW00240) of the heavy chain variable region  
 CC (VH) of the epidermal growth factor receptor (EGF-R)-specific mouse-  
 CC human chimeric antibody chMint5 was deduced from a cDNA clone  
 CC (AAT33445) obtd. by PCR amplification of murine Mint5 hybridoma DSM  
 CC ACC2150 cDNA. chMint5 comprises Mint5 VH and VL regions fused  
 CC to human C-gamma and CK regions. Constructs were expressed in  
 CC CHO cell transfectants. chMint5 shows lower immunogenicity than  
 CC Mint5 when administered to humans. It can be used in diagnostic  
 CC assays or used to produce immunotoxins or immunocytokines useful  
 CC for tumour therapy.

XX SQ Sequence 120 AA;

Query Match 77.3%; Score 68; DB 17; Length 120;  
 Best Local Similarity 75.0%; Pred. No. 0.0041;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTYLDTVQG 17

Db 51 lsngggstyypdvkg 66

RESULT 14  
 AAW66099

ID AAW66099 standard; Protein; 123 AA.

XX AC AAW66099;

DT 10-DEC-1998 (first entry)

DE anti-CD22 monoclonal antibody heavy chain variable region.

KW anti-CD22 monoclonal antibody heavy chain variable region; VL;  
 KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;  
 KW malignant B-cell; immunodiagnosis; RFB4 IgG.

XX OS Mammalia.

XX FH Key Location/Qualifiers

FT Misc-difference 121

FT /note= "Encoded by gtc"

XX PN WO9841641-A1.

XX PD 24-SEP-1998.

XX PF 19-MAR-1998; 98WO-US05453.

XX PR 20-MAR-1997; 97US-0041437.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Fitzgerald D, Kreitman R, Mansfield E, Pastan I;

XX DR WPI; 1998-521227/44.

XX DR N-ESDB; AAV07642.

XX PT Recombinant anti-CD22 antibodies and immuno-conjugates - of  
 XX PT antibodies linked to a therapeutic agent, e.g. Pseudomonas exotoxin  
 XX PT or a label; for inhibiting malignant B-cells

XX PS Claim 6; Fig 1; 71pp; English.

CC The invention claims for a recombinant immunoconjugate comprising  
 CC of a therapeutic agent (e.g. Pseudomonas exotoxin) or a detectable  
 CC label peptide bonded to a recombinant anti-CD22 antibody (RFB4 IgG)  
 CC having the present variable heavy (VH) chain with a cysteine residue

CC at amino acid 44 and a variable light (VL; AAW56098) chain with a  
 CC cysteine residue at amino acid 100. The immunconjugate is claimed  
 CC to inhibit the growth of malignant B-cells in vivo, such as rodent,  
 CC canine or primate B-cells. The anti-CD22 antibody is claimed useful  
 CC for detecting CD22 protein in a sample or in vivo in a mammal, and  
 CC can be used in diagnostic kits.  
 XX  
 SQ Sequence 123 AA;

Query Match 77.3%; Score 68; DB 19; Length 123;  
 Best Local Similarity 75.0%; Pred. No. 0.0043;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17  
 :||||| ||| |||:  
 Db 51 issgggttyypdtvkg 66

RESULT 15  
 AAW11919  
 ID AAW11919 standard; Protein; 119 AA.  
 XX AC AAW11919;  
 XX  
 DT 24-JUN-1997 (first entry)  
 XX  
 DE Humanised MAb SK48-E26 heavy chain.  
 XX  
 KW Interleukin-1 beta; IL-1 beta; recombinant antibody;  
 KW humanised antibody; chimeric antibody; antibody engineering;  
 KW monoclonal antibody; MAb; SK48-E26; inflammation; therapy.  
 XX  
 OS Chimeric Homo sapiens;.  
 OS Chimeric Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..30  
 FT /label= FR1  
 FT /note= "framework region 1"  
 FT Region 31..35  
 FT /label= CDR1  
 FT /note= "complementarity determining region 1  
 FT (Claim 10, page 48)"  
 FT Region 36..49  
 FT /label= FR2  
 FT /note= "framework region 2"  
 FT Region 50..66  
 FT /label= CDR2  
 FT /note= "complementarity determining region 2  
 FT (Claim 10, page 48)"  
 FT Region 67..98  
 FT /label= FR3  
 FT /note= "framework region 3"  
 FT Region 99..108  
 FT /label= CDR3  
 FT /note= "complementarity determining region 3  
 FT (Claim 10, page 48)"  
 FT Region 109..119  
 FT /label= FR4  
 FT /note= "framework region 4"  
 XX  
 PN WO9501997-A1.  
 XX  
 PD 19-JAN-1995.  
 XX  
 PF 07-JUL-1994; 94WO-US07659.  
 XX  
 PR 09-JUL-1993; 93US-0090534.  
 PR 04-MAR-1994; 94US-0206190.  
 XX  
 PA (SHIK ) SMITHKLINE BEECHAM CORP.

PI Gross MS, Hurle MR, Jackson JR, Jonak ZL, Theisen TW;  
 PI Young PR;  
 XX  
 DR WPI; 1995-066868/09.  
 DR N-PSDB; AAT51438.  
 XX  
 PT Recombinant and humanised chimeric antibodies against human  
 PT interleukin-1-beta - for preventing and treating  
 PT interleukin-mediated inflammatory disorders  
 XX  
 PS Claim 39; Page 40-41; 62pp; English.  
 XX  
 CC The heavy chain variable region (AAW11919) and light chain variable  
 CC region (AAW11920) of humanised anti-human interleukin-1 beta (IL-1  
 CC beta) murine monoclonal antibody (MAb) SK48-E26 comprise the  
 CC complementarity determining regions from MAb SK48-E26 (see also  
 CC AAW11917-18) grafted into human frameworks. The humanised antibody  
 CC can be produced in e.g. COS cells transfected with vectors carrying  
 CC humanised heavy and light chain nucleic acids (AAT51437-39) for use  
 CC in the treatment and prevention of IL-1 mediated inflammatory  
 CC disorders.  
 XX  
 SQ Sequence 119 AA;

Query Match 76.1%; Score 67; DB 16; Length 119;  
 Best Local Similarity 75.0%; Pred. No. 0.0059;  
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17  
 :||||| ||| |||:  
 Db 51 issgggttyypdtvkg 66

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:39 ; Search time 61.75 Seconds  
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6.724 Million cell updates/sec

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**Perfect score:** 88  
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 231628

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pcp.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
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1	68	77.3	125	1	US-08-331-398A-65	Sequence 65, Appl	
2	68	77.3	125	2	US-08-331-397B-55	Sequence 65, Appl	
3	68	77.3	125	2	US-08-759-804A-64	Sequence 64, Appl	
4	67	76.1	119	5	PCR-US94-07659-6	Sequence 6, Appl	
5	67	76.1	247	5	PCR-US94-07659-2	Sequence 6, Appl	
6	64	72.7	119	2	US-08-475-000-16	Sequence 16, Appl	
7	64	72.7	119	2	US-08-483-199-16	Sequence 16, Appl	
8	64	72.7	119	2	US-08-484-508-16	Sequence 16, Appl	
9	63	71.6	117	1	US-08-264-093-22	Sequence 22, Appl	
10	63	71.6	118	2	US-08-652-816A-11	Sequence 11, Appl	
11	63	71.6	120	1	US-08-264-093-14	Sequence 14, Appl	
12	62	70.5	117	4	US-08-752-693A-3	Sequence 3, Appl	
13	62	70.5	117	4	US-08-752-693A-4	Sequence 3, Appl	
14	62	70.5	118	1	US-08-328-362-2	Sequence 2, Appl	
15	62	70.5	136	1	US-08-253-877C-57	Sequence 57, Appl	
16	62	70.5	136	2	US-08-452-164A-57	Sequence 57, Appl	
17	62	70.5	136	4	US-08-976-183A-31	Sequence 31, Appl	
18	62	70.5	136	4	US-08-976-183A-32	Sequence 32, Appl	
19	62	70.5	136	4	US-08-976-183A-33	Sequence 33, Appl	
20	62	70.5	136	4	US-08-976-183A-34	Sequence 34, Appl	
21	62	70.5	150	4	US-08-976-183A-55	Sequence 55, Appl	
22	62	70.5	158	2	US-08-653-402B-6	Sequence 6, Appl	
23	62	70.5	158	2	US-08-653-402B-10	Sequence 10, Appl	
24	62	70.5	237	2	US-08-224-591-16	Sequence 16, Appl	
25	62	70.5	237	2	US-08-926-789-16	Sequence 16, Appl	
26	62	70.5	241	2	US-08-224-591-18	Sequence 18, Appl	
27	62	70.5	241	2	US-08-926-789-18	Sequence 18, Appl	

62	70.5	265	4	US-09-430-592A-5	Sequence 5, Appl
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60	68.2	120	2	US-08-438-197-28	Sequence 28, Appl
60	68.2	120	2	US-08-438-197-30	Sequence 30, Appl
60	68.2	120	2	US-08-438-197-32	Sequence 32, Appl
60	68.2	120	2	US-08-438-197-34	Sequence 34, Appl
60	68.2	120	2	US-08-438-197-40	Sequence 40, Appl
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60	68.2	120	5	PCT-US93-10555-98	Sequence 98, Appl
60	68.2	120	5	PCT-US93-10555-100	Sequence 100, Appl

## ALIGNMENTS

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NAME/KEY: Region  
LOCATION: 1..125  
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv  
OTHER INFORMATION: Heavy chain region"  
US-08-331-398A-65

Query Match 77.3%; Score 68; DB 1; Length 125;  
Best Local Similarity 75.0%; Pred. No. 0.0018;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGTTYLDTVQG 17  
Db 51 ISNGGGSTYYPDVKG 66

RESULT 2  
US-08-331-397B-65  
Sequence 65, Application US/08331397B  
Patent No. 5981726  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Benhar, Itai  
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-Specific Antibody Fragments, Fusion Proteins, and Uses Thereof  
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses Thereof  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,397B  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126120US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..125  
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv  
OTHER INFORMATION: Heavy chain region"  
US-08-331-397B-65

Query Match 77.3%; Score 68; DB 2; Length 125;  
Best Local Similarity 75.0%; Pred. No. 0.0018;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 VSSGGGTTYLDTVQG 17  
Db 51 ISNGGGSTYYPDVKG 66

RESULT 3  
US-08-759-804A-64  
Sequence 64, Application US/08759804A  
Patent No. 5990296  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Willingham, Mark  
APPLICANT: Fitzgerald, David J.  
APPLICANT: Brinkmann, Ulrich  
APPLICANT: Pai, Lee  
TITLE OF INVENTION: Tumor-Specific Antibody Fragments, Fusion Proteins, and Uses Thereof  
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/759,804A  
FILING DATE: 03-DEC-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/331,398  
FILING DATE: 28-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-126140US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..125  
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv  
OTHER INFORMATION: Heavy chain region"  
US-08-759-804A-64

Query Match 77.3%; Score 68; DB 2; Length 125;  
Best Local Similarity 75.0%; Pred. No. 0.0018;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGTTYLDTVQG 17  
Db 51 ISNGGGSTYYPDVKG 66

Db 51 ISNGGGSTYYPDVKG 66

## RESULT 4

PCT-US94-07659-6  
; Sequence 6, Application PC/TUS9407659  
; GENERAL INFORMATION:  
; APPLICANT: Young, Peter  
; APPLICANT: Gross, Mitchell  
; APPLICANT: Jonak, Zdenka L.  
; APPLICANT: Theisen, Timothy  
; APPLICANT: Hurler, Mark  
; APPLICANT: Jackson, Jeffrey R.  
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta  
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory  
; TITLE OF INVENTION: Disorders in Man  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corp.  
; ADDRESSEE: Intellectual Property  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07659  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/090,534  
; FILING DATE: 09-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50171-1  
; TELEPHONE: (610) 270-5024  
; TELEFAX: (610) 270-5090  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US94-07659-6

Query Match 76.1%; Score 67; DB 5; Length 119;  
Best Local Similarity 75.0%; Pred. No. 0.0024; 2; Mismatches 0; Gaps 0;  
Matches 12; Conservative 2; Indels 0; Gaps 0;

Qy 2 VSSGGGSTYLDTVQG 17  
:||||| ||| |||:|  
Db 51 ISNGGGSTYYPDVKG 66

## RESULT 5

PCT-US94-07659-2  
; Sequence 2, Application PC/TUS9407659  
; GENERAL INFORMATION:  
; APPLICANT: Young, Peter  
; APPLICANT: Gross, Mitchell  
; APPLICANT: Jonak, Zdenka L.  
; APPLICANT: Theisen, Timothy  
; APPLICANT: Hurler, Mark  
; APPLICANT: Jackson, Jeffrey R.  
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta

; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory  
; TITLE OF INVENTION: Disorders in Man  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corp.  
; ADDRESSEE: Intellectual Property  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07659  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/090,534  
; FILING DATE: 09-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50171-1  
; TELEPHONE: (610) 270-5024  
; TELEFAX: (610) 270-5090  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US94-07659-2

Query Match 76.1%; Score 67; DB 5; Length 247;  
Best Local Similarity 75.0%; Pred. No. 0.0052;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VSSGGGSTYLDTVQG 17  
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Db 70 ISSGGGTYPTVKG 85

## RESULT 6

US-08-475-000-16  
; Sequence 16, Application US/08475000  
; Patent No. 5811267  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,000  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: SAVEREIDE, PAUL  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0850.007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-475-000-16

Query Match 72.7%; Score 64; DB 2; Length 119;  
Best Local Similarity 68.8%; Pred. No. 0.0068;  
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGSTYYLDTVOG 17  
:|||||:|||||:|:|  
Db 51 ISSGGGNTYYPDSVKG 66

RESULT 7  
US-08-483-199-16  
Sequence 16, Application US/08483199  
Patent No. 5849877  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,199  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVEREIDE, PAUL  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0850.009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-199-16

Query Match 72.7%; Score 64; DB 2; Length 119;  
Best Local Similarity 68.8%; Pred. No. 0.0068;  
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGSTYYLDTVOG 17  
:|||||:|||||:|:|  
Db 51 ISSGGGNTYYPDSVKG 66

RESULT 8  
US-08-484-508-16  
Sequence 16, Application US/08484508  
Patent No. 5948647  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,508  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVEREIDE, PAUL  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0850.008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-508-16

Query Match 72.7%; Score 64; DB 2; Length 119;  
Best Local Similarity 68.8%; Pred. No. 0.0068;  
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGSTYYLDTVOG 17  
:|||||:|||||:|:|  
Db 51 ISSGGGNTYYPDSVKG 66

RESULT 9  
US-08-264-093-22  
Sequence 22, Application US/08264093  
Patent No. 5639863  
GENERAL INFORMATION:  
APPLICANT: Michael D. Dan  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO  
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE  
TITLE OF INVENTION: ANTIGEN  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ridout & Maybee  
STREET: 2300 Richmond-Adelaide Centre  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 2J7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage  
COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: MS-DOS 6.00  
; SOFTWARE: ASCII Editor  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/264,093  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA: NO. 5639863 applicable  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lake, James R.  
; REGISTRATION NUMBER: 31081  
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 868-1482  
; TELEFAX: (416) 362-0823  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not applicable  
; TOPOLOGY: linear  
; US-08-264-093-22

Query Match 71.6%; Score 63; DB 1; Length 17;  
Best Local Similarity 68.8%; Pred. No. 0.0012;  
Matches 11; Conservative 3; Mismatches 2; Indels 2; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17  
;||| ||||| ||:|  
Db 2 ISSNGGTTYADSVKG 17

RESULT 10  
US-08-652-816A-11  
; Sequence 11, Application US/08652816A  
; Patent No. 5872215  
; GENERAL INFORMATION:  
; APPLICANT: Osbourn, JK  
; APPLICANT: Allen, DJ  
; APPLICANT: McGafferty, JG  
; TITLE OF INVENTION: Specific binding members, materials and  
; NUMBER OF INVENTION: methods.  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,816A  
; FILING DATE: 23-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9125579.4  
; FILING DATE: 02-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9125579.8  
; FILING DATE: 02-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206372.6  
; FILING DATE: 23-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9525004.9  
; FILING DATE: 07-DEC-1995  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9610824.6  
; FILING DATE: 23-MAY-1996  
; PRIOR APPLICATION DATA: PCT/GB92/02240  
; APPLICATION NUMBER:  
; FILING DATE: 02-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/244,597  
; FILING DATE: 01-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David W. Clough  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/33308  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-652-816A-11

Query Match 71.6%; Score 63; DB 2; Length 118;  
Best Local Similarity 68.8%; Pred. No. 0.0096;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTTYLDTVQG 17  
;||| ||||| ||:|  
Db 51 ISSNGGTTYADSVKG 66

RESULT 11  
US-08-264-093-14  
; Sequence 14, Application US/08264093  
; Patent No. 5639863  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. Dan  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO  
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE  
; TITLE OF INVENTION: ANTIGEN  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ridout & Maybee  
; STREET: 2300 Richmond-Adelaide Centre  
; STREET: 101 Richmond Street West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 2J7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: MS-DOS 6.00  
; SOFTWARE: ASCII Editor  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/264,093  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA: NO. 5639863 applicable  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lake, James R.  
; REGISTRATION NUMBER: 31081  
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 868-1482  
; TELEFAX: (416) 362-0823  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not applicable  
; TOPOLOGY: linear  
; US-08-264-093-14



SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-08-752-693A-4

Query Match 70.5%; Score 62; DB 4; Length 117;  
Best Local Similarity 68.8%; Pred. No. 0.014;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17  
:|||||:|||||:  
Db 51 ISSGGSTYYLDSVKG 66

## RESULT 14

US-08-326-362-2  
; Sequence 2, Application US/08326362  
; Patent No. 5730981  
; GENERAL INFORMATION:  
; APPLICANT: Bosslet, Klaus  
; APPLICANT: Seeman, Gerhard  
; APPLICANT: Dippold, Wolfgang  
; TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,  
; TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/326,362  
; FILING DATE:

CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/032,863  
; FILING DATE: 17-MAR-1993  
; APPLICATION NUMBER: DE P 42 08 795.3  
; FILING DATE: 19-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Einaudi, Carol P.  
; REGISTRATION NUMBER: 32,220  
; REFERENCE/DOCKET NUMBER: 02481-1276-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 118 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-326-362-2

Query Match 70.5%; Score 62; DB 1; Length 118;  
Best Local Similarity 68.8%; Pred. No. 0.014;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17  
:|||||:|||||:  
Db 51 ISSGGSTYYRDSVKG 66

## RESULT 15

US-08-253-877C-57

; Sequence 57, Application US/08253877C  
; Patent No. 5773001

GENERAL INFORMATION:  
; APPLICANT: Hamann, Philip R.  
; APPLICANT: Hinman, Lois  
; APPLICANT: Hollander, Irwin  
; APPLICANT: Holcomb, Ryan  
; APPLICANT: Hallett, William  
; APPLICANT: Tsou, Hwei-Ru  
; APPLICANT: Weiss, Martin J.  
; TITLE OF INVENTION: Conjugates of Methylthio Antitumor  
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis  
; NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07470-8426  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/253,877C  
; FILING DATE: 03-JUN-1994  
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 32,368  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-831-3246  
; TELEFAX: 201-831-3305  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-253-877C-57

Query Match 70.5%; Score 62; DB 1; Length 136;  
Best Local Similarity 68.8%; Pred. No. 0.016;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGSTYYLDTVQG 17  
:|||||:|||||:  
Db 70 ISSGGSTYYLDSVKG 85

Search completed: August 19, 2002, 06:34:40  
Job time: 1201 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:04 ; Search time 78.53 Seconds  
(Without alignments)  
20.801 Million cell updates/sec

Title: US-09-339-922A-104

Perfect score: 91

Sequence: 1 KVSSGGSTYYPTVQG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	89.0	113	2 S26468	Ig heavy chain V r
2	81	89.0	117	1 HVMS34	Ig heavy chain pre
3	78	85.7	117	1 HVMS84	Ig heavy chain pre
4	77	84.6	108	2 PL0248	Ig heavy chain V r
5	77	84.6	111	2 PH1007	Ig heavy chain V r
6	74	81.3	108	2 PH1006	Ig heavy chain V r
7	74	81.3	118	2 S20641	Ig heavy chain V r
8	74	81.3	138	2 S09258	Ig heavy chain V r
9	72	79.1	113	2 S02717	Ig heavy chain V r
10	72	79.1	115	2 PH1538	Ig H chain V regio
11	72	79.1	117	1 HVMSRF	Ig heavy chain pre
12	72	79.1	119	2 PH1548	Ig H chain V regio
13	72	79.1	119	2 PH1549	Ig H chain V regio
14	70	76.9	111	2 S51211	Ig heavy chain V r
15	69	75.8	117	2 PH1552	Ig H chain V regio
16	68	74.7	117	2 PH1553	Ig H chain V regio
17	68	74.7	121	2 H27888	Ig heavy chain V r
18	68	74.7	254	2 B31790	Ig heavy chain V r
19	67	73.6	118	2 S00700	Ig heavy chain V r
20	67	73.6	119	2 PH0098	Ig heavy chain V r
21	67	73.6	124	2 I27888	Ig heavy chain V r
22	66	72.5	106	2 PH1008	Ig heavy chain V r
23	66	72.5	108	2 PH1011	Ig heavy chain V r
24	66	72.5	123	2 G37888	Ig heavy chain V r
25	65	71.4	83	2 S25913	Ig heavy chain V r
26	65	71.4	94	2 S14580	Ig heavy chain V r
27	65	71.4	102	2 S14581	Ig heavy chain V r
28	65	71.4	108	2 PH1010	Ig heavy chain V r
29	65	71.4	111	2 S40090	Ig heavy chain - m

30 65 71.4 119 2 F27888 Ig heavy chain V r  
31 65 71.4 119 2 B34353 anti-peptide Fab'  
32 65 71.4 120 2 S55336 Ig heavy chain V r  
33 65 71.4 120 2 S55337 Ig heavy chain V r  
34 65 71.4 122 2 E27888 Ig heavy chain V r  
35 64 70.3 70 2 PL0250 Ig heavy chain V r  
36 64 70.3 97 1 HVMS91 Ig heavy chain V r  
37 64 70.3 112 2 S26327 Ig heavy chain V r  
38 64 70.3 112 2 A27889 Ig heavy chain V r  
39 64 70.3 117 2 PL0249 Ig heavy chain V r  
40 64 70.3 117 2 PL0252 Ig heavy chain V r  
41 63 69.2 121 2 I27887 Ig heavy chain V r  
42 63 69.2 123 2 S63597 Ig heavy chain V r  
43 63 69.2 124 2 C27888 Ig heavy chain V r  
44 63 69.2 548 2 S38864 Ig epsilon chain C  
45 62 68.1 114 2 PH1009 Ig heavy chain V r

#### ALIGNMENTS

RESULT 1

S26468  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S26468  
R:Kavaler, J.  
submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <KAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 89.0%; Score 81; DB 2; Length 113;  
Best Local Similarity 87.5%; Pred. No. 2.3e-05;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGSTYYPTVQG 17

Db 47 ISSGGSTYYPTVKG 62

RESULT 2

HVMS34

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 31-Mar-1997

C:Accession: JT0502

R:Levy, N.S.; Malpietro, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0502

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A>Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 89.0%; Score 81; DB 1; Length 117;  
 Best Local Similarity 87.5%; Pred. No. 2.4e-05;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17  
 :|||||:|  
 Db 70 ISSGGGTTYPTVKG 85

## RESULT 3

HVMS84  
 Ig heavy chain precursor V region (5-84) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 31-Mar-1997  
 C:Accession: J0505  
 R:Levy, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
 J. Exp. Med. 169, 2007-2019, 1989  
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
 A:Reference number: J0501; MUID:89279149  
 A:Accession: J0505  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-117 <LEV>  
 A:Experimental source: strain BALB/cJ  
 A:Note: this sequence belongs to the VH7183 subfamily  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <WAT>  
 F:34-117/Domain: immunoglobulin homology <IMM>  
 F:41-115/Disulfide bonds: #status predicted

Query Match 85.7%; Score 78; DB 1; Length 117;  
 Best Local Similarity 81.2%; Pred. No. 6.9e-05;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17  
 :|||||:|  
 Db 70 ISNGGGTTYPTVKG 85

## RESULT 4

PL0248  
 Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
 C:Accession: PL0248  
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
 J. Exp. Med. 171, 263-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A:Reference number: PL0231; MUID:90111618  
 A:Accession: PL0248  
 A:Molecule type: mRNA  
 A:Residues: 1-108 <SHL>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-24/Region: framework 1  
 F:9-92/Domain: immunoglobulin homology <IMM>  
 F:25-29/Region: complementarity-determining 1  
 F:30-43/Region: framework 2  
 F:44-60/Region: complementarity-determining 2  
 F:61-92/Region: framework 3  
 F:93-99/Region: complementarity-determining 3  
 F:100-108/Region: framework 4

Query Match 84.6%; Score 77; DB 2; Length 108;  
 Best Local Similarity 81.2%; Pred. No. 9e-05;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17  
 :|||||:|

Db 45 ISSGGGTTYPDSVKG 60

## RESULT 5

PHI007  
 Ig heavy chain V region (clone 163-cl) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PHI007  
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective  
 A:Reference number: PH0971; MUID:92381444  
 A:Accession: PHI007  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <TIL>  
 A:Experimental source: B cell, strain [NZB x NZW]F1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.6%; Score 77; DB 2; Length 111;  
 Best Local Similarity 81.2%; Pred. No. 9.3e-05;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17  
 :|||||:|  
 Db 51 ISSGGGTTYPDSVKG 66

## RESULT 6

PHI006  
 Ig heavy chain V region (clone 202.33) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PHI006  
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective  
 A:Reference number: PH0971; MUID:92381444  
 A:Accession: PHI006  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-108 <TIL>  
 A:Experimental source: B cell, strain [NZB x NZW]F1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 74; DB 2; Length 108;  
 Best Local Similarity 75.0%; Pred. No. 0.00026;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17  
 : |||:|||||  
 Db 46 ISGGGNTYPTVKG 61

## RESULT 7

S20641  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C:Accession: S20641  
 R:Lozman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.  
 submitted to the EMBL Data Library, February 1992  
 A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice re  
 A:Reference number: S20639  
 A:Accession: S20641  
 A:Status: preliminary



A:Molecule type: DNA  
 A:Residues: 1-118 <LOS>  
 A:Cross-references: EMBL:X65003; NID:952602; PIDN:CAA46136.1; PID:g52603  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 74; DB 2; Length 118;  
 Best Local Similarity 75.0%; Pred. No. 0.00029;  
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VSSGGSTYYPDTVQG 17  
 Db 51 ISSGGNTYYPDSVKG 66

RESULT 8  
 S09258  
 Ig heavy chain V region precursor - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 23-Jul-1999  
 C:Accession: S09258  
 R:Hamada, H.; Maerzawa, K.; Tsuruo, T.  
 Nucleic Acids Res. 18, 1900, 1990  
 A:Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK  
 A:Reference number: S09258; MUID:90245594  
 A:Accession: S09258  
 A:Molecule type: DNA  
 A:Residues: 1-138 <HAM>  
 A:Cross-references: EMBL:X51719; NID:953207; PIDN:CAA36012.1; PID:g297545  
 C:Genetics:  
 A:Introns: 16/1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.3%; Score 74; DB 2; Length 130;  
 Best Local Similarity 75.0%; Pred. No. 0.00034;  
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VSSGGSTYYPDTVQG 17  
 Db 70 ISSGGNTYYPDSVKG 85

RESULT 9  
 S02717  
 Ig heavy chain V region (clone pH62) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C:Accession: S02717  
 R:Sollazzo, M.; Hasemann, C.A.; Meek, K.D.; Glotz, D.; Capra, J.D.; Zanetti, M.  
 submitted to the EMBL Data Library, February 1989  
 A:Reference number: S02717  
 A:Accession: S02717  
 A:Molecule type: DNA  
 A:Residues: 1-113 <SOL>  
 A:Cross-references: EMBL:Y00744; NID:952472; PIDN:CAA68713.1; PID:g1334095  
 A:Note: this sequence was determined from the differentiated gene  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 72; DB 2; Length 113;  
 Best Local Similarity 75.0%; Pred. No. 0.00056;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSSGGSTYYPDTVQG 17  
 Db 51 INSGGNTYYPDTVKG 66

RESULT 10  
 PH1538  
 Ig H chain V region (clone l3G12) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jan-2000  
 C:Accession: PH1538  
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.  
 J. Exp. Med. 177, 1105-1116, 1993  
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoforma  
 A:Reference number: PH1528; MUID:93210465  
 A:Accession: PH1538  
 A:Molecule type: mRNA  
 A:Residues: 1-115 <MUR>  
 A:Note: the stop codons X appear in residues 82, 85 and 106  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:14-99/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 72; DB 2; Length 115;  
 Best Local Similarity 75.0%; Pred. No. 0.00057;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSSGGSTYYPDTVQG 17  
 Db 50 INSGGNTYYPDTVKG 65

RESULT 11  
 HVMSRF  
 Ig heavy chain precursor V region (RF) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 31-Mar-1997  
 C:Accession: JT0503  
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
 J. Exp. Med. 169, 2007-2019, 1989  
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar  
 A:Reference number: JT0501; MUID:89279149  
 A:Accession: JT0503  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-117 <LEV>  
 A:Experimental source: strain BALB/cJ  
 A:Note: this sequence belongs to the VH7183 subfamily  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; hybridoma; immunoglobulin  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-117/Product: Ig heavy chain V region (RF) #status predicted <MAT>  
 F:34-117/Domain: immunoglobulin homology <IMM>  
 F:41-115/Disulfide bonds: #status predicted

Query Match 79.1%; Score 72; DB 1; Length 117;  
 Best Local Similarity 75.0%; Pred. No. 0.00058;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSSGGSTYYPDTVQG 17  
 Db 70 INSGGNTYYPDTVKG 85

RESULT 12  
 PH1548  
 Ig H chain V region (clone l2F4) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1548  
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.  
 J. Exp. Med. 177, 1105-1116, 1993  
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoforma  
 A:Reference number: PH1528; MUID:93210465

A:Accession: PH1548  
A:Molecule type: mRNA  
A:Residues: 1-119 <MUK>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 72; DB 2; Length 119;  
Best Local Similarity 75.0%; Pred. No. 0.00059;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17  
: : | | | | | | | | :  
DB 51 INSHGGTTYPTVKG 66

## RESULT 13

PH1549  
Ig H chain V region (clone 13F1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1549  
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.  
J. Exp. Med. 177, 1105-1116, 1993  
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans  
A:Reference number: PH1528; MUID:93210465  
A:Accession: PH1549  
A:Molecule type: mRNA  
A:Residues: 1-119 <MUK>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 72; DB 2; Length 119;  
Best Local Similarity 75.0%; Pred. No. 0.00059;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17  
: : | | | | | | | | :  
DB 51 INSHGGTTYPTVKG 66

## RESULT 14

S51211  
Ig heavy chain V region (AC7) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 01-Aug-1995 #sequence\_revision 01-Dec-1995 #text\_change 30-May-1997  
C:Accession: S51211; S58929  
R:Jarrin, A.; Andrieux, A.; Chapel, A.; Buchou, T.; Marguerie, G.  
FEBS Lett. 354, 169-172, 1994  
A:Title: A synthetic peptide with anti-platelet activity derived from a CDR of an anti-G  
A:Reference number: S51210; MUID:95046326  
A:Accession: S51211  
A:Molecule type: mRNA  
A:Residues: 9-111 <JAR>  
A:Accession: S58929  
A:Molecule type: protein  
A:Residues: 1-20 <JAR2>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 70; DB 2; Length 111;  
Best Local Similarity 75.0%; Pred. No. 0.0011;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17  
: : | | | | | | | | :  
DB 51 INSHGGTTYPTVKG 66

## RESULT 15

PH1552  
Ig H chain V region (clone 16E4) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jan-2000  
C:Accession: PH1552  
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.  
J. Exp. Med. 177, 1105-1116, 1993  
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoforma  
A:Reference number: PH1528; MUID:93210465  
A:Accession: PH1552  
A:Molecule type: mRNA  
A:Residues: 1-117 <MUK>

A:Note: the stop codon X appears in residue 87  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 69; DB 2; Length 117;  
Best Local Similarity 68.8%; Pred. No. 0.0017;  
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTTYPTVQG 17  
: : | | | | | | | | :  
DB 51 INTNGGTTYPTVKG 66

Search completed: August 19, 2002, 06:36:05  
Job time: 1286 sec



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OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0505; HVMS84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 54 FRAMEWORK-2.
FT DOMAIN 55 68 FRAMEWORK-3.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 85.7%; Score 78; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 2.5e-05;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGSTYYPDVTG 17
DB 70 ISNGGSTYYPDVTGK 85

RESULT 3
HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0503; HVMSRF.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.

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FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 79.1%; Score 72; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.00021;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGSTYYPDVTG 17
DB 70 ISNGGSTYYPDVTGK 85

RESULT 4
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0504; HVMS91.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 70.3%; Score 64; DB 1; Length 97;
Best Local Similarity 78.6%; Pred. No. 0.0029;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SGGGSTYYPDVTG 17
DB 52 SSGGSTYYPDVTGK 65

RESULT 5
HV57_MOUSE
ID HV57_MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

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RT "Early onset of somatic mutation in immunoglobulin VH genes during  
 the primary immune response."  
 RL J. Exp. Med. 168:2007-2019(1989).  
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.  
 DR PIR: JT0501; HVMS96.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region.  
 FT NON\_TER 98  
 SQ SEQUENCE 98 AA: 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 67.0%; Score 61; DB 1; Length 98;  
 Best Local Similarity 62.5%; Pred. No. 0.0085;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17  
 :||| |||||:|  
 Db 51 ISDGGTYYPDSVKG 66

## RESULT 6

HV58\_MOUSE  
 ID HV58\_MOUSE STANDARD; PRT; 117 AA.  
 AC P18529;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 5-76 precursor.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/CJ;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during  
 the primary immune response."  
 RL J. Exp. Med. 168:2007-2019(1989).  
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.  
 DR PIR: JT0506; HVMS57.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA: 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 67.0%; Score 61; DB 1; Length 117;  
 Best Local Similarity 68.8%; Pred. No. 0.01;  
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17  
 :||| |||||:|  
 Db 70 ISSGLXTYYPDSVKG 85

## RESULT 7

HV3C\_HUMAN

ID HV3C\_HUMAN STANDARD; PRT; 117 AA.  
 AC P01764;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-III region VH26 precursor.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81101090; PubMed=6450418;  
 RA Matthysens G., Rabbitts T.H.;  
 RT "Structure and multiplicity of genes for the human immunoglobulin  
 heavy chain variable region."  
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----

EMBL: J00236; AAA53516.1; -;  
 DR EMBL: M35415; AAA58735.1; -;  
 DR PIR: A02047; H3HU26.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1  
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA: 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 63.7%; Score 58; DB 1; Length 117;  
 Best Local Similarity 62.5%; Pred. No. 0.03;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17  
 :| ||||| :|  
 Db 70 ISGSGGTYYGDSVKG 85

## RESULT 8

HV3L\_HUMAN  
 ID HV3L\_HUMAN STANDARD; PRT; 119 AA.  
 AC P01773;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-III region BUR.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE (MVELOMA PROTEIN BUR).  
 RX MEDLINE=79151016; PubMed=107164;  
 RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;  
 RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal  
 IgA1 protease, digestion, Fab and Fc fragments, and the complete  
 amino acid sequence of the alpha 1 heavy chain."  
 RL J. Biol. Chem. 254:2865-2874(1979).  
 DR PIR: A02056; ALHUBR.  
 DR HSSP: P01772; 2IG2.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.

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DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Glycoprotein.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 58.2%; Score 53; DB 1; Length 119;
Best Local Similarity 56.2%; Pred. No. 0.18;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGSTYYPTVQV 17
:| | | | | | | | | |
Db 51 ISYGSBYADSVRG 66

RESULT 9
HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8814476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR; B28966; B28966.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 41 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 57.1%; Score 52; DB 1; Length 116;
Best Local Similarity 75.0%; Pred. No. 0.25;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGSTYYPTVQV 17
:| | | | | | | | | |
Db 73 GGSTYYADSVKG 84

RESULT 10
HV59_MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)

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DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO507; HVMS39.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 57.1%; Score 52; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 0.25;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGSTYYPTVQV 17
:| | | | | | | | | |
Db 70 ISGGVSYTYPPDSVKG 85

RESULT 11
CELFBACSU STANDARD; PRT; 442 AA.
AC P46320;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Probable 6-phospho-beta-glucosidase (EC 3.2.1.86).
GN CELF OR CELF OR LICH.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97144536; PubMed=8950303;
RA Tobisch S., Glaser P., Krueger S., Hecker M.;
RT "Identification and characterization of a new beta-glucoside
RT utilization system in Bacillus subtilis.";
RL J. Bacteriol. 179:496-506(1997).
RN [2]
RP SEQUENCE OF 1-305 FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE=97124196; PubMed=8969509;
RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
RA Miwa Y., Fujita Y.;
RT "Sequencing of a 65 kb region of the Bacillus subtilis genome
RT containing the lic and cel loci, and creation of a 177 kb contig
RT covering the gnt-sacXI region.";
RL Microbiology 142:3113-3123(1996).

```



RT "Cellobiose-6-phosphate hydrolase (Celf) of Escherichia coli:  
 RT characterization and assignment to the unusual family 4 of  
 RL glycosylhydrolases.";

CC J. Bacteriol. 181:7339-7345(1999).

CC -1- FUNCTION: HYDOLYZES A WIDE VARIETY OF P-BETA-GLUCOSIDES INCLUDING  
 CC CELLUBIOSE-6P, SALICIN-6P, ARBUTIN-6P, GENTIOBIOS-6P, METHYL-  
 CC BETA-GLUCOSIDE-6P AND P-NITROPHENYL-BETA-D-GLUCOPYRANOSIDE-6P.

CC -1- CATALYTIC ACTIVITY: 6-phospho-beta-D-glucoside-(1,4)-D-glucose +  
 CC H(2)O = D-glucose 6-phosphate + glucose.

CC -1- COFACTOR: NAD AND A DIVALENT METAL ION. MANGANESE, COBALT AND  
 CC NICKEL IONS ENHANCE ACTIVITY WHEREAS MAGNESIUM, CALCIUM,  
 CC STRONTIUM AND ZINC IONS DO NOT.

CC -1- PATHWAY: FERMENTATION OF THE BETA-GLUCOSIDES CELLOBIOSE,  
 CC ARBUTIN, AND SALICIN.

CC -1- SIMILARITY: BELONGS TO FAMILY 4 OF GLYCOSYL HYDROLASES.

CC -1- CAUTION: REF.1 AND REF.4 SEQUENCES DIFFER FROM THAT SHOWN IN  
 CC POSITIONS 371 ONWARD DUE TO NUMBER OF FRAMESHIFTS AS WELL AS OTHER  
 CC SEQUENCE ERRORS.

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CC EMBL; X52890; CAA37073.1; ALT\_FRAME.

DR EMBL; M64438; AAA23550.1; -.

DR EMBL; M64438; AAC74804.1; -.

DR EMBL; D90816; BAA15515.1; -.

DR EMBL; D90817; BAA15523.1; -.

DR EMBL; X66725; CAA47257.1; ALT\_FRAME.

DR EMBL; X66725; CAA47259.1; ALT\_FRAME.

PIR; S10874; S10874.

DR EcGene; EG10144; celf.

DR InterPro; IPR001088; Glyco\_hydro\_4.

DR Pfam; PF02056; Glyco\_hydro\_4; 1.

DR PRINTS; PR00732; GLYDRLASE4.

DR PRODOM; PD006892; Glyco\_hydro\_4; 1.

DR PROSITE; PS01324; GLYCOSYL\_HYDROL\_F4; 1.

DR Hydrolase; Glycosidase; NAD; Cobalt; Manganese; Nickel;

KW Complete proteome.

FT INIT\_MET 0 0

FT NP\_BIND 6 39 NAD (POTENTIAL).

FT ACT\_SITE 111 111 PROTON DONOR (BY SIMILARITY).

FT ACT\_SITE 355 355 NUCLEOPHILE (BY SIMILARITY).

SQ SEQUENCE 449 AA; 50381 MW; 1B36FFDE05E0AE56 CRC64;

Query Match 52.7%; Score 48; DB 1; Length 449;

Best Local Similarity 50.0%; Pred. No. 4.2;

Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17

Db 7 VTIGGSSYTPPELLGG 22

I: |||||:|:|:

RESULT 14

HV16\_MOUSE

ID HV16\_MOUSE STANDARD; PRT; 136 AA.

AC P01783;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region MOPC 21 precursor (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81234548; PubMed=6788376;

RA Bothwell A.D.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,

RA Baltimore D.;

RT "Heavy chain variable region contribution to the NPb family of  
 RL antibodies: somatic mutation evident in a gamma 2a variable region.";

RL Cell 24:625-637(1981).

RN [2]

RP SEQUENCE OF 17-136.

RA MEDLINE=77100368; PubMed=401950;

RA Adetugbo K., Milstein C., Secher D.S.;

RT "Molecular analysis of spontaneous somatic mutants.";

RL Nature 265:299-304(1977).

CC

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CC EMBL; J00522; AAD15290.1; -.

DR PIR; A02066; GIMS21.

DR HSSP; P01772; 2F84.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Signal.

FT NON\_TER 1 1

FT SIGNAL <1 16

FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.

FT DOMAIN 115 119 D SEGMENT.

FT DOMAIN 120 136 JH4 SEGMENT.

FT DISULFID 38 112

FT CONFLICT 75 78 HVAD -> DYAH (IN REF. 2).

FT CONFLICT 89 90 DN -> ND (IN REF. 2).

FT CONFLICT 115 115 W -> H (IN REF. 2).

FT CONFLICT 120 120 Y -> W (IN REF. 2).

FT NON\_TER 136 136

SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 51.6%; Score 47; DB 1; Length 136;

Best Local Similarity 50.0%; Pred. No. 1.7;

Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17

Db 67 ISSGSSTLHYADTVKG 82

I: ||||:|:|:|:

RESULT 15

HV02\_CANFA

ID HV02\_CANFA STANDARD; PRT; 117 AA.

AC P01785;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region MOO.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE OF 1-112.

RA MEDLINE=77242268; PubMed=407924;

RA Wasserman R.L., Capra J.D.;

RT "Primary structure of the variable regions of two canine

immunoglobulin heavy chains.";

RL Biochemistry 16:3160-3168(1977).

RN [2]

RP SEQUENCE OF 113-117.



RX MEDLINE=80077682; PubMed=117299;  
RA McCumber L.J., Capra J.D.;  
RT "The complete amino-acid sequence of a canine mu chain.";  
RL Mol. Immunol. 16:565-570(1979).  
CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A02068; MHDGMO.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT NON\_TER 117  
SQ SEQUENCE 117 AA; 12703 MW; FCE07309E0A84B35 CRC64;

Query Match 49.5%; Score 45; DB 1; Length 117;  
Best Local Similarity 57.1%; Pred. No. 3;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 4 SGGGSTYYPDTVQG 17  
Db 52 SSSGQTYADAVKG 65

Search completed: August 19, 2002, 06:59:09  
Job time: 1374 sec

GenCore version 4.5  
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# OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:12 ; Search time 140.4 Seconds  
(without alignments)  
20.947 Million cell updates/sec

Title: US-09-339-922a-104  
Perfect score: 91  
Sequence: 1 KVSSGGSTYYPDTVQG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

1: SPREMBL19:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	71.4	119	11 Q920E7	Q920E7 mus musculus
2	60	65.9	487	11 Q99KA4	Q99KA4 mus musculus
3	59	64.8	597	4 Q96BB9	Q96BB9 homo sapien
4	58	63.7	121	4 Q9UL71	Q9UL71 homo sapien
5	58	63.7	479	11 Q9LWP5	Q9LWP5 mus musculus
6	57	62.6	486	11 Q9L207	Q9L207 mus musculus
7	51	56.0	118	4 Q9UL72	Q9UL72 homo sapien
8	51	56.0	345	10 Q94HD3	Q94HD3 oryza sativ
9	51	56.0	440	16 Q92EC0	Q92EC0 listeria in
10	49	53.8	124	5 Q95TE1	Q95TE1 drosophila
11	49	53.8	421	2 Q9L260	Q9L260 streptomyc
12	48	52.7	440	16 Q9KSH2	Q9KSH2 vibrio chol
13	48	52.7	442	16 Q9KGC1	Q9KGC1 bacillus ha
14	48	52.7	480	11 Q9LXEL	Q9LXEL mus musculus
15	47	51.6	415	16 Q9X108	Q9X108 thermotoga
16	47	51.6	438	16 Q92ED4	Q92ED4 listeria in

17	47	51.6	441	16 Q9KEE0	Q9KEE0 bacillus ha
18	47	51.6	473	11 Q9D8L4	Q9D8L4 mus musculus
19	47	51.6	473	11 Q91Z05	Q91Z05 mus musculus
20	46	50.5	129	2 Q60111	Q60111 yersinia ps
21	46	50.5	258	5 Q9Y0E9	Q9Y0E9 drosophila
22	46	50.5	331	5 Q9VR49	Q9VR49 drosophila
23	46	50.5	426	2 Q9REW0	Q9REW0 erwinia chr
24	46	50.5	435	16 Q928S8	Q928S8 listeria in
25	46	50.5	724	16 Q926C6	Q926C6 rhizobium m
26	45	49.5	162	10 Q9FJ12	Q9FJ12 arabidopsis
27	45	49.5	446	2 Q59351	Q59351 escherichia
28	45	49.5	594	8 Q9T3A0	Q9T3A0 nephroselm
29	45	49.5	965	10 Q9FV66	Q9FV66 flavaria tr
30	45	49.5	1439	5 Q9VC41	Q9VC41 drosophila
31	44	48.4	211	11 Q9D8R6	Q9D8R6 mus musculus
32	44	48.4	348	16 Q92UR6	Q92UR6 rhizobium m
33	44	48.4	437	11 Q9R1A4	Q9R1A4 mus musculus
34	44	48.4	517	11 Q63206	Q63206 rattus norv
35	44	48.4	738	3 Q13658	Q13658 schizosacch
36	43	47.3	112	4 Q9HCC1	Q9HCC1 homo sapien
37	43	47.3	532	16 Q97IF3	Q97IF3 clostridium
38	43	47.3	798	2 Q9RKF0	Q9RKF0 streptomyc
39	43	47.3	857	5 Q9VR54	Q9VR54 drosophila
40	43	47.3	912	10 Q9SUE7	Q9SUE7 arabidopsis
41	43	47.3	962	12 Q89443	Q89443 african swi
42	43	47.3	1301	17 Q96Y03	Q96Y03 sulfolobus
43	43	47.3	2316	2 Q9FDJ9	Q9FDJ9 bacteroides
44	42.5	46.7	93	4 Q9UIV4	Q9UIV4 homo sapien
45	42.5	46.7	95	6 Q9GMH2	Q9GMH2 macaca mula

## ALIGNMENTS

### RESULT 1

ID Q920E7 PRELIMINARY; PRT; 119 AA.  
AC Q920E7;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE PTERIN-MIMICKING ANTI-IDIOTOPE HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaltis O., Cotton R.G.H.;  
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307937; AAL09421.1; -  
FT NON\_TER  
FT NON\_TER 119 119  
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match 71.4%; Score 65; DB 11; Length 119;  
Best Local Similarity 68.8%; Pred. No. 0.01; Indels 0; Gaps 0;  
Matches 11; Conservative 3; Mismatches 2;

### QY 2 VSSGGSTYYPDTVQG 17

Db 51 ISSGGSTYYPDSVKG 66  
:|||||:|||||:|

### RESULT 2

ID Q99KA4 PRELIMINARY; PRT; 487 AA.  
AC Q99KA4;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL 52.6 KDA PROTEIN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC004786; AAH04786.1; -.  
 DR HSP; P01810; 2FBJ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003600; Ig\_like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00409; Ig; 3.  
 DR SMART; SM00407; Igcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00410; IG\_Like; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 65.9%; Score 60; DB 11; Length 487;  
 Best Local Similarity 62.5%; Pred. No. 0.29; Indels 4; Gaps 0;  
 Matches 10; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

QY 2 VSSGGGTTYPTVQV 17  
 :||| ||||| :|||  
 Db 70 ISDGGSTYYPDNVKG 85

RESULT 3  
 Q96BB9 ID Q96BB9 PRELIMINARY; PRT; 597 AA.  
 AC Q96BB9  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL 55.0 KDA PROTEIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PRIMARY B-CELLS FROM TONSILS;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC015760; AAHL5760.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 64.8%; Score 59; DB 4; Length 597;  
 Best Local Similarity 62.5%; Pred. No. 0.52;  
 Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 2 VSSGGGTTYPTVQV 17  
 :||| ||||| :|||  
 Db 70 ISDGGSTYYPDNVKG 85

RESULT 4  
 Q9UL71 ID Q9UL71 PRELIMINARY; PRT; 121 AA.  
 AC Q9UL71  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035043; AAD56279.1; -.  
 DR HSP; P01772; 2FB4.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR NON\_TER 1  
 FT NON\_TER 121  
 FT SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 63.7%; Score 58; DB 4; Length 121;  
 Best Local Similarity 62.5%; Pred. No. 0.13;  
 Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 2 VSSGGGTTYPTVQV 17  
 :||| ||||| :|||  
 Db 51 ISDGGSTYYADSVKG 66

RESULT 5  
 Q91WP5 ID Q91WP5 PRELIMINARY; PRT; 479 AA.  
 AC Q91WP5  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL 51.6 KDA PROTEIN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=COLON;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC013656; AAHL3656.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 479 AA; 51603 MW; ECB2D087748584F CRC64;

Query Match 63.7%; Score 58; DB 11; Length 479;  
 Best Local Similarity 56.2%; Pred. No. 0.58;  
 Matches 9; Conservative 5; Mismatches 2; Indels 2; Gaps 0;

QY 2 VSSGGGTTYPTVQV 17  
 :||| ||||| :|||  
 Db 70 INSGNGTYYSDTMKG 85

RESULT 6  
 Q91Z07 ID Q91Z07 PRELIMINARY; PRT; 486 AA.  
 AC Q91Z07  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE HYPOTHETICAL 52.7 KDA PROTEIN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.; 2001) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC010324; AAH0324.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;  
  
 Query Match 62.6%; Score 57; DB 11; Length 486;  
 Best Local Similarity 64.3%; Pred. No. 0.85;  
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
 Qy 4 SGGSGTYPPTVQG 17  
 Db 71 TSGGNTYPDNVKG 84  
  
 RESULT 7  
 Q9UL72 PRELIMINARY; PRT; 118 AA.  
 AC Q9UL72;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-98277139; PubMed-9614934;  
 RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035042; AAD56278.1; -.  
 DR HSSP; P01772; 2FB4.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 FT NON\_TER 118 118  
 FT SEQUENCE 118 AA; 12872 MW; B4D1A594B2D5CCA CRC64;  
 SQ SEQUENCE 118 AA; 12872 MW; B4D1A594B2D5CCA CRC64;  
  
 Query Match 56.0%; Score 51; DB 4; Length 118;  
 Best Local Similarity 56.2%; Pred. No. 1.6;  
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
 Qy 2 VSSGGSTYPPTVQG 17  
 Db 50 VTYGGSSYADSVKG 65  
  
 RESULT 8  
 Q94HD3 PRELIMINARY; PRT; 345 AA.  
 AC Q94HD3;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PUTATIVE PROTEIN WITH SIMILARITY TO GLUCAN

DE ENDO-1,3-BETA-GLUCOSIDASE.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-NIPPONBARE;  
 RC Spiegel L., de la Bastide M., Nascimento L., Kirchoff K., King L.,  
 RA Preston R., Vil M.D., Baker J., Bell M., Zutavern T., Santos L.,  
 RA Miller B., Rodriguez S., Cunnius D.M., Kuit K., Ballija V., Shah R.,  
 RA Bahret A., Bal H., O'Shaughnessy A., Dedhia N., McCombie W.R.;  
 RA "Genomic Sequence for Oryza sativa, Nipponbare strain, clone  
 RT OSUNBA0045C13, from Chromosome 10.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NIPPONBARE;  
 RA McCombie W.R.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NIPPONBARE;  
 RA McCombie W.R.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NIPPONBARE;  
 RA Palmer L.E., Spiegel L., de la Bastide M., Nascimento L., Kirchoff K.,  
 RA King L., Preston R., Vil M.D., Baker J., Bell M., Zutavern T.,  
 RA Santos L., Miller B., Rodriguez S., Cunnius D.M., Kuit K., Ballija V.,  
 RA Shah R., Bahret A., Bal H., O'Shaughnessy A., Dedhia N.,  
 RA McCombie W.R.;  
 RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AC079634; AAK92657.1; -.  
 DR SEQUENCE 345 AA; 35127 MW; 43BFC3A924D08A94 CRC64;  
 SQ SEQUENCE 345 AA; 35127 MW; 43BFC3A924D08A94 CRC64;  
  
 Query Match 56.0%; Score 51; DB 10; Length 345;  
 Best Local Similarity 66.7%; Pred. No. 5.1;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
 Qy 4 SGGSGTYPPTV 15  
 Db 288 SGGSGCFYPDNI 299  
  
 RESULT 9  
 Q92EC0 PRELIMINARY; PRT; 440 AA.  
 ID Q92EC0;  
 AC Q92EC0;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE LIN0540 PROTEIN.  
 GN LIN0540.  
 OS Listeria innocua.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Listeria.  
 OX NCBI\_TaxID=1642;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CLIP 11262 / SEROVAR 6A;  
 RX PubMed-11679669;  
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,  
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,  
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deloux P.,  
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,  
 RA Etian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,  
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,  
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

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RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL596165; CAC95772.1; -.
DR ListiList; LIN00540; -.
KW Complete proteome.
SQ SEQUENCE 440 AA; 49273 MW; 5DAE3008B4241E83 CRC64;

Query Match 56.0%; Score 51; DB 16; Length 440;
Best Local Similarity 56.2%; Pred. No. 6.7;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 VSSGGSTYYPDTVOG 17
l: ||||| l: l:l
Db 8 VTIGGSSYTPELVEG 23

RESULT 10
Q95TE1 PRELIMINARY; PRT; 124 AA.
AC Q95TE1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE LD25304P.
GN CG12581.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY059451; AAL13357.1; -.
SQ SEQUENCE 124 AA; 13415 MW; C3280F3689AA469E CRC64;

Query Match 53.8%; Score 49; DB 5; Length 124;
Best Local Similarity 61.5%; Pred. No. 3.5;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGSTYYPDTVOG 17
||||| l:l:l
Db 106 GGGASYGPDVKG 118

RESULT 11
Q9L260 PRELIMINARY; PRT; 421 AA.
AC Q9L260
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE SUGAR HYDROLASE.
GN SC6D10.04.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;

```

```

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL138538; CAB71199.1; -.
DR InterPro; IPR001088; Glyco_hydro_4.
DR Pfam; PF02056; Glyco_hydro_4; 1.
DR PRINTS; PR00732; GLHYDRLASE4.
DR ProDom; PD006892; Glyco_hydro_4; 1.
KW Hydrolase.
SQ SEQUENCE 421 AA; 45017 MW; 3FCC9D4135567035 CRC64;

Query Match 53.8%; Score 49; DB 2; Length 421;
Best Local Similarity 61.5%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGGSTYYPDTVOG 17
||||| l: l:
Db 7 GGGSTYTPELIDG 19

RESULT 12
Q9KSH2 PRELIMINARY; PRT; 440 AA.
AC Q9KSH2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 6-PHOSHO-BETA-GLUCOSIDASE.
GN VC1284.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004207; AAF94443.1; -.
DR TIGR; VC1284; -.
DR InterPro; IPR001088; Glyco_hydro_4.
DR Pfam; PF02056; Glyco_hydro_4; 1.
DR PRINTS; PR00732; GLHYDRLASE4.
DR ProDom; PD006892; Glyco_hydro_4; 1.
KW Complete proteome.
SQ SEQUENCE 440 AA; 48512 MW; 65A3C3A1742C7486 CRC64;

Query Match 52.7%; Score 48; DB 16; Length 440;
Best Local Similarity 61.5%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:39:12 ; Search time 180.34 Seconds  
(without alignments)  
10.471 Million cell updates/sec

Title: US-09-339-922A-104  
Perfect score: 91  
Sequence: 1 KVSNGGSGSYPPDTVOG 17

Scoring table: BLOSSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq\_032802.\*

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6:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
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9:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
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19:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
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22:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	91	100.0	17	22	AAE06978
2	81	89.0	17	22	AAW00240
3	81	89.0	117	19	AAW76001
4	81	89.0	117	19	AAW76003
5	81	89.0	117	20	AAW06381
6	81	89.0	117	22	AAG63587
7	81	89.0	117	22	AAG63589
8	81	89.0	117	22	AAG61359
9	81	89.0	117	22	AAE061361
10	81	89.0	130	20	AAW06379
11	78	85.7	87	22	AAE06990

12	78	85.7	98	22	AAE06978	Mouse germline hea
13	78	85.7	120	17	AAW00240	EGF receptor chine
14	78	85.7	123	19	AAW66099	anti-CD22 monoclon
15	77	84.6	119	16	AAW11919	Humanised MAB SK48
16	77	84.6	125	22	AAW48937	Anti-TrkA murine m
17	77	84.6	247	16	AAW11917	Murine MAB SK48-E2
18	77	84.6	295	22	AAW48934	Anti-TrkA single c
19	74	81.3	98	22	AAE06981	Mouse germline hea
20	74	81.3	119	20	AAW69322	15D3 antibody heav
21	74	81.3	119	19	AAW32832	15D3 VH chain prot
22	74	81.3	119	20	AAW73503	Antibody 15D3 heav
23	74	81.3	138	13	AAW20064	MRK16-H chain. Ch
24	74	81.3	139	18	AAW21652	Humanised reshaped
25	74	81.3	139	18	AAW21656	Chimeric MAB 15 PC
26	74	81.3	140	18	AAW21654	Mouse MAB 15 heav
27	72	79.1	158	18	AAW19577	Mouse anti-idiotyp
28	72	79.1	158	18	AAW19577	Mouse anti-idiotyp
29	71	78.0	136	11	AAW06251	Variable region of
30	71	78.0	249	22	AAW20435	Anti-FIX/fixa anti
31	71	78.0	249	22	AAW20436	Anti-FIX/fixa anti
32	71	78.0	294	22	AAW20442	Anti-FIX/fixa anti
33	71	78.0	325	22	AAW20438	Anti-FIX/fixa anti
34	71	78.0	732	22	AAW20437	Anti-FIX/fixa anti
35	70	76.9	17	18	AAW27342	CDR2 from murine a
36	70	76.9	117	16	AAW79155	Human IgE receptor
37	70	76.9	117	18	AAW27357	Heavy chain variab
38	70	76.9	117	18	AAW27526	Heavy chain variab
39	70	76.9	117	18	AAW27354	Heavy chain variab
40	70	76.9	131	22	AAW84293	Amino acid sequenc
41	70	76.9	239	20	AAW73874	Human antiFc epsil
42	70	76.9	242	20	AAW73876	Human antiFc epsil
43	68	74.7	89	22	AAE06985	Mouse germline hea
44	68	74.7	117	16	AAW79157	Human IgE receptor
45	68	74.7	247	9	AAW80156	Biosynthetic antib

#### ALIGNMENTS

RESULT 1  
AAB61400  
ID AAB61400 standard; peptide; 17 AA.  
XX AAB61400;  
AC AAB61400;  
DT 03-APR-2001 (first entry)  
XX  
DE Enhanced LM609 VH CDR2 peptide.  
XX  
KW LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis.  
XX  
OS Unidentified.  
XX  
PN WO200078815-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 23-JUN-2000; 2000WO-US17454.  
XX  
PR 24-JUN-1999; 99US-0339922.  
XX  
(MOLE-) APPLIED MOLECULAR EVOLUTION.

PA Huse WD, Wu H;  
PI  
XX  
DR WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis -  
XX

PS Claim 1; Page 45; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

SQ Sequence 17 AA;

Query Match 100.0%; Score 91; DB 22; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.1e-07; Mismatches 0; Gaps 0;

Matches 17; Conservative 0; Indels 0; Indels 0; Gaps 0;

QY 1 KVSSGGGTYPTVQV 17

Db 1 kvssgggstypdtvqg 17

|||||

RESULT 2

AAB61399

ID AAB61399 standard; peptide; 17 AA.

XX AAB61399;

AC AAB61399;

XX AAB61399;

DT 03-APR-2001 (first entry)

XX Enhanced 6H6LH heavy chain CDR2.

DE

XX LM609; grafted antibody; alphaVbeta<sub>3</sub> integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

OS

XX WO200078815-A1.

PN 28-DEC-2000.

XX

PD 23-JUN-2000; 2000WO-US17454.

PF 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA Huse WD, Wu H;

XX WPI; 2001-050110/06.

DR Enhanced LM609 grafted antibodies exhibiting selective binding affinity

XX to alpha(V)beta<sub>3</sub> integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX Claim 4; Page 46; 132pp; English.

PS The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX SQ Sequence 17 AA;

Query Match 89.0%; Score 81; DB 22; Length 17;

Best Local Similarity 94.1%; Pred. No. 4e-06; Mismatches 1; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSGGGTYPTVQV 17

Db 1 kvssgggstypdtvqg 17

|||||

RESULT 3

AAW76001

ID AAW76001 standard; Protein; 117 AA.

XX AAW76001;

AC AAW76001;

XX 02-NOV-1998 (first entry)

DT

XX Vitaxin antibody heavy chain variable region protein fragment.

DE

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

XX Mus sp.

OS

XX WO9833919-A2.

PN 06-AUG-1998.

XX

PD 30-JAN-1998; 98WO-US01826.

PF 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

PI WPI; 1998-437472/37.

XX N-PSDB; AAV49820.

DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta<sub>3</sub>

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX Claim 1; Fig 1a; 129pp; English.

PS This sequence represents a fragment of the vitaxin antibody variable

XX heavy chain region. Vitaxin and the antibody LM609 bind selectively to

CC integrin alphaVbeta<sub>3</sub> and can be used to inhibit binding of alphaVbeta<sub>3</sub>

CC to a ligand and thus block integrin-mediated signal transduction. This is

CC useful in the treatment, prevention and diagnosis of alphaVbeta<sub>3</sub>-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.

CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,

CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,

CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity

CC more than 90 times greater than that of parent the parent antibody.

XX Sequence 117 AA;

SQ

Query Match 89.0%; Score 81; DB 19; Length 117;

Best Local Similarity 94.1%; Pred. No. 3.5e-05; Mismatches 1; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSGGGTYPTVQV 17





XX US2001011125-A1.  
 PN 02-AUG-2001.  
 XX 30-JAN-1997; 97US-0790540.  
 XX 30-JAN-1997; 97US-0790540.  
 XX (HUSE/) HUSE W D.  
 XX Huse WD;  
 PI WPI; 2001-496171/54.  
 XX N-PSDB; AAH74625.  
 XX New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer  
 XX Claim 1; Fig 1A; 25pp; English.  
 PS The present sequence represents the heavy chain variable region of the  
 XX grafted monoclonal antibody LM609. LM609 is a murine antibody which  
 CC specifically recognises the integrin alphavbeta3, and inhibits its  
 CC functional activity. The LM609 grafted antibody has the  
 CC complementarity determining regions (CDRs) substituted into a non-murine  
 CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis  
 CC of disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 CC an alphavbeta3-mediated disease.  
 XX Sequence 117 AA;  
 SQ Query Match 89.0%; Score 81; DB 22; Length 117;  
 Best Local Similarity 94.1%; Pred. No. 3.5e-05;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KVSSGGGSTYYPDVQV 17  
 Db ||||| ||||| |||||  
 50 kvssgggstyyldtvqg 66  
 RESULT 7  
 AAG63589  
 ID AAG63589 standard; Protein; 117 AA.  
 AC AAG63589;  
 XX 15-OCT-2001 (first entry)  
 DT A heavy chain variable region of LM609 antibody.  
 XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer.  
 XX Mus sp.  
 OS US2001011125-A1.  
 XX 02-AUG-2001.  
 PN 02-AUG-2001.  
 XX 30-JAN-1997; 97US-0790540.  
 XX 30-JAN-1997; 97US-0790540.  
 XX (HUSE/) HUSE W D.  
 XX Huse WD;  
 PI WPI; 2001-496171/54.  
 XX N-PSDB; AAH74625.  
 XX New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer  
 XX Claim 1; Fig 1A; 25pp; English.  
 PS The present sequence represents the heavy chain variable region of the  
 XX grafted monoclonal antibody LM609. LM609 is a murine antibody which  
 CC specifically recognises the integrin alphavbeta3, and inhibits its  
 CC functional activity. The LM609 grafted antibody has the  
 CC complementarity determining regions (CDRs) substituted into a non-murine  
 CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis  
 CC of disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 CC an alphavbeta3-mediated disease.  
 XX Sequence 117 AA;  
 SQ Query Match 89.0%; Score 81; DB 22; Length 117;  
 Best Local Similarity 94.1%; Pred. No. 3.5e-05;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KVSSGGGSTYYPDVQV 17  
 Db ||||| ||||| |||||  
 50 kvssgggstyyldtvqg 66  
 RESULT 7  
 AAG63589  
 ID AAG63589 standard; Protein; 117 AA.  
 AC AAG63589;  
 XX 15-OCT-2001 (first entry)  
 DT A heavy chain variable region of LM609 antibody.  
 XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer.  
 XX Mus sp.  
 OS US2001011125-A1.  
 XX 02-AUG-2001.  
 PN 02-AUG-2001.  
 XX 30-JAN-1997; 97US-0790540.  
 XX 30-JAN-1997; 97US-0790540.  
 XX (HUSE/) HUSE W D.  
 XX Huse WD;  
 PI WPI; 2001-496171/54.  
 XX N-PSDB; AAH74625.  
 XX New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer  
 XX Claim 1; Fig 1A; 25pp; English.  
 PS The present sequence represents the heavy chain variable region of the  
 XX grafted monoclonal antibody LM609. LM609 is a murine antibody which  
 CC specifically recognises the integrin alphavbeta3, and inhibits its  
 CC functional activity. The LM609 grafted antibody has the  
 CC complementarity determining regions (CDRs) substituted into a non-murine  
 CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis  
 CC of disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 CC an alphavbeta3-mediated disease.  
 XX Sequence 117 AA;  
 SQ Query Match 89.0%; Score 81; DB 22; Length 117;  
 Best Local Similarity 94.1%; Pred. No. 3.5e-05;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KVSSGGGSTYYPDVQV 17  
 Db ||||| ||||| |||||  
 50 kvssgggstyyldtvqg 66  
 RESULT 8  
 AAB61359  
 ID AAB61359 standard; protein; 117 AA.  
 AC AAB61359;  
 XX 03-APR-2001 (first entry)  
 DT Vitaxin heavy chain variable region protein.  
 XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 XX Unidentified.  
 OS WO200078815-A1.  
 XX 28-DEC-2000.  
 PD 23-JUN-2000; 2000WO-US17454.  
 XX 24-JUN-1999; 99US-0339922.  
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;  
 PI WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -

XX Disclosure; Fig 1; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX Sequence 117 AA;

Query Match 89.0%; Score 81; DB 22; Length 117;  
 Best Local Similarity 94.1%; Pred. No. 3.5e-05;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSEGGSTYYPTVQG 17  
 |||||

Db 50 kvssggstyyldtvqg 66

RESULT 9

AA61361  
 ID AAB61361 standard; protein; 117 AA.

XX AAB61361;

DT 03-APR-2001 (first entry)

XX Antibody LM609 heavy chain variable region protein.

XX LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US17454.

PR 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -

XX Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX Sequence 117 AA;

Query Match 89.0%; Score 81; DB 22; Length 117;  
 Best Local Similarity 94.1%; Pred. No. 3.5e-05;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSEGGSTYYPTVQG 17  
 |||||

Db 50 kvssggstyyldtvqg 66

RESULT 10

AA61361  
 ID AAY06379 standard; protein; 130 AA.

XX AAY06379;

XX 06-SEP-1999 (first entry)

XX Murine monoclonal antibody LM609 V kappa.

XX Humanised antibody; antibody humanisation; antibody engineering;  
 KW LM609; monoclonal antibody; complementarity determining region;  
 KW CDR grafting; mouse; human; integrin; apoptosis; angiogenesis;  
 KW cancer; therapy; diagnosis.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..2 /note= "vector-encoded residues"

FT Region 28..32 /note= "CDR1"

FT Region 47..63 /note= "CDR2"

FT Region 96..103 /note= "CDR3"

XX WO9929888-A1.

XX 17-JUN-1999.

XX 04-DEC-1998; 98WO-US25828.

XX 05-DEC-1997; 97US-0986016.

XX (SCRI ) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 1999-394979/33.

XX Production of humanized mouse monoclonal antibodies

XX Disclosure; Page 49-50; 55pp; English.

XX This sequence represents the light chain V kappa region of murine  
 CC monoclonal antibody LM609. LM609 is directed to integrin  
 CC alpha-v beta-3. It selectively promotes apoptosis of vascular  
 CC cells that have been stimulated to undergo angiogenesis, making it  
 CC a tool for cancer diagnosis and therapy. The invention provides

CC humanised antibodies, especially humanised LM609. In such humanized  
 CC antibodies, a light chain CDR from a mouse antibody such as LM609 is  
 CC grafted onto a human light chain, and a heavy chain CDR from a mouse  
 CC antibody is grafted onto a human antibody heavy chain to produce  
 CC libraries from which a humanised murine antibody having the desired  
 CC specificity is selected. By preserving the original CDR sequences  
 CC such as the HCDR3 and LCDR3 sequences of LM609 (see AAY06371-72), the  
 CC humanisation strategy ensures epitope conservation.

XX Sequence 130 AA;

Query Match 89.0%; Score 81; DB 20; Length 130;  
 Best Local Similarity 94.1%; Pred. No. 3.9e-05;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSSGGSTYYPDTVOG 17  
 ||||| ||||| |||||

DB 47 kvssggstyyldtvqg 63

RESULT 11

AAE06990  
 ID AAE06990 standard; Protein; 87 AA.

AC AAE06990;

DT 16-OCT-2001 (first entry)

DE Mouse germline heavy chain variable (VH) region, VH7183.13.

XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 XX neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioptasty; acquired immune deficiency syndrome;  
 KW AIDS; inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; VH; heavy chain variable region.

OS Mus sp.

PN WO200157226-A1.

XX 09-AUG-2001.

PF 02-FEB-2001; 2001WO-US03537.

PR 03-FEB-2000; 2000US-0497625.

XX (MILL-) MILLENNIUM PHARM INC.

PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

DR WPI; 2001-488888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor  
 PT 2-mediated disorder in a patient, comprises a binding specificity for  
 PT CCR2, and a non-human antigen binding region and human immunoglobulin

PS Disclosure; Page 159; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding  
 CC fragment, having binding specificity for CC-chemokine receptor 2  
 CC (CCR2), comprising an antigen binding region of non-human origin  
 CC and at least a portion of an immunoglobulin of human origin. The  
 CC humanised antibodies are useful for inhibiting the interaction of  
 CC a cell expressing CCR2. They are useful for inhibiting or treating  
 CC HIV infection. The proteins of the invention are useful for inhibiting  
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as  
 CC inflammatory disorder, autoimmune disorders such as rheumatoid

CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,  
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,  
 CC and in the manufacture of a medicament for treating CCR-2 mediated  
 CC disease. They are also useful for treating allergy, anaphylaxis,  
 CC malignancy, chronic and acute inflammation, histamine and IgE-  
 CC mediated allergic reaction, shock, stenosis, allograft rejection,  
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired  
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular  
 CC intervention, including angioplasty and/or stent placement in a mammal.  
 CC Humanised antibodies are also useful for inhibiting narrowing of the  
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of  
 CC a vessel in a mammal, preferably associated with vascular intervention.  
 CC The present sequence is mouse germline heavy chain variable (VH)  
 CC region, VH7183.13.

XX Sequence 87 AA;

Query Match 85.7%; Score 78; DB 22; Length 87;  
 Best Local Similarity 81.2%; Pred. No. 7.4e-05;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGSTYYPDTVOG 17

DB 40 isngggstyyptvkg 55

RESULT 12

AAE06978

ID AAE06978 standard; Protein; 98 AA.

AC AAE06978;

XX 16-OCT-2001 (first entry)

DE Mouse germline heavy chain variable (VH) region, V(H) 50.1.

XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioptasty; acquired immune deficiency syndrome;  
 KW AIDS; inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; VH; heavy chain variable region.

OS Mus sp.

PN WO200157226-A1.

XX 09-AUG-2001.

PF 02-FEB-2001; 2001WO-US03537.

PR 03-FEB-2000; 2000US-0497625.

XX (MILL-) MILLENNIUM PHARM INC.

PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

DR WPI; 2001-488888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor  
 PT 2-mediated disorder in a patient, comprises a binding specificity for  
 PT CCR2, and a non-human antigen binding region and human immunoglobulin

PS Disclosure; Page 154-155; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding  
 CC fragment, having binding specificity for CC-chemokine receptor 2  
 CC (CCR2), comprising an antigen binding region of non-human origin

CC and at least a portion of an immunoglobulin of human origin. The  
 CC humanised antibodies are useful for inhibiting the interaction of  
 CC a cell expressing CCR2. They are useful for inhibiting or treating  
 CC HIV infection. The proteins of the invention are useful for inhibiting  
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as  
 CC inflammatory disorder, autoimmune disorders such as rheumatoid  
 CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,  
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,  
 CC and in the manufacture of a medicament for treating CCR-2 mediated  
 CC disease. They are also useful for treating allergy, anaphylaxis,  
 CC malignancy, chronic and acute inflammation, histamine and IGE-  
 CC mediated allergic reaction, shock, stenosis, allograft rejection,  
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired  
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular  
 CC intervention, including angioplasty and/or stent placement in a mammal.  
 CC Humanised antibodies are also useful for inhibiting narrowing of the  
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of  
 CC a vessel in a mammal, preferably associated with vascular intervention.  
 CC The present sequence is mouse germline heavy chain variable (VH)  
 CC region, V(H)50.1.

XX SQ Sequence 98 AA;

Query Match 85.7%; Score 78; DB 22; Length 98;  
 Best Local Similarity 81.2%; Pred. No. 8.5e-05;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTYPTVQV 17  
 :|:|||||||:|  
 Db 51 isngggstyptvkg 66

RESULT 13

AAW00240  
 ID AAW00240 standard; Protein; 120 AA.

XX AC AAW00240;

XX DT 22-NOV-1996 (first entry)

XX DE EGF receptor chimeric MAb chMint5 VH chain.

XX KW Mouse-human chimeric antibody; monoclonal antibody; chMint5;  
 KW epidermal growth factor receptor; EGF-R; diagnosis; therapy;  
 KW immunotoxin; immunocytokine; tumour; cancer.

XX OS Mus musculus.

XX FH Key Location/Qualifiers  
 FT Region 31..35  
 FT /label= CDR1  
 FT Region 51..66  
 FT /label= CDR2  
 FT Region 99..109  
 FT /label= CDR3

XX PN W09627010-A1.

XX XX 06-SEP-1996.

XX XX 01-MAR-1996; 96WO-EP00805.

XX XX 01-MAR-1995; 95IT-OFT0036.

XX PA (ITU-Y) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.

XX PI Anastasi AM, Colnaghi MI, De Santis R, Di Massimo AM;  
 PI Ferrer Marsal C, Mele A;

XX DR WPI; 1996-412776/41.

XX DR N-PSDB; AAT33445.

XX

PT Murine/human chimeric monoclonal antibody, chMint5 specific for  
 PT EGF-R - shows a lower immunogenicity when administered to humans  
 XX  
 PS Claim 7; Page 15; 28pp; English.

XX The amino acid sequence (AAW00240) of the heavy chain variable region  
 CC (VH) of the epidermal growth factor receptor (EGF-R)-specific mouse-  
 CC human chimeric antibody chMint5 was deduced from a cDNA clone  
 CC (AA33445) obtd. by PCR amplification of murine Mint5 hybridoma DSM  
 CC ACC2150 cDNA. chMint5 comprises Mint5 VH and VL regions fused  
 CC to human C-gamma1 and CK regions. Constructs were expressed in  
 CC CHO cell transfectants. chMint5 shows lower immunogenicity than  
 CC Mint5 when administered to humans. It can be used in diagnostic  
 CC assays or used to produce immunotoxins or immunocytokines useful  
 CC for tumour therapy.

XX SQ Sequence 120 AA;

Query Match 85.7%; Score 78; DB 17; Length 120;  
 Best Local Similarity 81.2%; Pred. No. 0.00011;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTYPTVQV 17  
 :|:|||||||:|  
 Db 51 isngggstyptvkg 66

RESULT 14

AAW66099  
 ID AAW66099 standard; Protein; 123 AA.

XX AC AAW66099;

XX DT 10-DEC-1998 (first entry)

XX DE anti-CD22 monoclonal antibody heavy chain variable region.

XX KW anti-CD22 monoclonal antibody heavy chain variable region; VL;  
 KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;  
 KW malignant B-cell; immunodiagnosis; RFB4 IgG.

XX OS Mammalia.

XX FH Key Location/Qualifiers  
 FT Misc-difference 121  
 FT /note= "Encoded by gtc"

XX PN W09841641-A1.

XX PD 24-SEP-1998.

XX PF 19-MAR-1998; 98WO-US05453.

XX PR 20-MAR-1997; 97US-0041437.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Fitzgerald D, Kreitman R, Mansfield E, Pastan I;

XX DR WPI; 1998-521227/44.

XX DR N-PSDB; AAV07642.

XX PT Recombinant anti-CD22 antibodies and immuno-conjugates - of  
 PT antibodies linked to a therapeutic agent, e.g. Pseudomonas exotoxin  
 PT or a label; for inhibiting malignant B-cells

XX PS Claim 6; Fig 1; 71pp; English.

XX The invention claims for a recombinant immunoconjugate comprising  
 CC of a therapeutic agent (e.g. Pseudomonas exotoxin) or a detectable  
 CC label peptide bonded to a recombinant anti-CD22 antibody (RFB4 IgG)  
 CC having the present variable heavy (VH) chain with a cysteine residue

CC at amino acid 44 and a variable light (VL; AAW66098) chain with a  
 CC cysteine residue at amino acid 100. The immunconjugate is claimed  
 CC to inhibit the growth of malignant B-cells in vivo, such as rodent,  
 CC canine or primate B-cells. The anti-CD22 antibody is claimed useful  
 CC for detecting CD22 protein in a sample or in vivo in a mammal, and  
 CC can be used in diagnostic kits.

XX SQ Sequence 123 AA;

Query Match 85.7%; Score 78; DB 19; Length 123;  
 Best Local Similarity 81.2%; Pred. No. 0.00011;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 VSSGGGTYYPDTVOG 17  
 :|||||:|||||:  
 Db 51 issgggttyyptvkg 66

RESULT 15  
 AAW11919  
 ID AAW11919 standard; Protein; 119 AA.  
 XX AC AAW11919;  
 XX DT 24-JUN-1997 (first entry)  
 XX DE Humanised MAB SK48-E26 heavy chain.  
 XX KW Interleukin-1 beta; IL-1 beta; recombinant antibody;  
 KW humanised antibody; chimeric antibody; antibody engineering;  
 KW monoclonal antibody; MAB; SK48-E26; inflammation; therapy.  
 XX OS Chimeric Homo sapiens;.  
 OS Chimeric Mus sp.  
 XX FH Key Location/Qualifiers  
 FT Region 1..30  
 FT /label= FR1  
 FT /note= "framework region 1"  
 FT Region 31..35  
 FT /label= CDR1  
 FT /note= "complementarity determining region 1  
 FT (Claim 10, page 48)"  
 FT Region 36..49  
 FT /label= FR2  
 FT /note= "framework region 2"  
 FT Region 50..66  
 FT /label= CDR2  
 FT /note= "complementarity determining region 2  
 FT (Claim 10, page 48)"  
 FT Region 67..98  
 FT /label= FR3  
 FT /note= "framework region 3"  
 FT Region 99..108  
 FT /label= CDR3  
 FT /note= "complementarity determining region 3  
 FT (Claim 10, page 48)"  
 FT Region 109..119  
 FT /label= FR4  
 FT /note= "framework region 4"  
 XX PN WO9501997-A1.  
 XX PD 19-JAN-1995.  
 XX PF 07-JUL-1994; 94WO-US07659.  
 XX PR 09-JUL-1993; 93US-0090534.  
 XX PR 04-MAR-1994; 94US-0206190.  
 XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX

PI Gross MS, Hurle MR, Jackson JR, Jonak ZL, Theisen TW;  
 PI Young PR;  
 XX WPI; 1995-066868/09.  
 DR N-PSDB; AAT51438.  
 XX Recombinant and humanised chimeric antibodies against human  
 PT interleukin-1-beta - for preventing and treating  
 PT interleukin-mediated inflammatory disorders  
 XX Claim 39; Page 40-41; 62pp; English.  
 XX The heavy chain variable region (AAW11919) and light chain variable  
 CC region (AAW11920) of humanised anti-human interleukin-1 beta (IL-1  
 CC beta) murine monoclonal antibody (MAB) SK48-E26 comprise the  
 CC complementarity determining regions from MAB SK48-E26 (see also  
 CC AAW11917-18) grafted into human frameworks. The humanised antibody  
 CC can be produced in e.g. COS cells transfected with vectors carrying  
 CC humanised heavy and light chain nucleic acids (AAT51437-39) for use  
 CC in the treatment and prevention of IL-1 mediated inflammatory  
 CC disorders.  
 XX SQ Sequence 119 AA;

Query Match 84.6%; Score 77; DB 16; Length 119;  
 Best Local Similarity 81.2%; Pred. No. 0.00015;  
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 VSSGGGTYYPDTVOG 17  
 :|||||:|||||:  
 Db 51 issgggttyyptvkg 66

Search completed: August 19, 2002, 06:39:12  
 Job time: 1473 sec

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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:40 ; Search time 61.75 Seconds  
(without alignments)  
6.724 Million cell updates/sec

Title: US-09-339-922A-104

Perfect score: 91

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Scoring table: BLOSUM62

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Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	85.7	125	1	US-08-331-398A-65
2	78	85.7	125	2	US-08-331-397B-65
3	78	85.7	125	2	US-08-759-804A-64
4	77	84.6	119	5	PCT-US94-07659-6
5	77	84.6	247	5	PCT-US94-07659-2
6	74	81.3	119	2	US-08-475-000-16
7	74	81.3	119	2	US-08-483-199-16
8	74	81.3	119	2	US-08-484-508-16
9	72	79.1	158	2	US-08-653-402B-6
10	72	79.1	158	2	US-08-653-402B-10
11	65	71.4	32	4	US-08-525-539A-35
12	65	71.4	109	2	US-08-793-490-6
13	65	71.4	116	2	US-08-888-366-12
14	65	71.4	116	2	US-08-888-366-12
15	64	70.3	17	5	PCT-US93-08435-18
16	64	70.3	118	5	PCT-US93-08435-10
17	64	70.3	122	5	PCT-US93-08435-12
18	64	70.3	122	5	PCT-US93-08435-14
19	64	70.3	122	5	PCT-US93-08435-43
20	63	69.2	17	1	US-08-264-093-22
21	63	69.2	118	2	US-08-652-816A-11
22	63	69.2	120	1	US-08-264-093-14
23	62	68.1	118	1	US-08-326-362-2
24	62	68.1	135	4	US-08-579-378A-16
25	62	68.1	135	4	US-08-579-378A-20
26	62	68.1	443	5	PCT-US96-13152-4
27	61	67.0	123	1	US-08-356-272-3

28	61	67.0	300	2	US-08-661-052-4	Sequence 4, Appl
29	61	67.0	300	4	US-09-188-082-4	Sequence 4, Appl
30	61	67.0	301	2	US-08-661-052-14	Sequence 14, Appl
31	61	67.0	301	4	US-09-188-082-14	Sequence 14, Appl
32	61	67.0	553	2	US-08-661-052-16	Sequence 16, Appl
33	61	67.0	553	4	US-09-188-082-16	Sequence 16, Appl
34	60	65.9	120	2	US-08-428-197-20	Sequence 20, Appl
35	60	65.9	120	2	US-08-428-197-22	Sequence 22, Appl
36	60	65.9	120	2	US-08-428-197-24	Sequence 24, Appl
37	60	65.9	120	2	US-08-428-197-26	Sequence 26, Appl
38	60	65.9	120	2	US-08-428-197-28	Sequence 28, Appl
39	60	65.9	120	2	US-08-428-197-30	Sequence 30, Appl
40	60	65.9	120	2	US-08-428-197-32	Sequence 32, Appl
41	60	65.9	120	2	US-08-428-197-34	Sequence 34, Appl
42	60	65.9	120	2	US-08-428-197-40	Sequence 40, Appl
43	60	65.9	120	5	PCT-US93-10555-20	Sequence 20, Appl
44	60	65.9	120	5	PCT-US93-10555-22	Sequence 22, Appl
45	60	65.9	120	5	PCT-US93-10555-24	Sequence 24, Appl

#### ALIGNMENTS

RESULT 1  
US-08-331-398A-65  
; Sequence 65, Application US/08331398A  
; Patent No. 5608039  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Willingham, Mark  
; APPLICANT: Fitzgerald, David  
; APPLICANT: Brinkmann, Ulrich  
; APPLICANT: Pai, Lee  
; TITLE OF INVENTION: 'Single Chain B3 Antibody Fusion Proteins  
; TITLE OF INVENTION: and Their Uses (as amended)  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/331,398A  
; FILING DATE: 28-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-1261100S  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 125 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:

; NAME/KEY: Region  
 ; LOCATION: 1..125  
 ; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv  
 ; OTHER INFORMATION: Heavy chain region"  
 US-08-331-398A-65

Query Match 85.7%; Score 78; DB 1; Length 125;  
 Best Local Similarity 81.2%; Pred. No. 0.0001;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17  
 :|:|||||||||:|  
 Db 51 ISNGGGTYYPDTVKG 66

RESULT 2  
 US-08-331-397B-65  
 ; Sequence 65, Application US/08331397B  
 ; Patent No. 5981726  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pastan, Ira  
 ; APPLICANT: Benhar, Itai  
 ; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-  
 ; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses  
 ; TITLE OF INVENTION: Thereof  
 ; NUMBER OF SEQUENCES: 68  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew  
 ; STREET: One Market Plaza, Steuart Street Plaza  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105-1492

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/331,397B  
 ; FILING DATE: 28-OCT-1994

; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/767,331  
 ; FILING DATE: 30-SEP-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/596,289  
 ; FILING DATE: 12-OCT-1990

; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hunter, Tom  
 ; REGISTRATION NUMBER: 38,498  
 ; REFERENCE/DOCKET NUMBER: 015280-126120US  
 ; TELEPHONE: (415) 543-9600  
 ; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 65:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 125 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear

; MOLECULE TYPE: protein  
 ; FEATURE:  
 ; NAME/KEY: Region  
 ; LOCATION: 1..125

; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv  
 ; OTHER INFORMATION: Heavy chain region"  
 US-08-331-397B-65

Query Match 85.7%; Score 78; DB 2; Length 125;  
 Best Local Similarity 81.2%; Pred. No. 0.0001;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17  
 :|:|||||||||:|

Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VSSGGGTYYPDTVQG 17  
 :|:|||||||||:|  
 Db 51 ISNGGGTYYPDTVKG 66

RESULT 3  
 US-08-759-804A-64  
 ; Sequence 64, Application US/08759804A  
 ; Patent No. 5990296  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pastan, Ira  
 ; APPLICANT: Willingham, Mark  
 ; APPLICANT: Fitzgerald, David J.  
 ; APPLICANT: Brinkmann, Ulrich  
 ; APPLICANT: Pal, Lee

; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,  
 ; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof  
 ; NUMBER OF SEQUENCES: 68  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/759,804A  
 ; FILING DATE: 03-DEC-1996

; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/331,398  
 ; FILING DATE: 28-OCT-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/767,331  
 ; FILING DATE: 30-SEP-1991

; APPLICATION NUMBER: US 07/596,289  
 ; FILING DATE: 12-OCT-1990  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Weber, Ellen L.  
 ; REGISTRATION NUMBER: 32,762  
 ; REFERENCE/DOCKET NUMBER: 015280-126140US  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 64:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 125 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear

; MOLECULE TYPE: protein  
 ; FEATURE:  
 ; NAME/KEY: Region  
 ; LOCATION: 1..125

; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv  
 ; OTHER INFORMATION: Heavy chain region"  
 US-08-759-804A-64

Query Match 85.7%; Score 78; DB 2; Length 125;  
 Best Local Similarity 81.2%; Pred. No. 0.0001;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGTYYPDTVQG 17  
 :|:|||||||||:|



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Db 51 ISSGGGTYYPDTVKG 66
;
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; STREET: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07659-2

Query Match 84.6%; Score 77; DB 5; Length 247;
Best Local Similarity 81.2%; Pred. No. 0.00029;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGTYYPDTVQG 17
; :||||| :|||||:
Db 70 ISSGGGTYYPDTVKG 85

RESULT 6
US-08-475-000-16
; Sequence 16, Application US/08475000
; Patent No. 5811267
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424

Db 51 ISSGGGTYYPDTVKG 66
;
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurler, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; STREET: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07659-6

Query Match 84.6%; Score 77; DB 5; Length 119;
Best Local Similarity 81.2%; Pred. No. 0.00014;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSSGGGTYYPDTVQG 17
; :||||| :|||||:
Db 51 ISSGGGTYYPDTVKG 66

RESULT 5
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurler, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
```

ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0850.007  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-475-000-16

Query Match 81.3%; Score 74; DB 2; Length 119;  
Best Local Similarity 75.0%; Pred. No. 0.00038;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGSTYPDTVQG 17  
:|||||:|||||:|  
Db 51 ISSGGGTYPPDSVK 66

RESULT 7  
US-08-483-199-16  
Sequence 16, Application US/08483199  
Patent No. 5849877  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,199  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0850.009  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-199-16

Query Match 81.3%; Score 74; DB 2; Length 119;  
Best Local Similarity 75.0%; Pred. No. 0.00038;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGSTYPDTVQG 17  
:|||||:|||||:|  
Db 51 ISSGGGTYPPDSVK 66

RESULT 8  
US-08-484-508-16  
Sequence 16, Application US/08484508  
Patent No. 5948647  
GENERAL INFORMATION:  
APPLICANT: RING, DAVID B.  
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION  
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,508  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0850.008  
TELEPHONE: (510) 601-385  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-508-16

Query Match 81.3%; Score 74; DB 2; Length 119;  
Best Local Similarity 75.0%; Pred. No. 0.00038;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSSGGGSTYPDTVQG 17  
:|||||:|||||:|  
Db 51 ISSGGGTYPPDSVK 66

RESULT 9  
US-08-653-402B-6  
Sequence 6, Application US/08653402B  
Patent No. 5969107  
GENERAL INFORMATION:  
APPLICANT: CARCELLER, Ana  
APPLICANT: ROSELL, Elisabet  
APPLICANT: GOMEZ, Alicia  
APPLICANT: ADEN, Jaume  
APPLICANT: PIULATS, Jaume  
TITLE OF INVENTION: Anti-idiotypic antibodies which induce an  
TITLE OF INVENTION: Immune response against epidermal growth factor receptor.  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.  
STREET: 2200 Clarendon Boulevard, Suite 1400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22201  
COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/653,402B  
;; FILING DATE: 24-MAY-1996  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 95107967.2  
;; FILING DATE: 26-MAY-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lebovitz, Richard M.  
;; REGISTRATION NUMBER: 37,067  
;; REFERENCE/DOCKET NUMBER: MERCK 1781  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-243-6410  
;; TELEFAX: 703-243-6410  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 158 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-653-402B-6

Query Match 79.1%; Score 72; DB 2; Length 158;  
Best Local Similarity 75.0%; Pred. No. 0.001;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTYTPDVTQV 17  
Db 70 INSGGTYTPDVTKG 85

RESULT 10  
US-08-653-402B-10  
;; Sequence 10, Application US/08653402B  
;; Patent No. 5969107  
;; GENERAL INFORMATION:  
;; APPLICANT: CARCELLER, Ana  
;; APPLICANT: ROSELL, Elisabeth  
;; APPLICANT: GOMEZ, Alicia  
;; APPLICANT: ADEN, Jaume  
;; APPLICANT: PIULATS, Jaume  
;; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an  
;; immune response against epidermal growth factor receptor.  
;; NUMBER OF SEQUENCES: 13  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.  
;; STREET: 2200 Clarendon Boulevard, Suite 1400  
;; CITY: Arlington  
;; STATE: Virginia  
;; COUNTRY: U.S.A.  
;; ZIP: 22201  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/653,402B  
;; FILING DATE: 24-MAY-1996  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 95107967.2  
;; FILING DATE: 26-MAY-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lebovitz, Richard M.  
;; REGISTRATION NUMBER: 37,067  
;; REFERENCE/DOCKET NUMBER: MERCK 1781  
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 703-243-6333  
;; TELEFAX: 703-243-6410  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 158 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-653-402B-10

Query Match 79.1%; Score 72; DB 2; Length 158;  
Best Local Similarity 75.0%; Pred. No. 0.001;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSSGGGTYTPDVTQV 17  
Db 70 INSGGTYTPDVTKG 85

RESULT 11  
US-08-525-539A-35  
;; Sequence 35, Application US/08525539A  
;; Patent No. 6309636  
;; GENERAL INFORMATION:  
;; APPLICANT: DO COUTO, FERNANDO J.R.  
;; APPLICANT: CERIANI, ROBERTO L.  
;; APPLICANT: PETERSON, JERRY A.  
;; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
;; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
;; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
;; NUMBER OF SEQUENCES: 81  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 755 Page Mill Road  
;; CITY: Palo Alto  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 94304-1018  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/525,539A  
;; FILING DATE: 14-SEP-1995  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: DYLAN, TYLER  
;; REGISTRATION NUMBER: 37,612  
;; REFERENCE/DOCKET NUMBER: 27633-20001.21  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 813-5600  
;; TELEFAX: (415) 494-0792  
;; TELEX: 706141  
;; INFORMATION FOR SEQ ID NO: 35:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 32 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-525-539A-35

Query Match 71.4%; Score 65; DB 4; Length 32;  
Best Local Similarity 68.8%; Pred. No. 0.0021;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGGTYTPDVTQV 17  
Db 2 ISSGGTYTPDVTKG 17

RESULT 12  
US-08-793-490-6  
; Sequence 6, Application US/08793490  
; Patent No. 5968824  
; GENERAL INFORMATION:  
; APPLICANT: Spruce, Barbara A  
; APPLICANT: Prescott, Alan  
; APPLICANT: Bottger, Angelika  
; APPLICANT: Dewar, Deborah A  
; TITLE OF INVENTION: Agents for Inducing Apoptosis and Applications of Said  
; FILE REFERENCE: ME A9701  
; CURRENT APPLICATION NUMBER: US/08/793,490  
; EARLIER FILING DATE: 1997-04-28  
; EARLIER APPLICATION NUMBER: GB 9419285.3  
; EARLIER FILING DATE: 1994-09-23  
; EARLIER APPLICATION NUMBER: GB 9417444.8  
; EARLIER FILING DATE: 1994-08-30  
; EARLIER APPLICATION NUMBER: PCT/GB95/02037  
; EARLIER FILING DATE: 1995-08-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequence  
; OTHER INFORMATION: encoded by anti-proenkephalin immunoglobulin heavy  
; OTHER INFORMATION: chain variable domain genes  
US-08-793-490-6

Query Match 71.4%; Score 65; DB 2; Length 109;  
Best Local Similarity 68.8%; Pred. No. 0.0074;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 2 VSSGGSTYYPDVVOG 17  
:|||||:|||||:  
Db 50 ISSGGSTYYPDVSVKG 65

RESULT 13  
US-08-888-366-10  
; Sequence 10, Application US/08888366  
; Patent No. 5972656  
; GENERAL INFORMATION:  
; APPLICANT: Lopez, Osvaldo  
; APPLICANT: Wylie, Dwane E.  
; APPLICANT: Wagner, Fred W.  
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/888,366  
; FILING DATE: 03-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/187,407  
; FILING DATE: 27-JAN-1994  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/990,542  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/493,299  
; FILING DATE: 14-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/324,392  
; FILING DATE: 14-MAR-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 8648.39USC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-888-366-10

Query Match 71.4%; Score 65; DB 2; Length 116;  
Best Local Similarity 68.8%; Pred. No. 0.0079;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSSGGSTYYPDVVOG 17  
:|||||:|||||:  
Db 45 ISSGGSTYYPDVSVKG 60

RESULT 14  
US-08-888-366-12  
; Sequence 12, Application US/08888366  
; Patent No. 5972656  
; GENERAL INFORMATION:  
; APPLICANT: Lopez, Osvaldo  
; APPLICANT: Wylie, Dwane E.  
; APPLICANT: Wagner, Fred W.  
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/888,366  
; FILING DATE: 03-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/187,407  
; FILING DATE: 27-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,542  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/493,299  
; FILING DATE: 14-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/324,392  
; FILING DATE: 14-MAR-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.

REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 8648.39USC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-888-366-12

Query Match 71.4%; Score 65; DB 2; Length 116;  
Best Local Similarity 68.8%; Pred. No. 0.0079;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VSSGGSTYYPDVTQV 17  
Db 45 ISSGGSTYYPDVSKG 60

## RESULT 15

PCT-US93-08435-18  
Sequence 18, Application PC/TUS9308435  
GENERAL INFORMATION:  
APPLICANT: SmithKline Beecham, Corporation  
APPLICANT: U. S. Government, Secretary of  
APPLICANT: the Navy  
APPLICANT: U. S. Government, Secretary of  
APPLICANT: the Army  
TITLE OF INVENTION: Novel Antibodies for Conferring Passive  
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Box 457, 321 Norristown Road  
CITY: Spring House  
STATE: PA  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08435  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/941,654  
FILING DATE: 09-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: SBC F50107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9200  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
PCT-US93-08435-18

Query Match 70.3%; Score 64; DB 5; Length 17;  
Best Local Similarity 64.7%; Pred. No. 0.0015;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KVSSGGSTYYPDVTQV 17  
Db 1 EISDGGSTYYPDVTG 17

Search completed: August 19, 2002, 06:34:40  
Job time: 1201 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:05 ; Search time 78.53 Seconds  
(without alignments)  
9.789 Million cell updates/sec

Title: US-09-339-922A-106

Perfect score: 44

Sequence: 1 HLHGSPAS 8

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	84.1	572	2	B48521
2	36	81.8	1115	2	billirubin oxidase
3	34	77.3	220	2	protein T5E21.11 [
4	34	77.3	220	2	phosphoglycerate d
5	34	77.3	224	2	phosphoglycerate d
6	34	77.3	762	2	transcription fact
7	34	77.3	1294	2	hypothetical prote
8	33	75.0	277	2	bacteriophage phiC
9	33	75.0	277	2	hypothetical prote
10	33	75.0	346	2	conserved hypothet
11	33	75.0	413	2	phage-related inte
12	33	75.0	761	2	hypothetical prote
13	33	75.0	796	2	hypothetical prote
14	32	72.7	95	2	protein F46F5.11 [
15	32	72.7	208	2	inverted repeat co
16	32	72.7	209	2	A56644
17	32	72.7	218	2	pyrazinamidase/nic
18	32	72.7	219	1	hypothetical prote
19	32	72.7	219	1	pyrazinamidase/nic
20	32	72.7	219	2	hypothetical 23.4K
21	32	72.7	225	2	hypothetical prote
22	32	72.7	312	2	hypothetical prote
23	32	72.7	331	2	conserved hypothet
24	32	72.7	327	2	transcription regu
25	32	72.7	335	2	T18247
26	32	72.7	350	2	glyceraldehyde 3-p
27	32	72.7	350	2	H81662
28	32	72.7	352	2	sorbitol dehydroge
29	32	72.7	364	2	photosystem II pro
					O-methyltransferas
					JQ2268

30	32	72.7	385	2	S56224	hypothetical prote
31	32	72.7	388	2	AC2011	hypothetical prote
32	32	72.7	405	2	S62789	11beta-hydroxyster
33	32	72.7	444	2	C89768	conserved hypotet
34	32	72.7	449	2	H69862	Nat-transporting A
35	32	72.7	500	2	B83910	hypothetical prote
36	32	72.7	574	1	S11032	5'-nucleotidase (E
37	32	72.7	980	2	T39630	valine-tRNA ligase
38	32	72.7	1104	1	SYBYVT	valine--tRNA ligas
39	32	72.7	1603	2	D89407	protein R10E8.6 [I
40	32	72.7	1696	2	T24146	hypothetical prote
41	32	72.7	2121	2	T27406	hypothetical prote
42	31	70.5	98	2	PC6012	thuf protein - Rho
43	31	70.5	178	2	S50637	hypothetical prote
44	31	70.5	222	2	AH0991	cell division ATP-
45	31	70.5	237	2	T07820	hypothetical prote

#### ALIGNMENTS

RESULT 1

B48521

billirubin oxidase (EC 1.3.3.5) - fungus (Myrothecium verrucaria)

C;Species: Myrothecium verrucaria

C;Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000

C;Accession: B48521; A48521

R;Koikeda, S.; Ando, K.; Kaji, H.; Inoue, T.; Murao, S.; Takeuchi, K.; Samejima, T.  
J. Biol. Chem. 268, 18801-18809, 1993

A;Title: Molecular cloning of the gene for billirubin oxidase from Myrothecium verruca

A;Reference number: A48521; MUID:93366794

A;Accession: B48521

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-572 <KO1>

A;Cross-references: GB:D14081; NID:g436236; PIDN:BARA03166.1; PID:g456710

A;Note: sequence extracted from NCBI backbone (NCBIN:136730, NCBI:P:136732)

A;Accession: A48521

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-572 <KO12>

A;Cross-references: GB:D14081; NID:g436236; PIDN:BARA03166.1; PID:g456710

A;Note: sequence extracted from NCBI backbone (NCBIN:136728, NCBI:P:136729)

C;Keywords: oxidoreductase

Query Match 84.1%; Score 37; DB 2; Length 572;  
Best Local Similarity 85.7%; Pred. No. 22;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HLHGSPA 7

|||||

Db 132 HLHGSPS 138

RESULT 2

F86280

protein T5E21.11 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C;Accession: F86280

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719

A;Accession: F86280

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A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1115 <STO>
A:Cross-references: GB:AE005172; NID:g7527726; PIDN:AAF63175.1; GSPDB:GN00141
C:Genetics:
A:Gene: T5E21.11
A:Map position: 1
C:Superfamily: valine--trna ligase

Query Match      81.8%; Score 36; DB 2; Length 1115;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSPA 7
Db 396 HLHGKFA 402

RESULT 3
A:Title: phosphoglycerate dehydrogenase homolog lmo1813 [imported] - Listeria monocytogenes (strain
A:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AE1301
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1301
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99891.1; PID:gl6411267; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1813

Query Match      77.3%; Score 34; DB 2; Length 220;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSPA 7
Db 46 HLHGSPA 52

RESULT 4
A:Title: phosphoglycerate dehydrogenase homolog lin1927 [imported] - Listeria innocua (strain Cl
A:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AE1673
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1673
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97157.1; PID:gl6414428; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
```

```
A:Gene: lin1927

Query Match      77.3%; Score 34; DB 2; Length 220;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSPA 7
Db 46 HLHGSPA 52

RESULT 5
A:Title: transcription factor TRF - fruit fly (Drosophila melanogaster)
A:Species: Drosophila melanogaster
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: S37740; S29720; S31869; S31871
R:Crowley, T.E.; Hoey, T.; Liu, J.K.; Jan, Y.N.; Jan, L.Y.; Tjian, R.
Nature 361, 557-561, 1993
A:Title: A new factor related to TATA-binding protein has highly restricted expressio
A:Reference number: S29720; MUID:93156846
A:Accession: S37740
A:Molecule type: DNA
A:Residues: 1-224 <CRO1>
A:Cross-references: EMBL:X70838; NID:gl1137; PIDN:CAA50186.1; PID:gl1138
A:Accession: S29720
A:Molecule type: mRNA
A:Residues: 1-224 <CRO2>
A:Cross-references: EMBL:X70837; NID:gl1135; PIDN:CAA50185.1; PID:gl1136
C:Genetics:
A:Gene: FlyBase:Trf
A:Cross-references: FlyBase:FBgn0010287
A:Introns: 52/2
C:Superfamily: transcription initiation factor IID
C:Keywords: DNA binding; transcription factor

Query Match      77.3%; Score 34; DB 2; Length 224;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSPAS 8
Db 161 HVHGQFSS 168

RESULT 6
B70838
A:Title: hypothetical protein Rv0197 - Mycobacterium tuberculosis (strain H37RV)
A:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: B70838
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987
A:Accession: B70838
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-762 <COL>
A:Cross-references: GB:AL021928; GB:AL123456; NID:g3261522; PIDN:CAAL7319.1; PID:g290
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0197
C:Superfamily: formate dehydrogenase

Query Match      77.3%; Score 34; DB 2; Length 762;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
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Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFA 7  
 Db 326 HLHSSFA 332

RESULT 7  
 T35044  
 bacteriophage phiC31 resistance protein pgly - Streptomyces coelicolor  
 C;Species: Streptomyces coelicolor  
 C;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 01-Dec-2000  
 C;Accession: T35044; T30203  
 R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, August 1998  
 A;Reference number: Z21566  
 A;Accession: T35044  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Molecule type: translated from GB/EMBL/DDBJ  
 A;Residues: 1-1294 <SEE>  
 A;Cross-references: EMBL:AL031371; PIDN:CAA20546.1; GSPDB:GN00070; SCOEDB:SC4G2.09  
 A;Experimental source: strain A3(2)  
 R;Bedford, D.J.; Laity, C.; Buttner, M.J.  
 J. Bacteriol. 177, 4681-4689, 1995  
 A;Title: Two genes involved in the phase-variable phi C31 resistance mechanism of Strept  
 A;Reference number: 220777; MUID:95370146  
 A;Accession: T30203  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-372, 'N', 374-913, 'I', 915-1002, 'A', 1004-1294 <BED>  
 A;Cross-references: EMBL:L37531; NID:g576537; PID:g576538; PIDN:AAB00365.1  
 C;Genetics:  
 A;Gene: pgly; SCOEDB:SC4G2.09

Query Match 77.3%; Score 34; DB 2; Length 1294;  
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8  
 Db 72 YLHGSFGS 79

RESULT 8  
 F97615  
 hypothetical protein AGR\_C\_3868 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
 C;Species: Agrobacterium tumefaciens  
 C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
 C;Accession: F97615  
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,  
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A;Reference number: A97359; PMID:11743194  
 A;Accession: F97615  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-277 <KUR>  
 A;Cross-references: GB:AE007869; PIDN:AAK87879.1; PID:gl515157269; GSPDB:GN00169  
 C;Genetics:  
 A;Gene: AGR\_C\_3868  
 A;Map position: circular chromosome

Query Match 75.0%; Score 33; DB 2; Length 277;  
 Best Local Similarity 85.7%; Pred. No. 62;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LHGSFAS 8  
 Db 79 LHGSFSS 85

RESULT 11  
 S77339  
 hypothetical protein sll1723 - Synechocystis sp. (strain PCC 6803)  
 C;Species: Synechocystis sp.

RESULT 9  
 AD2838  
 conserved hypothetical protein Atu2132 [imported] - Agrobacterium tumefaciens (strain  
 C;Species: Agrobacterium tumefaciens  
 C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
 C;Accession: AD2838  
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo  
 ; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl  
 erage, G.; Gillet, W.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam  
 ster, E.W.  
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A;Reference number: AB2577; PMID:11743193  
 A;Accession: AD2838  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-277 <KUR>  
 A;Cross-references: GB:AE008688; PIDN:AAL43122.1; PID:gl7740595; GSPDB:GN00186  
 A;Experimental source: strain C58 (Dupont)  
 C;Genetics:  
 A;Gene: Atu2132  
 A;Map position: circular chromosome

Query Match 75.0%; Score 33; DB 2; Length 277;  
 Best Local Similarity 85.7%; Pred. No. 62;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFAS 8  
 Db 79 LHGSFSS 85

RESULT 10  
 AF3161  
 phage-related integrase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) p  
 C;Species: Agrobacterium tumefaciens  
 C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
 C;Accession: AF3161  
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo  
 ; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl  
 Science 294, 2317-2323, 2001  
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam  
 ster, E.W.  
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A;Reference number: AB2577; PMID:11743193  
 A;Accession: AF3161  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-346 <KUR>  
 A;Cross-references: GB:AE008687; PIDN:AAL45708.1; PID:gl7743437; GSPDB:GN00188  
 A;Experimental source: strain C58 (Dupont)  
 C;Genetics:  
 A;Gene: intX  
 A;Genome: plasmid

Query Match 75.0%; Score 33; DB 2; Length 346;  
 Best Local Similarity 85.7%; Pred. No. 77;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFAS 8  
 Db 116 LHGAFAFAS 122



A:Variety: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999  
 C:Accession: S77339  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpō, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* s.  
 A:Reference number: S74322; MUID:97061201  
 A:Accession: S77339  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-413 <KAN>  
 A:Cross-references: EMBL:D90906; GB:AB001339; NID:gl652492; PTID:BAAL7442.1; PTID:dl01817  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 75.0%; Score 33; DB 2; Length 413;  
 Best Local Similarity 75.0%; Pred. No. 92;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8  
 ||| |||  
 Db 128 HLHAHFAS 135

RESULT 12  
 T05299  
 hypothetical protein F26P21.30 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 24-Nov-1999  
 C:Accession: T05299  
 R:Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De ewes, H.W.; Mayer, K.F.X.; Schueller, C.  
 submitted to the Protein Sequence Database, October 1998  
 A:Reference number: Z15407  
 A:Accession: T05299  
 A:Molecule type: DNA  
 A:Residues: 1-761 <BEV>  
 A:Cross-references: EMBL:AL031804  
 A:Experimental source: cultivar Columbia; BAC clone F26P21  
 C:Genetics:  
 A:Map position: 4  
 A:Introns: 123/2; 167/2; 221/3; 262/3; 281/3; 348/3; 385/3; 398/2; 450/3; 484/3; 492/3;  
 A:Note: F26P21.30  
 C:Superfamily: Arabidopsis thaliana hypothetical protein F26P21.30

Query Match 75.0%; Score 33; DB 2; Length 761;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSF 6  
 |||||  
 Db 267 HLHGSY 272

RESULT 13  
 E88029  
 protein F46F5.11 [imported] - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
 C:Accession: E88029  
 R:anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological  
 A:Reference number: A75000; MUID:99069613; PMID:9851916  
 A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele  
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
 A:Accession: E88029  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-796 <STO>

A:Cross-references: GB:chr\_II; PIDN:AC78189.1; PID:g3886038; GSPDB:GN00020; CESP:F46F  
 C:Genetics:  
 A:Gene: F46F5.11  
 A:Map position: 2

Query Match 75.0%; Score 33; DB 2; Length 796;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSF 6  
 |||||  
 Db 601 HLHGSY 606

RESULT 14  
 A56644  
 inverted repeat component hypothetical protein IR3 - equine herpesvirus 1  
 C:Species: equine herpesvirus 1  
 C:Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 08-Oct-1999  
 C:Accession: A56644  
 R:Holden, V.R.; Harty, R.N.; Yalamanchili, R.R.; O'Callaghan, D.J.  
 DNA Seq. 3, 143-152, 1992  
 A:Title: The IR3 gene of equine herpesvirus type 1: a unique gene regulated by sequen  
 A:Reference number: A56644; MUID:93112995  
 A:Accession: A56644  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-95 <HOL>  
 A:Cross-references: GB:M92043; NID:g330912; PIDN:AAA68888.1; PID:g330913  
 A:Note: sequence extracted from NCBI backbone (NCBIN:121461, NCBI:P:121462)  
 C:Genetics:  
 A:Gene: IR3

Query Match 72.7%; Score 32; DB 2; Length 95;  
 Best Local Similarity 75.0%; Pred. No. 33;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8  
 ||| |||  
 Db 20 HLHALFAS 27

RESULT 15  
 AC2830  
 pyrazinamidase/nicotinamidase [imported] - Agrobacterium tumefaciens (strain C58, Dup  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
 C:Accession: AC2830  
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam  
 ster, E.W.  
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; PMID:11743193  
 A:Accession: AC2830  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-208 <KUR>  
 A:Cross-references: GB:AE008688; PIDN:AAL43057.1; PID:gl7740524; GSPDB:GN00186  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: pncA  
 A:Map position: circular chromosome

Query Match 72.7%; Score 32; DB 2; Length 208;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HGSFAS 8  
| | | | |  
Db 54 HGSFAS 59

Search completed: August 19, 2002, 05:36:07  
Job time: 1288 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:09 ; Search time 51.81 seconds  
(without alignments)  
5.979 Million cell updates/sec

Title: US-09-339-922A-106

Perfect score: 44

Sequence: 1 HLHGSFAS 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	37	84.1	572	1 BLRO_MYRVE	Q12737 myrothecium
2	36	81.8	1107	1 SYV_ARATH	P93736 arabidopsis
3	35	79.5	394	1 IPOUL_DROME	P24350 drosophila
4	34	77.3	358	1 YC07_KLEPN	Q48453 klebsiella
5	32	72.7	213	1 PNCA_ECOLI	P21369 escherichia
6	32	72.7	222	1 SDHB_PEPAS	P33074 peptostrept
7	32	72.7	335	1 G3P_CHLMU	Q9PJN6 chlamydia m
8	32	72.7	352	1 PSBD_CHLVU	P56319 chlorella v
9	32	72.7	364	1 ZRP4_MAIZE	P47917 zea mays (m
10	32	72.7	385	1 YF00_YEAST	P43567 saccharomyc
11	32	72.7	400	1 DH12_RAT	P50233 rattus norv
12	32	72.7	405	1 DH12_HUMAN	P80365 homo sapien
13	32	72.7	574	1 SNTD_HUMAN	P21589 homo sapien
14	32	72.7	980	1 SYV_SCHPO	O75005 schizosacch
15	32	72.7	1104	1 SYV_YEAST	P07806 saccharomyc
16	31	70.5	178	1 YEW4_YEAST	P40081 saccharomyc
17	31	70.5	887	1 YLX8_CAEEL	P46504 caenorhabdi
18	30	68.2	176	1 TRAF_AGR75	Q44350 agrobacteri
19	30	68.2	176	1 TRAF_AGR76	Q44364 agrobacteri
20	30	68.2	176	1 TRAF_AGR79	P15595 agrobacteri
21	30	68.2	197	1 EGG5_FASHE	P07915 fasciola he
22	30	68.2	244	1 T2FC_YEAST	P35189 saccharomyc
23	30	68.2	272	1 MCBC_ECOLI	P23185 escherichia
24	30	68.2	317	1 YDC1_YEAST	Q02896 saccharomyc
25	30	68.2	376	1 CYB_PLABE	O99253 plasmodium
26	30	68.2	376	1 CYB_PLACH	O99256 plasmodium
27	30	68.2	376	1 CYB_PLAFA	Q02768 plasmodium
28	30	68.2	382	1 CYB_PLAVS	O63696 plasmodium
29	30	68.2	427	1 AROA_STRPN	Q9S400 streptococc
30	30	68.2	445	1 GLNA_LACDE	P45627 lactobacill
31	30	68.2	529	1 ENP3_HUMAN	O75355 homo sapien
32	30	68.2	768	1 LEM3_RAT	P98106 rattus norv
33	30	68.2	906	1 FOX2_CANTR	P22414 candida tro

#### ALIGNMENTS

RESULT 1					
BLRO_MYRVE	34	30	68.2	946	1 YIN7_YEAST
ID	BLRO_MYRVE	STANDARD;	PRT;	572 AA.	
AC	Q12737;				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	Bilirubin oxidase precursor (EC 1.3.3.5).				
OS	Myrothecium verrucaria.				
OC	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Myrothecium.				
OX	NCBI_TaxID=5532;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN=MT-1;				
RX	MEDLINE=93366794; PubMed=8360171;				
RA	Koike S., Ando K., Kaji H., Inoue T., Murao S., Takeuchi K.,				
RA	Samejima T.;				
RT	"Molecular cloning of the gene for bilirubin oxidase from Myrothecium				
RT	verrucaria and its expression in yeast.";				
RL	J. Biol. Chem. 268:18801-18809(1993).				
CC	-1- FUNCTION: OXIDATION OF BILIRUBIN AND OTHER TETRAPYRROLES.				
CC	-1- CATALYTIC ACTIVITY: Bilirubin + O(2) = biliverdin + H(2)O.				
CC	-1- CONFACITOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH				
CC	CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2				
CC	OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR. CONTAINS 2 BLUE COPPER				
CC	ATOMS PER MOLECULE.				
CC	-1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.				
CC	-1- SIMILARITY: CONTAINS 2 PLASTOCYANIN-LIKE DOMAINS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL; D14081; BAA03166.1; .				
DR	EMBL; D12579; BAA02123.1; .				
DR	InterPro; IPR001117; Cu-oxidase.				
DR	Pfam; PF00394; Cu-oxidase; 1.				
CC	Signal; Copper; Metal-binding; Oxidoreductase; Glycoprotein; Repeat.				
FT	SIGNAL 1 19 PROBABLE.				
FT	PROPEP 20 38				
FT	CHAIN 39 572				
FT	DOMAIN 98 194				
FT	DOMAIN 404 526				
FT	METAL 132 132				
FT	METAL 134 134				
FT	METAL 172 172				
FT	METAL 174 174				
FT	METAL 436 436				
FT	METAL 439 439				
FT	METAL 441 441				
FT	METAL 494 494				
FT	METAL 495 495				

P40462 saccharomyc  
O75185 homo sapien  
Q49409 mycoplasma  
O14514 homo sapien  
O61493 mus musculus  
O60673 homo sapien  
P91303 caenorhabdi  
P37750 escherichia  
P52563 halobacteri  
P08203 escherichia  
P06190 salmonella  
P37680 escherichia

```

FT METAL          496 496 COPPER (TYPE 3) (BY SIMILARITY).
FT METAL          500 500 COPPER (TYPE 1) (BY SIMILARITY).
FT METAL          503 503 COPPER (TYPE 1) (BY SIMILARITY).
FT CARBOHYD       510 510 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD       520 520 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE       572 AA; 63947 MW; 5842D641303E5EFF CRC64;

Query Match      84.1%; Score 37; DB 1; Length 572;
Best Local Similarity 85.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLHGSFA 7
    |||||
Db 132 HLHGSFS 138

RESULT 2
SYV_ARATH
ID SYV_ARATH STANDARD; PRT; 1107 AA.
AC P93736;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VAL1-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VALRS).
GN VALRS.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=97352801; PubMed=9207094;
RA Zhang J.Z., Somerville C.R.;
RT "Suspensor-derived polyembryony caused by altered expression of
RL valyl- tRNA synthetase in the tw2 mutant of Arabidopsis.";
Proc. Natl. Acad. Sci. U.S.A. 94:7349-7355(1997).
CC -|- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC + L-valyl-tRNA(Val).
CC -|- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; U89986; AAB49704.1; -.
CC EMBL; U93308; AAB51589.1; -.
CC HSSP; P96142; IGAX.
CC InterPro; IPR002300; tRNA-synt_la.
CC InterPro; IPR001412; tRNA-synt_I.
CC InterPro; IPR002303; tRNA-synt_val.
CC Pfam; PF00133; tRNA-synt_1; 1.
CC PRINTS; PR00986; TRNASYNTHAL.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SITE 177 187 "HIGH" REGION.
FT SITE 694 698 "KMSKS" REGION.
FT BINDING 697 697 ATP (BY SIMILARITY).
SQ SEQUENCE 1107 AA; 125894 MW; ED71F237DF24E51B CRC64;

Query Match      81.8%; Score 36; DB 1; Length 1107;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLHGSFA 7
    |||||

```

```

Db 388 HLHGKFA 394
RESULT 3
IPOU_DROME
ID IPOU_DROME STANDARD; PRT; 394 AA.
AC P24350; Q26465; O77214;
DT 01-MAR-1992 (Rel. 21, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Inhibitory POU protein (I-POU) (Abnormal chemosensory jump 6 protein).
GN IPOU OR ACJ6.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM I-POU).
RX MEDLINE=91204052; PubMed=1673230;
RA Treacy M.N., He X., Rosenfeld M.G.;
RT "I-POU: a POU-domain protein that inhibits neuron-specific gene
RT activation.";
RL Nature 350:577-584(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM TI-POU).
RC STRAIN=CANTON-S;
RA Clyne P.J., Certel S., de Bruyne M., Zaslavsky L., Johnson W.,
RA Carlson J.R.;
RT "The odor-specificities of a subset of olfactory receptor neurons are
RT governed by Acj6, a POU domain transcription factor.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 318-375 FROM N.A. (ISOFORM TI-POU).
RX MEDLINE=92154665; PubMed=1346754;
RA Treacy M.N., Neilson L.I., Turner E.E., He X., Rosenfeld M.G.;
RT "Twin of I-POU: a two amino acid difference in the I-POU homeodomain
RT distinguishes an activator from an inhibitor of transcription.";
RL Cell 68:491-505(1992).
RN [4]
RP DNA-BINDING.
RX MEDLINE=97140288; PubMed=8986770;
RA Turner E.E.;
RT "Similar DNA recognition properties of alternatively spliced
RT Drosophila POU factors.";
Proc. Natl. Acad. Sci. U.S.A. 93:15097-15101(1996).
CC -|- FUNCTION: MODULATES GENE TRANSCRIPTION.
CC -|- SUBCELLULAR LOCATION: Nuclear.
CC -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS; I-POU (SHOWN HERE) AND TI-
CC POU/TWIN-OF-I-POU; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -|- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE CENTRAL NERVOUS
CC SYSTEM.
CC -|- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
CC TO CLASS-4 POU.
CC -|- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT THAT I-POU HOMEOBOX IS
CC UNABLE TO BIND DNA BECAUSE IT LACKS TWO N-TERMINAL BASIC RESIDUES.
CC -----
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CC -----
CC EMBL; X58436; CAA41342.1; -.
CC EMBL; AF086816; AAC35369.1; -.
CC EMBL; S82271; AAB21441.1; -.
CC EMBL; S82267; AAB21441.1; JOINED.
CC FTR; SI4795; SI4795.
CC HSSP; PI4859; IOCT.
CC TRANSFAC; T01898; -.
CC FlyBase; FBgn0000028; acj6.

```



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CC -----  
DR EMBL; M26934; AAA23447.1; -;  
DR EMBL; AE000271; AAC74838.1; ALT\_INIT.  
DR EMBL; D90820; BAA15559.1; -;  
DR EMBL; D90821; BAA15566.1; -;  
DR PIR; J00048; QOECA5.  
DR Ecogen; EG1135; pncA.  
DR InterPro; IPR000868; Isochorismatase.  
DR Pfam; PF00857; Isochorismatase; 1.  
KW Hydrolase; Complete proteome.  
SQ SEQUENCE 213 AA; 23362 MW; B9F8D946FA18433F CRC64;  
  
Query Match 72.7%; Score 32; DB 1; Length 213;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 HGSFAS 8  
Db 58 HGSFAS 63  
  
RESULT 6  
SDHB\_PEPAS  
ID SDHB\_PEPAS STANDARD; PRT; 222 AA.  
AC P33074;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE L-serine dehydratase, beta chain (EC 4.2.1.13) (L-serine deaminase)  
DE (SDH) (L-SD).  
GN SDHB.  
OS Peptostreptococcus asaccharolyticus (Peptococcus asaccharolyticus).  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Peptoniphilus.  
ON "Genome sequences of Clostridium trachomatis MoPn and Chlamydia  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 14963;  
RX MEDLINE=97386436; PubMed=9244285;  
RA Holmster A.E., Textor S., Buckel W.;  
RT "Cloning and expression of the genes coding for the L-serine  
dehydratase from Peptostreptococcus asaccharolyticus: relationship of  
the iron-sulfur protein to both L-serine dehydratases from Escherichia  
coli.";  
RT J. Bacteriol. 179:4937-4941(1997).  
RN [2]  
RP SEQUENCE OF 4-19.  
RC STRAIN=ATCC 14963;  
RX MEDLINE=91293139; PubMed=2065681;  
RA Grabowski R., Buckel W.;  
RT "Purification and properties of an iron-sulfur-containing and  
pyridoxal-phosphate-independent L-serine dehydratase from  
Peptostreptococcus asaccharolyticus.";  
RT Eur. J. Biochem. 199:89-94(1991).  
RL -1- CATALYTIC ACTIVITY: L-serine + H(2)O -> pyruvate + NH(3) + H(2)O.  
CC -1- COFACTOR: IRON-SULFUR (4FE-4S).  
CC -1- PATHWAY: GLUCONEOGENESIS FROM SERINE.  
CC -1- SUBUNIT: HETEROCTAMER OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.  
CC -1- SIMILARITY: BELONGS TO THE IRON-SULFUR DEPENDENT L-SERINE  
DEHYDRATASE FAMILY.  
CC -----  
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CC -----  
CC EMBL; U76260; AAC45545.1; -;  
CC

DR PIR; S16376; S16376.  
DR InterPro; IPR002912; ACT.  
DR Pfam; PF01842; ACT; 1.  
KW Lyase; Iron-sulfur; 4Fe-4S; Glucoconeogenesis.  
SQ SEQUENCE 222 AA; 24151 MW; 3A2A624EC3104C08 CRC64;  
  
Query Match 72.7%; Score 32; DB 1; Length 222;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 LHGSFA 7  
Db 47 LHGSFA 52  
  
RESULT 7  
G3P\_CHLMU  
ID G3P\_CHLMU STANDARD; PRT; 335 AA.  
AC Q9PJN6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Glycerinaldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).  
GN GAP OR TC0792.  
OS Chlamydia muridarum.  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=83560;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MoPn / Nigg;  
RX MEDLINE=20150255; PubMed=10684935;  
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Bass S.,  
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Dodson R.,  
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., McElroy S.L.,  
RA Winn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
RA Eisen J., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
pneumoniae AR39.";  
RL Nucleic Acids Res. 28:1397-1406(2000).  
CC -1- CATALYTIC ACTIVITY: D-glycerinaldehyde 3-phosphate + phosphate +  
NAD(+) -> 3-phospho-D-glyceroyl phosphate + NADH.  
CC -1- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.  
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE  
DEHYDROGENASE FAMILY.  
CC -----  
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CC -----  
CC EMBL; AE002347; AAF39595.1; -;  
DR TIGR; TC0792;  
DR InterPro; IPR000173; GAP\_DH.  
DR Pfam; PF00044; gpdh; 1.  
DR Pfam; PF02800; gpdh.C; 1.  
DR PRINTS; PR00078; G3PDHGRNAS.  
DR PROSITE; PS00071; GAPDH; 1.  
KW Glycolysis; NAD; Oxidoreductase; Complete proteome.  
FT BINDING 151 151  
FT GLYCERALDEHYDE 3-PHOSPHATE (BY  
SIMILARITY).  
FT ACT\_SITE 178 178  
FT ACTIVATES THIOL GROUP DURING CATALYSIS  
(BY SIMILARITY).  
FT SEQUENCE 335 AA; 36240 MW; BELLCF546FB17FD2 CRC64;  
SQ  
  
Query Match 72.7%; Score 32; DB 1; Length 335;  
Best Local Similarity 100.0%; Pred. No. 32;  
  
QY 2 LHGSFA 7  
Db 47 LHGSFA 52

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HGSFAS 8  
| | | | |  
DB 50 HGSFAS 55

RESULT 8  
PSBD\_CHLVU STANDARD; PRT; 352 AA.  
AC P56319;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Photosystem II D2 protein (Photosystem Q(A) protein) (PSII D2  
protein).  
GN PSBD.  
OS Chlorella vulgaris.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;  
OC Chlorellaceae; Chlorella.  
OX NCBI\_TaxID=3077;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IAM C-27 / TANIYA;  
RX MEDLINE=97303241; PubMed=9159184;  
RA Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,  
TSUDZUKI J., NAKASHIMA K., TSUDZUKI T., SUZUKI Y., HAMADA A., OHTA T.,  
INAMURA A., YOSHINAGA K., SUGIURA M.;  
RT "Complete nucleotide sequence of the chloroplast genome from the  
green alga *Chlorella vulgaris*: the existence of genes possibly  
involved in chloroplast division.";  
RT Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).  
RL  
CC -!- FUNCTION: THIS IS ONE OF THE TWO REACTION CENTER PROTEINS OF PSII,  
D2 PROTEIN IS NEEDED FOR ASSEMBLY OF A STABLE PSII COMPLEX.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast  
thylakoid membrane.  
CC -!- SIMILARITY: BELONGS TO THE REACTION CENTER L/M CHAINS / PSBA /  
PSBD FAMILY.

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CC  
CC EMBL; AB001684; BAA57876.1; -;  
DR HSP; P02955; IDOP.  
DR InterPro; IPR000484; Photo\_RC.  
DR Pfam; PF00124; photoRC; 1.  
DR ProDom; PD000551; Photo\_RC; 1.  
DR PROSITE; PS00244; REACTION\_CENTER; 1.  
KW Transmembrane; Electron transport; Thylakoid; Photosystem II;  
KW Chloroplast; Iron.  
FT TRANSMEM 35 56 POTENTIAL.  
FT TRANSMEM 108 128 POTENTIAL.  
FT TRANSMEM 141 163 POTENTIAL.  
FT TRANSMEM 191 217 POTENTIAL.  
FT TRANSMEM 266 286 POTENTIAL.  
FT METAL 214 214 IRON (NON HEME).  
FT METAL 224 224 IRON (NON HEME).  
FT METAL 268 268 IRON (NON HEME).  
SQ SEQUENCE 352 AA; 39429 MW; 0F8FD072C9FD139 CRC64;  
Query Match 72.7%; Score 32; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFA 7  
| | | | |

DB 116 LHGSFA 121

RESULT 9  
ZRP4\_MAIZE STANDARD; PRT; 364 AA.  
AC P47917;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE O-methyltransferase ZRP4 (EC 2.1.1.-) (OMT).  
GN ZRP4.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NKH31; TISSUE=Root;  
RX MEDLINE=94105316; PubMed=8278520;  
RA Held B.M., Wang H., John I., Wurtele E.S., Colbert J.T.;  
RT "An mRNA putatively coding for an O-methyltransferase accumulates  
preferentially in maize roots and is located predominantly in the  
region of the endodermis.";  
RT Plant Physiol. 102:1001-1008(1993).  
RL  
CC -!- FUNCTION: MAY BE INVOLVED IN THE O-METHYLATION OF SUBERIN  
PHENYLPROPANOID PRECURSORS.  
CC -!- TISSUE SPECIFICITY: ACCUMULATES PREFERENTIALLY IN THE ROOTS AND IS  
LOCATED PREDOMINANTLY IN THE REGION OF THE ENDODERMIS, LOW LEVELS  
ARE SEEN IN THE LEAVES, STEMS, AND OTHER SHOOT ORGANS.  
CC -!- SIMILARITY: TO OTHER OMTS REQUIRING S-ADENOSYL-L-METHIONINE AS  
SUBSTRATE.

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CC  
CC EMBL; L14063; AAA18532.1; -;  
DR MaizeDB; 63528; -;  
DR InterPro; IPR001601; Meth-transf.  
DR InterPro; IPR001077; Methyltransf\_2.  
DR InterPro; IPR000051; SAM\_bind.  
DR Pfam; PF00891; Methyltransf\_2; 1.  
KW Transferase; Methyltransferase.  
SQ SEQUENCE 364 AA; 39583 MW; FB8AD93AD5A6611D CRC64;

Query Match 72.7%; Score 32; DB 1; Length 364;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8  
| | | | |  
DB 46 HLHGSFAS 53

RESULT 10  
YFDO\_YEAST STANDARD; PRT; 385 AA.  
AC P43567;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 41.9 kDa protein in HAC1-CAK1 intergenic region.  
GN YFLO30W.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

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OX NCBI_TaxID=4932;
RN SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae.;
RL Nat. Genet. 10:261-268(1995).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL; D50617; BAA09208.1; -.
DR SGD; S0001864; YFL030W.
DR InterPro; IPR000192; AminoTransf_class_V.
DR Pfam; PF00266; aminotran_5; 1.
DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
KW Hypothetical protein; Pyridoxal phosphate.
FT BINDING 201 201 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 385 AA; 41907 MW; 460D5DCCAB8FDF79F CRC64;

Query Match 72.7%; Score 32; DB 1; Length 385;
Best Local Similarity 62.5%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8
DB 230 HVHGFSS 237

RESULT 11
DH12_RAT
ID DH12_RAT STANDARD; PRT; 400 AA.
AC P50233;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Corticosteroid 11-beta-dehydrogenase, isozyme 2 (EC 1.1.1.146) (11-
DE DH2) (11-beta-hydroxysteroid dehydrogenase 2) (11-beta-HSD2) (NAD-
DE dependent 11-beta-hydroxysteroid dehydrogenase).
GN HSD11B2 OR HSD11K.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney;
RX MEDLINE=95377198; PubMed=7649078;
RA Zhou M.Y., Gomez-Sanchez E.P., Cox D.L., Cosby D.,
RA Gomez-Sanchez C.E.;
RT "Cloning, expression, and tissue distribution of the rat nicotinamide
RT adenine dinucleotide-dependent 11 beta-hydroxysteroid
RT dehydrogenase.";
RL Endocrinology 136:3729-3734(1995).
CC -!- FUNCTION: HAS A ROLE IN MODULATING GLUCOCORTICOID ACTIVITY BOTH AT
CC THE LEVEL OF THE MINERALOCORTICOID RECEPTOR AND THE GLUCOCORTICOID
CC RECEPTOR. USES NADH WHILE 11-DH1 USES NADPH. CATALYZES NON
CC REVERSIBLY THE CONVERSION OF CORTISOL TO THE INACTIVE METABOLITE
CC CORTISONE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: A 11-BETA-HYDROXYSTEROID + NAD(+) = A

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CC 11-OXOSTEROID + NADH.
CC -!- SUBCELLULAR LOCATION: Microsomal.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC -----
DR EMBL; U22424; AAA87007.1; -.
DR HSP; P14061; IPDU.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD; Microsome.
FT NE_BIND 82 111 NAD (BY SIMILARITY).
FT ACT_SITE 232 232 BY SIMILARITY.
SQ SEQUENCE 400 AA; 43726 MW; A1BAAA328E2F189D CRC64;

Query Match 72.7%; Score 32; DB 1; Length 400;
Best Local Similarity 83.3%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSF 6
DB 302 HLHGQF 307

RESULT 12
DH12_HUMAN
ID DH12_HUMAN STANDARD; PRT; 405 AA.
AC P80365; Q13194;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Corticosteroid 11-beta-dehydrogenase, isozyme 2 (EC 1.1.1.146) (11-
DE DH2) (11-beta-hydroxysteroid dehydrogenase 2) (11-beta-HSD2) (NAD-
DE dependent 11-beta-hydroxysteroid dehydrogenase).
GN HSD11B2 OR HSD11K.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95163772; PubMed=7859916;
RA Albiston A.L., Obeyesekere V.R., Smith R.E., Krozowski Z.S.;
RT "Cloning and tissue distribution of the human 11 beta-hydroxysteroid
RT dehydrogenase type 2 enzyme.";
RL Mol. Cell. Endocrinol. 105:R11-R17(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96079108; PubMed=8530071;
RA Agarwal A.K., Rogerson F.M., Mune T., White P.C.;
RT "Gene structure and chromosomal localization of the human HSD11K gene
RT encoding the kidney (type 2) isozyme of 11 beta-hydroxysteroid
RT dehydrogenase.";
RL Genomics 29:195-199(1995).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96190749; PubMed=8611140;
RA Brown R.W., Chapman K.E., Kotelevtsev Y., Yau J.L., Lindsay R.S.,
RA Brett L., Leckie C., Murad P., Lyons V., Mullins J.J.,
RA Edwards C.R.W., Seckl J.R.;
RT "Cloning and production of antisera to human placental 11 beta-

```



RT hydroxysteroid dehydrogenase type 2.";  
 RL Biochem. J. 313:1007-1017(1996).  
 [4]  
 RN VARIANTS AME CYS-208 AND CYS-213.  
 RX MEDLINE=95400319; PubMed=7670488;  
 RA Mune T., Rogerson F.M., Nikkila H., Agarwal A.K., White P.C.;  
 RT "Human hypertension caused by mutations in the kidney isozyme of 11  
 beta-hydroxysteroid dehydrogenase.";  
 RL Nat. Genet. 10:394-399(1995).  
 CC -|- FUNCTION: HAS A ROLE IN MODULATING GLUCOCORTICOID ACTIVITY BOTH AT  
 CC THE LEVEL OF THE MINERALOCORTICOID RECEPTOR AND THE GLUCOCORTICOID  
 CC RECEPTOR. USES NADH WHILE 11-DH1 USES NADPH. CATALYZES NON  
 CC REVERSIBLY THE CONVERSION OF CORTISOL TO THE INACTIVE METABOLITE  
 CC CORTISONE.  
 CC -|- CATALYTIC ACTIVITY: A 11-BETA-HYDROXYSTEROID + NAD(+) = A  
 CC 11-OXOSTEROID + NADH.  
 CC -|- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -|- TISSUE SPECIFICITY: FOUND IN PLACENTA, KIDNEY, PANCREAS, PROSTATE,  
 CC OVARY, SMALL INTESTINE AND COLON.  
 CC -|- DISEASE: DEFECTS IN HSD11B2 ARE THE CAUSE OF A POTENTIALLY FATAL  
 CC FORM OF CHILDHOOD HYPERTENSION TERMED APPARENT MINERALOCORTICOID  
 CC EXCESS (AME). IT IS THOUGHT THAT INACTIVATION OF HSD11B2 PERMITS  
 CC CORTISOL TO OCCUPY THE RENAL MINERALOCORTICOID RECEPTOR AND  
 CC THEREBY CAUSE SODIUM RETENTION AND HYPERTENSION.  
 CC -|- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
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 -----  
 DR EMBL; U14631; AAA91969.1; -;  
 DR EMBL; U27317; AAB48544.1; -;  
 DR EMBL; U26726; AAC50356.1; -;  
 DR HSSP; P14061; IFDW.  
 DR MIM; 218030; -;  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PROSITE; PS00061; adh\_short; 1.  
 KW Oxidoreductase; NAD; Microsome; Disease mutation.  
 FT NP\_BIND 82 111 NAD (BY SIMILARITY).  
 FT ACT\_SITE 232 232 BY SIMILARITY.  
 FT VARIANT 208 208 R -> C (IN AME).  
 FT FTIG=VAR\_006958.  
 FT VARIANT 213 213 R -> C (IN AME).  
 FT FTIG=VAR\_006959.  
 FT CONFLICT 148 148 L -> F (IN REF. 2).  
 FT CONFLICT 148 148 L -> V (IN REF. 3).  
 FT SEQUENCE 405 AA; 44140 MW; 4AB7538269913F24 CRC64;  
 SQ  
 Query Match 72.7%; Score 32; DB 1; Length 405;  
 Best Local Similarity 83.3%; Pred. No. 38;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 HLHGSF 6  
 Db 302 HLHGQF 307  
 RESULT 13  
 ID 5NTD\_HUMAN STANDARD; PRT; 574 AA.  
 AC P21589; O75520;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 5'-nucleotidase precursor (EC 3.1.3.5) (5'-nucleotidase) (5'-NT)  
 DE (CD73 antigen).

GN NT5 OR NTE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Placenta;  
 RX MEDLINE=90361037; PubMed=2129526;  
 RA Misumi Y., Ogata S., Ohkubo K., Hirose S., Ikehara Y.;  
 RT "Primary structure of human placental 5'-nucleotidase and  
 RT identification of the glycolipid anchor in the mature form.";  
 RL Eur. J. Biochem. 191:563-569(1990).  
 RN [2]  
 RP SEQUENCE OF 1-113 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=96144293; PubMed=8566797;  
 RA Hansen K.R., Resta R., Webb C.F., Thompson L.F.;  
 RT "Isolation and characterization of the promoter of the human 5'-  
 RT nucleotidase (CD73)-encoding gene.";  
 RL Gene 167:307-312(1995).  
 RN [3]  
 RP SEQUENCE OF 359-489 FROM N.A.  
 RC TISSUE=Leukocyte;  
 RA Zanon L., Rosi F., Pagani R., Marinello E.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 27-40.  
 RC TISSUE=Placenta;  
 RX MEDLINE=91058583; PubMed=2173922;  
 RA Klemens M.R., Sherman W.R., Holmberg N.J., Ruedi J.M., Low M.G.,  
 RA Thompson L.F.;  
 RT "Characterization of soluble vs membrane-bound human placental 5'-  
 RT nucleotidase.";  
 RL Biochem. Biophys. Res. Commun. 172:1371-1377(1990).  
 RN [5]  
 RP DISEASE.  
 RX MEDLINE=98313134; PubMed=9651114;  
 RA Rosi F., Agostinho A.B., Carlucci F., Zanon L., Porcelli B.,  
 RA Marinello E., Galleni P., Tabucchi A.;  
 RT "Behaviour of human lymphocytic isoenzymes of 5'-nucleotidase.";  
 RL Life Sci. 62:2257-2266(1998)  
 CC -|- FUNCTION: HYDROLYZES EXTRACELLULAR NUCLEOTIDES INTO MEMBRANE  
 CC PERMEABLE NUCLEOSIDES.  
 CC -|- CATALYTIC ACTIVITY: A 5'-ribonucleotide + H(2)O = a ribonucleoside  
 CC + phosphate.  
 CC -|- COFACTOR: ZINC.  
 CC -|- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
 CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -|- DISEASE: THERE IS A DECREASE IN THE ACTIVITY OF NT5 IN B-CELL  
 CC CHRONIC LYMPHOCYTIC LEUKEMIA.  
 CC -|- SIMILARITY: BELONGS TO THE 5'-NUCLEOTIDASE FAMILY.  
 CC -|- DATABASE: NAME=PROW; NOTE=CD guide CD73 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd73.htm".  
 -----  
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 -----  
 DR EMBL; X55740; CAA39271.1; -;  
 DR EMBL; U21730; AAA96950.1; -;  
 DR EMBL; AF069067; AAC98672.1; -;  
 DR PIR; S11032; S11032.  
 DR HSSP; P07024; ZUSH.  
 DR MIM; 129190; -;  
 DR InterPro; IPR002224; 5\_nucleotidase.  
 DR InterPro; IPR000934; Ser\_thr\_phosphatse.  
 DR Pfam; PF01009; 5\_nucleotidase; 1.  
 DR Pfam; PF02872; 5\_nucleotidase; 1.

DR PROSITE: PS00785; 5\_NUCLEOTIDASE\_1; 1.  
 DR PROSITE: PS00786; 5\_NUCLEOTIDASE\_2; 1.  
 KW Hydrolase; Signal; GPI-anchor; Glycoprotein; Zinc.  
 FT SIGNAL 1 26  
 FT CHAIN 27 549 5'-NUCLEOTIDASE.  
 FT PROPEP 550 574 REMOVED IN NATURE FORM.  
 FT LIPID 549 549 GPI-ANCHOR.  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 376 376 T -> A (IN REF. 3).  
 SQ SEQUENCE 574 AA; 63367 MW; A99AF170AB7EAECE CRC64;

Query Match 72.7%; Score 32; DB 1; Length 574;  
 Best Local Similarity 71.4%; Pred. No. 55;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFA 7  
 | | | | |  
 Db 553 HCHGSFS 559

RESULT 14  
 SYV\_SCHPO STANDARD; PRT; 980 AA.  
 AC 075005;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Probable valyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.9)  
 DE (Valine--trNA ligase) (VALRS).  
 GN SPBC1709.02C OR SPBC1734.18C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RA Lyne M., Rajandream M.A., Barrell B.G., Rieger M.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate  
 CC + L-valyl-tRNA(Val).  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (Probable).  
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.  
 CC  
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 CC  
 CC EMBL; AL031856; CAA21312.1; -.  
 CC EMBL; AL031852; CAA21241.1; -.  
 CC HSSP; P96142; LGAX.  
 DR InterPro; IPR002300; trNA-synt\_la.  
 DR InterPro; IPR001412; trNA-synt\_I.  
 DR InterPro; IPR002303; trNA-synt\_val.  
 DR Pfam; PF00133; trNA-synt.1; 1.  
 DR PRINTS; PR00986; TRNASYNTHAL.  
 DR PROSITE; PS00178; AA\_TRNA\_LIGASE\_I; 1.  
 KW Hypothetical protein; Aminoacyl-tRNA synthetase; Protein biosynthesis;  
 KW Ligase; ATP-binding; Mitochondrion; Transit peptide.  
 FT TRANSIT 1 ?  
 FT CHAIN 1 980 PROBABLE VALYL-TRNA SYNTHETASE.  
 FT SITE 139 149 "HIGH" REGION.  
 FT SITE 652 656 "KMSKS" REGION.  
 FT BINDING 655 655 ATP (BY SIMILARITY).

SQ SEQUENCE 980 AA; 111316 MW; BB91FAF976030C3C CRC64;

Query Match 72.7%; Score 32; DB 1; Length 980;  
 Best Local Similarity 83.3%; Pred. No. 95;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSF 6  
 | | | | |  
 Db 351 HLHGKF 356

RESULT 15  
 SYV\_YEAST STANDARD; PRT; 1104 AA.  
 AC P07806;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Valyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.9)  
 DE (Valine--trNA ligase) (VALRS).  
 GN VAS1 OR YGR094W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87222321; PubMed=3294828;  
 RA Jordana X., Chatton B., Paz-Weisshaar M., Buhler J.-M., Cramer F.,  
 RA Ebel J.-P., Fasiolo F.;  
 RT "Structure of the yeast valyl-tRNA synthetase gene (VASI) and the  
 RT homology of its translated amino acid sequence with Escherichia coli  
 RT isoleucyl-tRNA synthetase.";  
 RL J. Biol. Chem. 262:7189-7194(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wedler H., Scharfe M., Wedler E., Wambutt R.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Hernandez K., Weber N., Wipfli P., Schmidheini T.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-78 FROM N.A.  
 RX MEDLINE=88087140; PubMed=3275649;  
 RA Chatton B., Walter P., Ebel J.-P., Lacroite F., Fasiolo F.;  
 RT "The yeast VAS1 gene encodes both mitochondrial and cytoplasmic  
 RT valyl-tRNA synthetases.";  
 RL J. Biol. Chem. 263:52-57(1988).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate  
 CC + L-valyl-tRNA(Val).  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.  
 CC -!- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS  
 CC BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.  
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.  
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 CC  
 CC EMBL; J02719; AAA35207.1; -.  
 CC EMBL; Z72879; CAA37097.1; -.  
 CC EMBL; M18392; AAA35205.1; -.  
 CC EMBL; M18392; AAA35206.1; -.  
 CC PIR; A29871; SYBYVT.  
 CC HSSP; P96142; LGAX.  
 CC SGD; S0003326; VAS1.  
 CC InterPro; IPR002300; trNA-synt\_la.

DR InterPro; IPR001412; trna-synt\_I.  
 DR InterPro; IPR002303; trna-synt\_val.  
 DR Pfam; PF00133; trna-synt\_1; 1.  
 DR PRINTS; PR00986; TRNASYNTHVAL.  
 DR PROSITE; PS00178; AA\_TRNA\_LIGASE\_I; 1.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Mitochondrion; Transit peptide; Alternative initiation.  
 FT TRANSIT 1 47 MITOCHONDRION.  
 FT CHAIN 48 1104 VALYL-TRNA SYNTHETASE, MITOCHONDRIAL  
 FT ISOFORM.  
 FT CHAIN 47 1104 VALYL-TRNA SYNTHETASE, CYTOPLASMIC  
 FT ISOFORM.  
 FT INIT\_MET 47 47 FOR CYTOPLASMIC ISOFORM.  
 FT SITE 190 200 "HIGH" REGION.  
 FT SITE 703 707 "KMSKS" REGION.  
 FT BINDING 706 706 ATP (BY SIMILARITY).  
 FT CONFLICT 147 147 A -> G (IN REF. 1).  
 FT CONFLICT 540 540 R -> K (IN REF. 1).  
 SQ SEQUENCE 1104 AA; 125769 MW; 6493AEF37ECD4A7C CRC64;

Query Match 72.7%; Score 32; DB 1; Length 1104;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLHGSF 6  
 |||||  
 Db 402 HLHGKF 407

Search completed: August 19, 2002, 06:59:10  
 Job time: 1375 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:13 ; Search time 140.4 Seconds  
(without alignments)  
9.857 Million cell updates/sec

Title: US-09-339-922A-106

Perfect score: 44

Sequence: 1 HLHGSFAS 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	84.1	254	10 O82093	O82093 prunus arce
2	37	84.1	254	10 O9FUM3	O9FUM3 prunus aviu
3	37	84.1	602	3 O9P8C3	O9P8C3 acronium
4	36	81.8	105	10 Q42273	Q42273 arabidopsis
5	36	81.8	214	10 O9FE97	O9FE97 arabidopsis
6	36	81.8	240	10 O9FUTO	O9FUTO arabidopsis
7	36	81.8	1115	10 O9MA22	O9MA22 arabidopsis
8	35	79.5	389	5 O9VXW1	O9VXW1 arabidopsis
9	35	79.5	494	10 Q9LSH2	Q9LSH2 arabidopsis
10	35	79.5	581	5 Q9VSO9	Q9VSO9 drosophila
11	34	77.3	83	4 Q9H374	Q9H374 homo sapien
12	34	77.3	220	16 Q92AJ5	Q92AJ5 listeria in
13	34	77.3	224	5 Q27896	Q27896 drosophila
14	34	77.3	762	16 O53648	O53648 mycobacteri
15	34	77.3	1294	2 O86682	O86682 streptomyc
16	34	77.3	1294	2 O53942	O53942 streptomyc

17	33	75.0	81	2	O50075	Q50075 mycobacteri
18	33	75.0	192	10	O9FUQ9	O9FUQ9 oryza meyer
19	33	75.0	219	10	O9FN71	O9FN71 arabidopsis
20	33	75.0	322	10	O9SPK6	O9SPK6 haematococc
21	33	75.0	413	16	P73402	P73402 synechocyst
22	33	75.0	527	12	Q91SH3	Q91SH3 guinea pig
23	33	75.0	710	2	O936V8	O936V8 prochloroco
24	33	75.0	713	10	O9ASW9	O9ASW9 arabidopsis
25	33	75.0	761	10	O82634	O82634 arabidopsis
26	33	75.0	796	5	O9TXX9	O9TXX9 caenorhabdi
27	33	75.0	1413	5	O9VJ38	O9VJ38 drosophila
28	33	75.0	1424	5	O9VJ39	O9VJ39 drosophila
29	32	72.7	95	12	O05535	O05535 equine herp
30	32	72.7	105	12	O9Q911	O9Q911 avian adeno
31	32	72.7	209	10	O9SX97	O9SX97 arabidopsis
32	32	72.7	286	2	O93IC9	O93IC9 staphylococ
33	32	72.7	294	13	O98S10	O98S10 brachydanio
34	32	72.7	299	8	O9TNI8	O9TNI8 adiantum ca
35	32	72.7	306	2	O9RIV6	O9RIV6 streptomyc
36	32	72.7	312	16	O99XE0	O99XE0 staphylococ
37	32	72.7	315	13	O9YGT8	O9YGT8 brachydanio
38	32	72.7	329	13	O98S11	O98S11 brachydanio
39	32	72.7	331	3	O94066	O94066 candida alb
40	32	72.7	350	16	O927H5	O927H5 listeria in
41	32	72.7	368	5	O9VKF7	O9VKF7 drosophila
42	32	72.7	442	2	O9S0L8	O9S0L8 staphylococ
43	32	72.7	443	2	O93AC9	O93AC9 pseudomonas
44	32	72.7	444	16	O99XC5	O99XC5 staphylococ
45	32	72.7	449	16	O31658	O31658 bacillus su

ALIGNMENTS

RESULT 1

O82093 ID O82093 PRELIMINARY; PRT; 254 AA.  
AC O82093; 1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE EXPANSIN.  
GN PA-EXPL.  
OS Prunus armeniaca (Apricot).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
OX NCBI\_TaxID=36596;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERGERON; TISSUE=MESOCARP PLUS EXOCARP;  
RA Mbequie-A-Mbequie D., Gomez R.-M., Fills-Lycaon B.;  
RT "Molecular cloning and nucleotide sequence of expansin 1 (PA-Exp1)  
from apricot fruit";  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U93167; AAC33529.1; -;  
DR InterPro; IPR000882; Pollen\_allergen.1.  
DR Pfam; PF01357; Pollen\_allergen; 1.  
DR PRINTS; PR01225; EXPANSIN.FAMILY.  
DR PRODOM; PD002179; Pollen\_allergen; 1.  
SQ SEQUENCE 254 AA; 27264 MW; 88068D75932FD0E1 CRC64;

Query Match 84.1%; Score 37; DB 10; Length 254;

Best Local Similarity 85.7%; Pred. No. 13; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLHGSFA 7

Db 21 HLHGAFA 27

RESULT 2

Q9FUM3 Q9FUM3 PRELIMINARY; PRT; 254 AA.  
 AC Q9FUM3;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE EXPANSIN 1.  
 GN EXP1 OR EXP2.  
 OS Prunus avium (Cherry), and  
 OS Prunus cerasus.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=42229, 140311;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.avium;  
 RA Wu Z., Wiersma P.A.;  
 RT "Differential Expression of Expansin Genes Isolated from Sweet Cherry  
 (Prunus avium L.) During Fruit Ripening."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.cerasus; TISSUE=RIPENING FRUIT;  
 RA Yoo S.-D., Gao Z., Cantini C., Loeschner W., van Nocker S.;  
 RT "Coordinated expression of genes encoding expansins and other cell  
 wall-modifying enzymes is associated with pectin-related changes in  
 the cell wall during ripening of cherry (P. cerasus) fruit."  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF297521; AAG13982.1; -;  
 DR EMBL; AF350937; AAK48846.1; -;  
 DR InterPro; IPR000882; Pollen\_allergen.  
 DR Pfam; PF01357; Pollen\_allergen; 1.  
 DR PRINTS; PR01225; EXPANSINFAMILY.  
 DR ProDom; PD002179; Pollen\_allergen; 1.  
 SQ SEQUENCE 254 AA; 27278 MW; 953A7EB2491FD0E1 CRC64;

Query Match 84.1%; Score 37; DB 10; Length 254;  
 Best Local Similarity 85.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7  
 |||||  
 DB 21 HLHGAF 27

RESULT 3  
 Q9P8C3 Q9P8C3 PRELIMINARY; PRT; 602 AA.  
 AC Q9P8C3;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE POLYPHENOL OXIDASE PRECURSOR.  
 GN PPOA.  
 OS Acremonium murorum.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreales; Hypocreaceae; mitosporic Hypocreaceae; Acremonium.  
 OX NCBI\_TaxID=45278;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CBS 157.72;  
 RX MEDLINE=21268855; PubMed=11375170;  
 RA Gouka R.J., van der Heiden M., Swarthoff T., Verrips C.T.;  
 RT "Cloning of a phenol oxidase gene from Acremonium murorum and its  
 expression in Aspergillus awamori."  
 RL Appl. Environ. Microbiol. 67:2610-2616(2001).  
 DR EMBL; AJ271104; CAB75422.1; -;  
 KW Signal.  
 RN [2]  
 RP SIGNAL.  
 FT SIGNAL.  
 SQ SEQUENCE 602 AA; 66920 MW; 0303D991405228A3 CRC64;

Query Match 84.1%; Score 37; DB 3; Length 602;  
 Best Local Similarity 85.7%; Pred. No. 32;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7  
 |||||  
 DB 154 HLHGSFS 160

RESULT 4  
 Q42273 Q42273 PRELIMINARY; PRT; 105 AA.  
 AC Q42273;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE HSP26A HOMOLOGUE (FRAGMENT).  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=DRY SEEDS OF A.THALIANA ECOTYPE COLUMBIA;  
 RA Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;  
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z34012; CAA03973.1; -;  
 DR InterPro; IPR004045; GST\_N.  
 DR Pfam; PF02798; GST\_N; 1.  
 FT NON\_TER 105 105  
 SQ SEQUENCE 105 AA; 12376 MW; 7FDC76BEC069ECD4 CRC64;

Query Match 81.8%; Score 36; DB 10; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFAS 8  
 |||||  
 DB 11 LHGSFAS 17

RESULT 5  
 Q9FE97 Q9FE97 PRELIMINARY; PRT; 214 AA.  
 AC Q9FE97;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE GLUTATHIONE S-TRANSFERASE-LIKE PROTEIN.  
 GN GST14B.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=99087489; PubMed=9872454;  
 RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.  
 RT Sequence features of the regions of 1,013,767 bp covered by sixteen  
 RT physically assigned pl and TAC clones."  
 RL DNA Res. 5:297-308(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wagner U., Mauch F.;  
 RT "Analysis of the glutathione S-transferase family in Arabidopsis

RT thaliana.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB015469; BAB11498.1; -;  
 DR EMBL: AF288180; AAG30129.1; -;  
 KW Transferase.  
 SQ SEQUENCE 214 AA; 24673 MW; 644A7B5E201D30D3 CRC64;

Query Match 81.8%; Score 36; DB 10; Length 214;

Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHGSFAS 8

|||||

Db 11 LHGSFAS 17

RESULT 6

Q9FUT0

ID Q9FUT0 PRELIMINARY; PRT; 240 AA.

AC Q9FUT0;

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE GLUTATHIONE S-TRANSFERASE.

GN GSTL4.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Wagner U., Mauch F.;

RT "Analysis of the glutathione S-transferase family in Arabidopsis

thaliana";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF288179; AAG30128.1; -;

DR InterPro: IPR004045; GST\_N.

KW Transferase.

SQ SEQUENCE 240 AA; 27612 MW; D0872464356EA2FB CRC64;

Query Match

Best Local Similarity 100.0%; Score 36; DB 10; Length 240;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHGSFAS 8

|||||

Db 11 LHGSFAS 17

RESULT 7

Q9MA22

ID Q9MA22 PRELIMINARY; PRT; 1115 AA.

AC Q9MA22;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE T5E21.11.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,

Shinn P., Tambunga G., Altafi H., Bei Q., Chin C., Chiou J., Choi E.,

Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B.,

Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,

Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,

Thaveri A., Torlumi M., Vaysberg M., Yu G., Federspiel N.A.,

RA Theologis A., Ecker J.R.;

RT "Genomic sequence for Arabidopsis thaliana BAC T5E21 from chromosome

I.";

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC010657; AAF63175.1; -;

DR HSSP: P96142; IGAX.

DR InterPro: IPR002300; tRNA-synt\_1a.

DR InterPro: IPR001412; tRNA-synt\_1.

DR InterPro: IPR002301; tRNA-synt\_1le.

DR InterPro: IPR002303; tRNA-synt\_val.

DR Pfam: PF00133; tRNA-synt\_1; 1.

DR PRINTS: PR00986; TRNASYNTHAL.

DR PROSITE: PS00178; AA\_TRNA\_LIGASE\_I; 1.

SQ SEQUENCE 1115 AA; 126675 MW; 4F383F79B656B0D1 CRC64;

Query Match

Best Local Similarity 85.7%; Score 36; DB 10; Length 1115;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLHGSPA 7

|||||

Db 396 HLHGKFA 402

RESULT 8

Q9VXW1

ID Q9VXW1 PRELIMINARY; PRT; 389 AA.

AC Q9VXW1;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE CG9151 PROTEIN.

GN ACJ6 OR CG9151.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,

Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Splier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -!- SIMILARITY: WITH OTHER HOMEBOX PROTEINS.  
 DR EMBL; AE003498; AAF48447.1; -.  
 DR HSSP; P10037; 1AU7.  
 DR FlyBase; FBgn0000028; acj6.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR000157; pou; 1.  
 DR PROSITE; PS00028; POU DOMAIN.  
 DR SMART; SM00383; Hox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 DR PROSITE; PS00035; POU\_1; 1.  
 DR PROSITE; PS00465; POU\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 SQ SEQUENCE 389 AA; 4284 MW; 4AAB56FD4F07721 CRC64;

Query Match 79.5%; Score 35; DB 5; Length 389;  
 Best Local Similarity 75.0%; Pred. No. 51;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HLHGSFAS 8  
 Db 165 HLHGSVHS 172  
 |||||: |

RESULT 9  
 ID Q9LSH2 PRELIMINARY; PRT; 494 AA.  
 AC Q9LSH2;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE GLUTAMATE DECARBOXYLASE.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
 RT clones.";  
 RL DNA Res. 7:131-135(2000).  
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 DR EMBL; AB026646; BAB02870.1; -.  
 DR InterPro; IPR002129; Pyridoxal\_dec.  
 DR Pfam; PF00282; Pyridoxal\_dec; 1.  
 KW Decarboxylase; Lyase; Pyridoxal phosphate.  
 SQ SEQUENCE 494 AA; 55770 MW; 7985F175E54DF262 CRC64;

Query Match 79.5%; Score 35; DB 10; Length 494;  
 Best Local Similarity 75.0%; Pred. No. 66;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HLHGSFAS 8  
 Db 12 HLHSTFAS 19  
 ||||: |||

RESULT 10  
 ID Q9VS09 PRELIMINARY; PRT; 581 AA.  
 AC Q9VS09;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE CG8645 PROTEIN.  
 GN CG8645.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer J.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003560; AAF50621.1; -.  
 DR HSSP; P39061; IKOE.  
 DR FlyBase; FBgn0035732; CG8645.  
 DR InterPro; IPR000087; Collagen.  
 DR InterPro; IPR002088; PPTA.  
 DR Pfam; PF01391; Collagen; 3.

DR PROSITE; PS00904; PPTA; UNKNOWN1.  
SQ SEQUENCE 581 AA; 60772 MW; 19BC1E48CB477FE7 CRC64;

Query Match 79.5%; Score 35; DB 5; Length 581;  
Best Local Similarity 87.5%; Pred. No. 78;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLKGSFAS 8  
||| |||||  
DB 507 HLKGSFAS 514

RESULT 11  
Q9H374  
ID Q9H374 PRELIMINARY; PRT; 83 AA.  
AC Q9H374;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE PRO102.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,  
RA Xu W., Gao F., Liu M., He F.;  
RT "Functional prediction of the coding sequences of 75 new genes deduced  
RT by analysis of cDNA clones from human fetal liver."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF130105; AAG3530.1; -  
SQ SEQUENCE 83 AA; 9799 MW; 6F76AF9B9BDBD4B5 CRC64;

Query Match 77.3%; Score 34; DB 4; Length 83;  
Best Local Similarity 85.7%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLKGSFA 7  
||| ||| |  
DB 14 HLKGSIA 20

RESULT 12  
Q92AJ5  
ID Q92AJ5 PRELIMINARY; PRT; 220 AA.  
AC Q92AJ5;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE LIN1927 PROTEIN.  
GN LIN1927.  
OS Listeria innocua.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.  
OX NCBI\_TaxID=1642;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CLIP 11262 / SEROVAR 6A;  
RX PubMed=11679669;  
RA Baquero F., Frangeul L., Buchrieser C., Rusniok C., Amend A.,  
RA Glaser P., Berche P., Bloeker H., Brandt P., Chakraborty T.,  
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,  
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,  
RA Entian K.-D., Fshhi H., Garcia-del Portillo F., Garrido P.,  
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkut G.,  
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,  
RA Nordisiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,  
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;  
RT "Comparative genomics of *Listeria* species.";  
RL Science 294:849-852(2001).  
DR EMBL; AL596170; CAC97157.1; -.  
DR Listlist; LIN01927; -.  
KW Complete proteome.  
SQ SEQUENCE 220 AA; 23860 MW; F50CDC3E026F97AE CRC64;

Query Match 77.3%; Score 34; DB 16; Length 220;  
Best Local Similarity 85.7%; Pred. No. 44;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLKGSFA 7  
||| |||||  
DB 46 HLKGSFA 52

RESULT 13  
Q27896  
ID Q27896 PRELIMINARY; PRT; 224 AA.  
AC Q27896;  
DT 01-JAN-1999 (TREMBLrel. 09, Created)  
DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE TBP-RELATED FACTOR.  
GN TRP OR CG7562.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
RC STRAIN=CANTON-S; TISSUE=TESTIS;  
RX MEDLINE=93156846; PubMed=8429912;  
RA Crowley T.E., Hoey T., Liu J.-K., Jan Y.N., Jan L.Y., Tjian R.;  
RT "A new factor related to TATA-binding protein has highly restricted  
RT expression patterns in *Drosophila*."  
RL Nature 361:557-561(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY.  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,



RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2183-2195(2000).  
CC -1- FUNCTION: ACTS AS A TRANSCRIPTION FACTOR. BINDS TO THE TATA BOX  
CC PROMOTER ELEMENT WHICH LIES CLOSE TO THE POSITION OF TRANSCRIPTION  
CC INITIATION.  
CC -1- FUNCTION: MAY BE ESSENTIAL FOR EMBRYONIC DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- TISSUE SPECIFICITY: PRIMARY SPERMATOCYTES IN THE ADULT TESTIS AND  
CC IN A SUBSET OF CELLS IN THE DORSAL MEDIAL REGION OF THE EMBRYONIC  
CC CENTRAL NERVOUS SYSTEM.  
CC -1- SIMILARITY: WEAK, WITH BACTERIAL POLYMERASE SIGMA-FACTORS. HIGH,  
CC WITH TBP.  
DR EMBL: X70837; CAA50185.1; -;  
DR EMBL: X70838; CAA50186.1; -;  
DR EMBL: AE003619; AAF52600.1; -;  
DR HSSP: P20226; 1TGH.  
DR FlyBase: FBgn010287; Trf.  
DR InterPro: IPR000814; TFID.  
DR Pfam: PF00352; TBP; 2.  
DR PRINTS; PR00686; TIFACTORIID.  
DR PROSITE; PS00351; TFID; 2.  
KW Transcription regulation; DNA-binding; Nuclear protein; Repeat.  
FT DOMAIN 51 218 2 X TFID REPEATS.  
FT REPEAT 51 127 1.  
FT REPEAT 141 218 2.  
FT SEQUENCE 224 AA; 25455 MW; CA619BE4BA726460 CRC64;  
SQ

Query Match 77.3%; Score 34; DB 5; Length 224;  
Best Local Similarity 62.5%; Pred. No. 45;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSEFAS 8  
|:|:| |:  
DB 161 HVHGQFSS 168

RESULT 14  
O53648 PRELIMINARY; PRT; 762 AA.  
AC O53648  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 82.6 KDA PROTEIN.  
GN RV0197 OR MTV033.05.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV.  
RX MEDLINE=98295987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garner T., Churcher C., Harris D.,  
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,  
Hornsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,  
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
RT "Deciphering the biology of *Mycobacterium tuberculosis* from the  
RT complete genome sequence.";  
RL Nature 393:537-544(1998).  
DR EMBL: AL021928; CAA17319.1; -;

DR TuberculList: Rv0197; -;  
DR InterPro: IPR001467; Molybdopterin.  
DR Pfam: PF00384; molybdopterin; 3.  
DR Pfam: PF01568; molybdop\_binding; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 762 AA; 82571 MW; 73PFF9DD5D14BCCE CRC64;  
Query Match 77.3%; Score 34; DB 16; Length 762;  
Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSEFA 7  
|:|:| |:  
DB 326 HLHSSFA 332

RESULT 15  
O86682 PRELIMINARY; PRT; 1294 AA.  
AC O86682  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE BACTERIOPHAGE (PHIC31) RESISTANCE GENE PGLY.  
GN PGLY.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Seeger K.J., Harris D.;  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RX MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,  
RA Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
DR EMBL: AL031371; CAA20546.1; -;  
SQ SEQUENCE 1294 AA; 141187 MW; 5515825E3087B4F1 CRC64;  
Query Match 77.3%; Score 34; DB 2; Length 1294;  
Best Local Similarity 75.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSEFAS 8  
|:|:| |:  
DB 72 YLHGSEFGS 79

Search completed: August 19, 2002, 06:58:15  
Job time: 1405 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run On: August 19, 2002, 06:39:12 ; Search time 180.34 seconds  
(without alignments)  
4.927 Million cell updates/sec

Title: US-09-339-922A-106

Perfect score: 44

Sequence: 1 HLHGFAS 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

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19:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
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21:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	8	22	AA61401
2	37	84.1	10	19	AAW76037
3	37	84.1	10	22	AA61395
4	37	84.1	21	22	AA81503
5	37	84.1	21	22	AA20098
6	37	84.1	572	14	AA40843
7	37	84.1	578	22	AA81506
8	37	84.1	583	22	AA81505
9	37	84.1	583	22	AA20097
10	37	84.1	602	21	AA69204
11	36	81.8	240	21	AAG42074

12	36	81.8	242	21	AAG54727
13	35	79.5	95	21	AAG47207
14	35	79.5	97	21	AAG11600
15	35	79.5	389	22	AB84263
16	35	79.5	494	21	AAG13764
17	35	79.5	507	21	AAG13763
18	35	79.5	581	22	AB860799
19	34	77.3	112	22	AAE01420
20	34	77.3	224	22	AB863359
21	34	77.3	736	22	ABG17921
22	33	75.0	10	19	AAW76020
23	33	75.0	10	22	AB81378
24	33	75.0	99	22	AAU45647
25	33	75.0	187	22	AAU45960
26	33	75.0	322	21	AA811111
27	33	75.0	1413	22	AB860857
28	33	75.0	1424	22	AB860854
29	32	72.7	31	20	AA80315
30	32	72.7	66	22	AB817631
31	32	72.7	66	22	AA823960
32	32	72.7	157	22	AA001883
33	32	72.7	176	21	AA812100
34	32	72.7	198	21	AA812099
35	32	72.7	208	21	AA839024
36	32	72.7	209	21	AA836752
37	32	72.7	215	22	AA835514
38	32	72.7	226	21	AA836751
39	32	72.7	330	22	AA875161
40	32	72.7	346	22	AB824308
41	32	72.7	368	22	AB861162
42	32	72.7	405	18	AAW18677
43	32	72.7	451	22	AB824306
44	32	72.7	475	21	AA833985
45	32	72.7	493	22	AB829667

#### ALIGNMENTS

RESULT 1  
AA61401  
ID AA61401 standard; peptide; 8 AA.  
AC AA61401;  
XX  
XX 03-APR-2001 (first entry)  
XX  
XX Enhanced LM609 VH CDR3 peptide.  
DE  
DE LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis.  
KW  
XX  
XX Unidentified.  
XX  
XX WO200078815-A1.  
XX  
XX 28-DEC-2000.  
XX  
XX 23-JUN-2000; 2000WO-US17454.  
XX  
XX 24-JUN-1999; 99US-0339922.  
XX  
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX  
XX Huse WD, Wu H;  
XX  
XX WPT; 2001-050110/06.  
XX  
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis -  
XX

PS Claim 1; Page 45; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta<sub>3</sub> integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 44; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8  
 | | | | | | | |  
 Db 1 hlhgsfas 8

RESULT 2

AAW76037  
 ID AAW76037 standard; Protein; 10 AA.

XX AC AAW76037;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-H region CDR3 protein fragment #13.

XX KW Vitaxin; antibody; variable region; heavy chain; integrin;  
 LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;  
 KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; AAV49874.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta<sub>3</sub>  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis

XX PS Claim 62; Page 43; 129pp; English.

XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody  
 CC LM609 heavy and light chain variable region. LM609 and the antibody  
 CC vitaxin bind selectively to integrin alphavbeta<sub>3</sub> and can be used to  
 CC inhibit binding of alphavbeta<sub>3</sub> to a ligand and thus block  
 CC integrin-mediated signal transduction. This is useful in the treatment,  
 CC prevention and diagnosis of alphavbeta<sub>3</sub>-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
 CC antibodies contain non-murine framework regions so are suitable for use  
 CC in humans. Enhanced types of LM609 have affinity more than 90 times  
 CC greater than that of parent the parent antibody.

XX SQ Sequence 10 AA;

Query Match 84.1%; Score 37; DB 19; Length 10;  
 Best Local Similarity 87.5%; Pred. No. 0.63;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8  
 | | | | | | | |  
 Db 3 hnhgsfas 10

RESULT 3

AAAB61395  
 ID AAB61395 standard; peptide; 10 AA.

XX AC AAB61395;

XX DT 03-APR-2001 (first entry)

XX DE Multiple mutant VH CDR3 #1.

XX KW LM609; grafted antibody; alphavbeta<sub>3</sub> integrin; angiogenesis;  
 XX inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI; 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -

XX PS Disclosure; Page 42; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta<sub>3</sub> integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX SQ Sequence 10 AA;

Query Match 84.1%; Score 37; DB 22; Length 10;  
 Best Local Similarity 87.5%; Pred. No. 0.63;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSFAS 8  
 | | | | |  
 Db 3 hnhgsfas 10

RESULT 4  
 AAB81503  
 ID AAB81503 standard; peptide; 21 AA.  
 XX AC AAB81503;  
 XX DT 18-JUN-2001 (first entry)  
 XX DE Stachybotrys chartarum phenol oxidising enzyme peptide #1.  
 XX KW Stachybotrys chartarum; phenol oxidising enzyme; detergent;  
 KW paper production; pulp production; textile; food industry; bleaching.  
 XX OS Stachybotrys chartarum.  
 XX PN WO200121748-A1.  
 XX PD 29-MAR-2001.  
 XX PF 06-SEP-2000; 2000WO-EP08840.  
 XX PR 22-SEP-1999; 99EP-0203120.  
 XX PA (UNIL ) UNILEVER NV.  
 PA (UNIL ) UNILEVER PLC.  
 PA (HIND-) HINDUSTAN LEVER LTD.  
 XX PI Convents D, Doornink M, De Vries CH, Wang H;  
 XX WPI; 2001-273462/28.  
 XX DR New detergent compositions comprising a phenol oxidizing enzyme useful  
 PT in detergent or cleaning compositions, fiber treatment, processing,  
 PT finishing or production, paper and pulp production, or in starch  
 PT processing applications -  
 XX Example 2; Page 27; 46pp; English.  
 XX CC The present sequence is a fragment of the Stachybotrys chartarum  
 CC phenol oxidising enzyme. It was obtained by subjecting the enzyme to SDS  
 CC polyacrylamide gel electrophoresis, treating the isolated fraction  
 CC with urea and iodoacetamide, and digesting with enzyme endoLysC.  
 CC The invention relates to detergent compositions comprising one or more  
 CC surfactants and a phenol oxidising enzyme having at least 68% identity to  
 CC the Stachybotrys chartarum phenol oxidising enzyme. Phenol oxidising  
 CC enzymes may be used in the detergent, paper, pulp, textile and food  
 CC industries. They are used for preventing the transfer of dyes in solution  
 CC from one textile to another during detergent washing, or in modifying the  
 CC colour associated with dyes and coloured compounds having different  
 CC chemical structures, such as in pulp and paper bleaching, bleaching the  
 CC colour of stains on fabric and in detergent and textile applications.  
 XX Sequence 21 AA;  
 SQ

Query Match 84.1%; Score 37; DB 22; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 1.4;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7  
 | | | | |  
 Db 14 hlhgsfs 20

RESULT 5  
 AAB20098  
 ID AAB20098 standard; Peptide; 21 AA.

XX AAB20098;  
 AC 23-APR-2001 (first entry)  
 DT Stachybotrys chartarum phenol oxidase B peptide.  
 XX Phenol oxidising enzyme; phenol oxidase B; bleach; pulp; paper;  
 DE textile; detergent.  
 KW Stachybotrys chartarum.  
 XX US6168936-B1.  
 XX PN 02-JAN-2001.  
 XX PD 22-SEP-1999; 99US-0401476.  
 XX PF 22-SEP-1999; 99US-0401476.  
 XX PR (GEMV ) GENENCOR INT INC.  
 XX PA Wang H;  
 XX PI WPI; 2001-136715/14.  
 XX DR New phenol oxidizing enzyme, also useful in the detergent, paper and  
 XX pulp, textile or food industries, especially in modifying the colour  
 XX associated with dyes and coloured compounds, as well as in anti-dye  
 XX transfer applications -  
 XX Example 2; Column 13; 23pp; English.  
 XX CC The present sequence is that of an isolated peptide of the  
 CC phenol oxidase B enzyme of Stachybotrys chartarum M0CL 38898. The  
 CC peptide was isolated from purified enzyme by endoLysC digestion  
 CC and HPLC separation. A primer (see AAF30030) based on the peptide  
 CC was used in the PCR amplification of the S. chartarum phenol  
 CC oxidase B gene (spob, see AAF30029). The invention provides phenol  
 CC oxidising enzymes such as S. chartarum phenol oxidase B (see  
 CC AAB20097), or enzymes having at least 68% identity to it, nucleic  
 CC acids encoding them, expression vectors, filamentous fungus and  
 CC yeast host cells, and methods for the recombinant production of the  
 CC enzymes. The phenol oxidising enzymes are useful for bleaching  
 CC pulp and paper, fabric stains, and in detergent and textile  
 CC applications.  
 XX Sequence 21 AA;  
 SQ

Query Match 84.1%; Score 37; DB 22; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 1.4;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7  
 | | | | |  
 Db 14 hlhgsfs 20

RESULT 6  
 AAR40843  
 ID AAR40843 standard; Protein; 572 AA.  
 XX AC AAR40843;  
 XX DT 24-FEB-1994 (first entry)  
 XX DE Bilirubin oxidase.  
 XX KW Bilirubin; oxidase; analytical; BO; expression vector; PCR;  
 KW polymerase chain reaction.  
 XX OS Myrothecium verrucaria.

XX Key Location/Qualifiers  
 FT Peptide 1..38  
 FT /label= sig\_peptide  
 FT 39..534  
 FT Protein  
 FT /label= mat\_protein  
 XX  
 PN JF05199882-A.  
 XX  
 PD 10-AUG-1993.  
 XX  
 XX 24-JAN-1992; 92JP-0034126.  
 XX  
 PR 24-JAN-1992; 92JP-0034126.  
 XX  
 XX (AMANO ) AMANO PHARM KK.  
 PA  
 XX WPI; 1993-284681/36.  
 DR  
 DR N-PSDB; AAQ47790.  
 XX  
 PT Bilirubin oxidase prepn. useful as an analytical enzyme - by  
 PT culturing bilirubin oxidase in transformant culture  
 XX  
 PS Claim 1; Page 29-32; 32pp; Japanese.  
 XX  
 CC The sequence encodes bilirubin oxidase. The protein produced has a  
 CC 38 amino acid signal peptide which is removed to give the mature  
 CC protein (AAR40843).  
 XX  
 SQ Sequence 572 AA;

Query Match 84.1%; Score 37; DB 14; Length 572;  
 Best Local Similarity 85.7%; Pred. No. 42;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7  
 |||||: 138 hlhgsfs 138  
 Db

RESULT 7  
 AAB81506  
 ID AAB81506 standard; Protein; 578 AA.  
 AC  
 XX AAB81506;  
 XX  
 DT 18-JUN-2001 (first entry)  
 XX  
 DE Bilirubin oxidase.  
 XX  
 KW Bilirubin oxidase; phenol oxidising enzyme; phenol oxidase B;  
 KW detergent; paper production; pulp production; textile; food industry;  
 KW bleaching.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200121748-A1.  
 PN  
 XX  
 PD 29-MAR-2001.  
 XX  
 PF 06-SEP-2000; 2000WO-EP08840.  
 XX  
 PR 22-SEP-1999; 99EP-0203120.  
 XX  
 XX (UNIL ) UNILEVER NV.  
 PA (UNIL ) UNILEVER PLC.  
 PA (HIND-) HINDUSTAN LEVER LTD.  
 XX  
 XX Convents D, Doornink M, De Vries CH, Wang H;  
 PI  
 XX WPI; 2001-273462/28.  
 DR  
 XX

PT New detergent compositions comprising a phenol oxidizing enzyme useful  
 PT in detergent or cleaning compositions, fiber treatment, processing,  
 PT finishing or production, paper and pulp production, or in starch  
 PT processing applications -  
 XX  
 PS Example 4; Fig 4; 46pp; English.  
 XX  
 CC The present sequence was used for comparison with the Stachybotrys  
 CC chartarum phenol oxidising enzyme. The invention relates to detergent  
 CC compositions comprising one or more surfactants and a phenol oxidising  
 CC enzyme having at least 68% identity to the Stachybotrys chartarum phenol  
 CC oxidising enzyme. Phenol oxidising enzymes may be used in the detergent,  
 CC paper, pulp, textile and food industries. They are used for preventing  
 CC the transfer of dyes in solution from one textile to another dye and  
 CC detergent washing, or in modifying the colour associated with dyes and  
 CC coloured compounds having different chemical structures, such as in pulp  
 CC and paper bleaching, bleaching the colour of stains on fabric and in  
 CC detergent and textile applications.  
 XX  
 SQ Sequence 578 AA;

Query Match 84.1%; Score 37; DB 22; Length 578;  
 Best Local Similarity 85.7%; Pred. No. 43;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSFA 7  
 |||||: 135 hlhgsfs 141  
 Db

RESULT 8  
 AAB81505  
 ID AAB81505 standard; Protein; 583 AA.  
 AC  
 XX AAB81505;  
 XX  
 DT 18-JUN-2001 (first entry)  
 XX  
 DE Stachybotrys chartarum phenol oxidase B enzyme.  
 XX  
 KW Stachybotrys phenol oxidase B; spoB; phenol oxidising enzyme;  
 KW detergent; paper production; pulp production; textile; food industry;  
 KW bleaching.  
 XX  
 OS Stachybotrys chartarum.  
 XX  
 XX WO200121748-A1.  
 PN  
 XX  
 PD 29-MAR-2001.  
 XX  
 PF 06-SEP-2000; 2000WO-EP08840.  
 XX  
 PR 22-SEP-1999; 99EP-0203120.  
 XX  
 XX (UNIL ) UNILEVER NV.  
 PA (UNIL ) UNILEVER PLC.  
 PA (HIND-) HINDUSTAN LEVER LTD.  
 XX  
 XX Convents D, Doornink M, De Vries CH, Wang H;  
 PI  
 XX WPI; 2001-273462/28.  
 DR N-PSDB; AAF82586.  
 XX  
 PT New detergent compositions comprising a phenol oxidizing enzyme useful  
 PT in detergent or cleaning compositions, fiber treatment, processing,  
 PT finishing or production, paper and pulp production, or in starch  
 PT processing applications -  
 XX  
 PS Claim 1; Fig 2; 46pp; English.  
 XX  
 CC The present sequence is a Stachybotrys chartarum phenol oxidising  
 CC enzyme. The invention relates to detergent compositions comprising one or

CC more surfactants and a phenol oxidising enzyme having at least 68%  
 CC identity to the Stachybotrys chartarum phenol oxidising enzyme. Phenol  
 CC oxidising enzymes may be used in the detergent, paper, pulp, textile and  
 CC food industries. They are used for preventing the transfer of dyes in  
 CC solution from one textile to another during detergent washing, or in  
 CC modifying the colour associated with dyes and coloured compounds having  
 CC different chemical structures, such as in pulp and paper bleaching,  
 CC bleaching the colour of stains on fabric and in detergent and textile  
 CC applications.  
 XX  
 SQ Sequence 583 AA;

Query Match 84.1%; Score 37; DB 22; Length 583;  
 Best Local Similarity 85.7%; Pred. No. 43;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 7  
 Db 135 hlhgfs 141  
 |||||:

RESULT 9  
 AAB20097  
 ID AAB20097 standard; Protein; 583 AA.  
 XX  
 AC AAB20097;

DT 23-APR-2001 (first entry)

XX Stachybotrys chartarum phenol oxidase B.

XX Phenol oxidising enzyme; phenol oxidase B; spoB gene; bleach;  
 KW pulp; paper; textile; detergent.

XX Stachybotrys chartarum.

XX US6168936-B1.

XX 02-JAN-2001.

XX 22-SEP-1999; 99US-0401476.

XX 22-SEP-1999; 99US-0401476.

XX (GEMV ) GENENCOR INT INC.

XX Wang H;

XX WPI; 2001-136715/14.

DR N-PSDB; AAF30028, AAF20029.

XX New phenol oxidizing enzyme, also useful in the detergent, paper and  
 PT pulp, textile or food industries, especially in modifying the colour  
 PT associated with dyes and coloured compounds, as well as in anti-dye  
 PT transfer applications -

XX Claim 1; Fig 2; 23pp; English.

XX The present sequence is that of Stachybotrys chartarum MUCL 38898  
 CC phenol oxidase B, as deduced from isolated genomic DNA (see  
 CC AAF30028). The invention provides phenol oxidising enzymes such  
 CC as phenol oxidase B, or enzymes having at least 68% identity to  
 CC it, nucleic acids encoding them, expression vectors, filamentous  
 CC fungus and yeast host cells, and methods for the recombinant  
 CC production of the phenol oxidising enzymes. The enzymes are useful  
 CC for bleaching pulp and paper, fabric stains, and in detergent and  
 CC textile applications. They show optimal activity at pH range 5-11,  
 CC 7-10.5 or 8-10, and at 20-60 or 20-40 degree C.

XX Sequence 583 AA;

Query Match 84.1%; Score 37; DB 22; Length 583;  
 Best Local Similarity 85.7%; Pred. No. 43;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 7  
 Db 135 hlhgfs 141  
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RESULT 10  
 AAY69204  
 ID AAY69204 standard; Protein; 602 AA.  
 XX  
 AC AAY69204;

DT 30-MAY-2000 (first entry)

XX Amino acid sequence of a phenol oxidising enzyme.

XX Phenol oxidizing enzyme; fungus; redox reaction; detergent; bleaching;  
 KW fabric; pulp; paper; decolourisation; plant-derived food product;  
 KW coloured compound; porphyrin; tannin; polyphenol; carotenoid;  
 KW anthocyanin; Maillard reaction product.

XX Acremonium murorum.

XX WO200005349-A1.

XX 03-FEB-2000.

XX 13-JUL-1999; 99WO-EP04922.

XX 21-JUL-1998; 98EP-0202454.

XX (UNIL ) UNILEVER NV.

PA (UNIL ) UNILEVER PLC.

PA (HIND-) HINDUSTAN LEVER LTD.

XX Convents D, Gouka RJ, Van Der Heiden M, Swarthoff T, Verrips CT;

XX WPI; 2000-195101/17.

DR N-PSDB; AAZ61243.

XX Phenol-oxidizing enzyme from Acremonium, used in detergent compositions  
 PT for bleaching stains on fabrics -

XX Claim 5; Page 41-43; 45pp; English.

XX The present sequence represents a phenol oxidizing enzyme from the  
 CC fungus Acremonium murorum. The enzyme has the CBS accession number  
 CC 157.72. The enzyme catalyses redox reactions and is specific for  
 CC molecular oxygen as the electron acceptor. The phenol oxidising enzyme  
 CC is specifically used in detergents for bleaching strains on fabrics,  
 CC but also for bleaching pulp and paper and for decolourisation of  
 CC plant-derived food products. The enzyme has a pH optimum in the  
 CC alkaline to neutral range and can bleach a wide variety of coloured  
 CC compounds, e.g. porphyrins, tannins, polyphenols, carotenoids,  
 CC anthocyanins and Maillard reaction products.

XX Sequence 602 AA;

Query Match 84.1%; Score 37; DB 21; Length 602;  
 Best Local Similarity 85.7%; Pred. No. 44;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 7  
 Db 154 hlhgfs 160  
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RESULT 11  
 AAG42074

ID AAG42074 standard; Protein; 240 AA.  
AC AAG42074;  
XX 18-OCT-2000 (first entry)  
DT  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52426.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
XX 06-SEP-2000.  
PD  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
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XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
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PR 25-MAR-1999; 99US-0126264.  
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PR 01-APR-1999; 99US-0127462.  
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PR 08-APR-1999; 99US-0128714.  
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Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHGSFAS 8
Db 11 lhgsfas 17

RESULT 12
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ID AAG54727 standard; Protein; 242 AA.
XX
AC AAG54727;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69855.
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 25-MAR-1999; 99US-0126264.
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XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

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XX 18-OCT-2000 (first entry)

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XX Protein identification; signal transduction pathway; metabolic pathway;

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XX Arabidopsis thaliana.

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KW Drosophila; developmental biology; cell signalling; insecticide;  
pharmaceutical.

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OS Drosophila melanogaster.

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PN WO200171042-A2.

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PF 23-MAR-2001; 2001WO-US09231.

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PR 11-JUL-2000; 2000US-0614150.

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PA (PEKE ) PE CORP NY.

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PI Venter JC, Adams M, Li PWD, Myers EW;

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DR WPI; 2001-656860/75.

DR N-PSDB; ABL08366.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
XX Disclosure; SEQ ID NO 19581; 21pp + Sequence Listing; English.  
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XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
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GenCore version 4.5  
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OM protein - protein search, using sw model

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Title: US-09-339-922A-106

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; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
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Query Match      84.1%; Score 37; DB 4; Length 21;
Best Local Similarity 85.7%; Pred. No. 0.42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 HLHGSPA 7
DB      14 HLHGSPS 20

```

```

RESULT 2
US-09-401-476-4
; Sequence 4, Application US/09401476
; Patent No. 6168936
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes
; FILE REFERENCE: GC584
; CURRENT APPLICATION NUMBER: US/09/401,476
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Stachybotrys charatum
US-09-401-476-4

```

```

Query Match      84.1%; Score 37; DB 4; Length 572;

```

Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 7  
| | | | |  
Db 132 HLHGSA 138

RESULT 3  
US-09-401-476-2  
; Sequence 2, Application US/09401476  
; Patent No. 6168936  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Huaming  
; TITLE OF INVENTION: No. 6168936el Phenol Oxidizing Enzymes  
; FILE REFERENCE: GC584  
; CURRENT APPLICATION NUMBER: US/09/401.476  
; CURRENT FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 583  
; TYPE: PRT  
; ORGANISM: Stachybotrys chartarum  
US-09-401-476-2

Query Match 84.1%; Score 37; DB 4; Length 583;  
Best Local Similarity 85.7%; Pred. No. 14;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 7  
| | | | |  
Db 135 HLHGSA 141

RESULT 4  
US-08-655-821-16  
; Sequence 16, Application US/08655821  
; Patent No. 5846718  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Ying  
; TITLE OF INVENTION: IDENTIFICATION OF PYRAZINAMIDE-RESISTANT  
; TITLE OF INVENTION: MYCOBACTERIA AND METHODS FOR TREATING  
; TITLE OF INVENTION: MYCOBACTERIAL INFECTIONS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/655,821  
; FILING DATE: 31-MAY-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ellison, Eldora L.  
; REGISTRATION NUMBER: 39,967  
; REFERENCE/DOCKET NUMBER: 07662/003001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 213 amino acids

; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-655-821-16

Query Match 72.7%; Score 32; DB 2; Length 213;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HGSEAS 8  
| | | | |  
Db 58 HGSEAS 63

RESULT 5  
US-08-519-081-2  
; Sequence 2, Application US/08519081  
; Patent No. 5883240  
; GENERAL INFORMATION:  
; APPLICANT: Baker Medical Research, Institute  
; TITLE OF INVENTION: Genetic sequences encoding  
; TITLE OF INVENTION: glucocorticoid dehydrogenases and uses therefor  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/519,081  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 405 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-519-081-2

Query Match 72.7%; Score 32; DB 2; Length 405;  
Best Local Similarity 83.3%; Pred. No. 87;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLHGSA 6  
| | | | |  
Db 302 HLHGSA 307

RESULT 6  
US-08-754-369-2  
; Sequence 2, Application US/08754369  
; Patent No. 5965372  
; GENERAL INFORMATION:  
; APPLICANT: Baker Medical Research, Institute  
; TITLE OF INVENTION: Genetic sequences encoding  
; TITLE OF INVENTION: glucocorticoid dehydrogenases and uses therefor  
; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/754,369  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 405 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-754-369-2

Query Match 72.7%; Score 32; DB 2; Length 405;  
Best Local Similarity 83.3%; Pred. No. 87;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLHGSF 6  
Db 302 HLHGQF 307

RESULT 7  
US-08-637-759B-375  
; Sequence 375, Application US/08637759B  
; Patent No. 5876931  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/637,759B  
; FILING DATE: 03-MAY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/02875  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPMS 101  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 375:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 384 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; US-08-637-759B-375

Query Match 70.5%; Score 31; DB 2; Length 384;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLHGSFA 7  
Db 154 YLHGAF 160

RESULT 8  
US-08-871-355A-375  
; Sequence 375, Application US/08871355A  
; Patent No. 6015669  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/871,355A  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/02875  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPMS 101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 375:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 384 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; US-08-871-355A-375

Query Match 70.5%; Score 31; DB 3; Length 384;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;



QY 1 HLHGSA 7  
:|||||  
Db 154 YLHGAF 160

## RESULT 9

US-09-201-945-375  
; Sequence 375, Application US/09201945  
; Patent No. 6342215  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/201.945  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/637,759  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPS 101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 375:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 384 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEetical: NO  
US-09-201-945-375

Query Match 70.5%; Score 31; DB 4; Length 384;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 7  
:|||||  
Db 154 YLHGAF 160

## RESULT 10

US-09-154-802-1  
; Sequence 1, Application US/09154802  
; Patent No. 5989822  
; GENERAL INFORMATION:  
; APPLICANT: Y. Tom Tang  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: ATP SYNTHASE SUBUNIT HOMOLOG  
; FILE REFERENCE: PF-0596 US  
; CURRENT APPLICATION NUMBER: US/09/154.802

; CURRENT FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: 1887516  
US-09-154-802-1

Query Match 68.2%; Score 30; DB 2; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 5  
:|||||  
Db 27 HLHGSA 31

## RESULT 11

US-09-373-029-1  
; Sequence 1, Application US/09373029  
; Patent No. 6036954  
; GENERAL INFORMATION:  
; APPLICANT: Y. Tom Tang  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: ATP SYNTHASE SUBUNIT HOMOLOG  
; FILE REFERENCE: PF-0596 US  
; CURRENT APPLICATION NUMBER: US/09/373.029  
; CURRENT FILING DATE: 1999-08-11  
; EARLIER APPLICATION NUMBER: 09/154,802  
; EARLIER FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: 1887516  
US-09-373-029-1

Query Match 68.2%; Score 30; DB 3; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGSA 5  
:|||||  
Db 27 HLHGSA 31

## RESULT 12

US-08-702-153-2  
; Sequence 2, Application US/08702153  
; Patent No. 5955332  
; GENERAL INFORMATION:  
; APPLICANT: PREVOTS, Fabien  
; APPLICANT: TOLOU, Sandrine  
; APPLICANT: DALOYAU, Marl ne  
; TITLE OF INVENTION: Nucleic acid sequences and plasmids  
; TITLE OF INVENTION: comprising at least one phage resistance mechanism,  
; TITLE OF INVENTION: bacteria containing them, and their use  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street N.W., Suite 500  
; CITY: Washington, D.C.  
; COUNTRY: USA

ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,153  
FILING DATE: 23-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95 09980  
FILING DATE: 22-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16781/625  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 346 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-702-153-2

Query Match 68.2%; Score 30; DB 2; Length 346;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HLHGS 5  
Db 194 HLHGS 198  
RESULT 13  
US-08-702-153-4  
Sequence 4, Application US/08702153  
Patent No. 595332  
GENERAL INFORMATION:  
APPLICANT: PREVOTS, Fabien  
APPLICANT: TOLOU, Sandrine  
APPLICANT: DALOYAU, Marl ne  
TITLE OF INVENTION: Nucleic acid sequences and plasmids  
TITLE OF INVENTION: comprising at least one phage resistance mechanism,  
TITLE OF INVENTION: bacteria containing them, and their use  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,153  
FILING DATE: 23-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95 09980  
FILING DATE: 22-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16781/625

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 346 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-702-153-4  
Query Match 68.2%; Score 30; DB 2; Length 346;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HLHGS 5  
Db 194 HLHGS 198  
RESULT 14  
US-09-240-639-4  
Sequence 4, Application US/09240639  
Patent No. 6350447  
GENERAL INFORMATION:  
APPLICANT: Chadwick, Brian Paul  
APPLICANT: Frischauf, Anna-Maria  
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE  
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS  
FILE REFERENCE: 9598-066  
CURRENT APPLICATION NUMBER: US/09/240,639  
CURRENT FILING DATE: 1998-01-29  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 529  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-240-639-4

Query Match 68.2%; Score 30; DB 4; Length 529;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HLHGS 5  
Db 127 HLHGS 131  
RESULT 15  
US-09-036-987A-2  
Sequence 2, Application US/09036987A  
Patent No. 6143526  
GENERAL INFORMATION:  
APPLICANT: Baltz, Richard H.  
APPLICANT: Broughton, Mary C.  
APPLICANT: Crawford, Kathryn P.  
APPLICANT: Madduri, Krishnamurthy  
APPLICANT: Merlo, Donald J.  
APPLICANT: Treadway, Patti J.  
APPLICANT: Turner, Jan R.  
APPLICANT: Waldron, Clive  
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
TITLE OF INVENTION: Production  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dow Agrosciences LLC Patent Department  
STREET: 9330 Zionsville Road  
CITY: Indianapolis  
STATE: Indiana

; COUNTRY: USA  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/036,987A  
; FILING DATE: 09-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stuart, Donald R  
; REGISTRATION NUMBER: 28,479  
; REFERENCE/DOCKET NUMBER: 50,608  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317)337-4816  
; TELEFAX: (317)337-4847  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2595 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-036-987A-2

Query Match 68.2%; Score 30; DB 4; Length 2595;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLHGS 5  
|  
|  
|  
|  
|  
Db 1100 HLHGS 1104

Search completed: August 19, 2002, 06:34:42  
Job time: 1203 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:07 ; Search time 78.53 Seconds  
(without alignments)  
13.460 Million cell updates/sec

Title: US-09-339-922A-108

Perfect score: 56

Sequence: 1 QASQSIHNLH 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	82.1	106	2	Ig kappa chain V r
2	46	82.1	123	2	Ig kappa chain pre
3	45	80.4	102	2	Ig kappa chain V r
4	45	80.4	104	2	Ig kappa chain V r
5	45	80.4	107	2	anti-glycoprotein
6	45	80.4	107	2	anti-glycoprotein
7	45	80.4	138	2	Ig kappa chain pre
8	44	78.6	107	2	anti-glycoprotein
9	42	75.0	107	2	Ig kappa chain V r
10	41	73.2	96	2	Ig kappa chain V r
11	41	73.2	103	2	Ig kappa chain V r
12	39	69.6	62	2	Ig kappa chain V r
13	39	69.6	87	2	Ig kappa chain V r
14	39	69.6	88	2	Ig kappa chain V r
15	39	69.6	88	2	Ig kappa chain V r
16	39	69.6	95	2	Ig kappa chain V r
17	39	69.6	108	2	Ig kappa chain V r
18	39	69.6	110	2	Ig kappa chain V r
19	39	69.6	117	2	Ig kappa chain V r
20	39	69.6	117	2	Ig kappa chain V r
21	39	69.6	127	2	Ig kappa chain V r
22	39	69.6	129	1	Ig kappa chain pre
23	39	69.6	129	2	Ig kappa chain V r
24	37	66.1	106	2	Ig kappa chain (an
25	37	66.1	122	2	Ig kappa chain - h
26	37	66.1	1085	2	hypothetical prote
27	37	66.1	10797	2	probable peptide s
28	36	64.3	115	1	Ig kappa chain pre
29	36	64.3	115	2	Ig kappa chain pre

30 36 64.3 117 1 K4RBF2 Ig kappa chain pre  
31 36 64.3 122 2 S40314 Ig kappa chain - h  
32 36 64.3 506 2 A81191 hypothetical prote  
33 36 64.3 833 2 F81989 hypothetical prote  
34 35.5 63.4 93 2 S17634 Ig kappa chain V r  
35 35 62.5 92 1 KVRB38 Ig kappa chain V r  
36 35 62.5 93 2 S38564 Ig kappa chain V r  
37 35 62.5 107 2 B28044 Ig kappa chain V r  
38 35 62.5 107 2 A28044 Ig kappa chain V r  
39 35 62.5 107 2 D48677 Ig kappa chain V-J  
40 35 62.5 107 2 B49026 Ig kappa chain (cl  
41 35 62.5 107 2 S69901 Ig kappa chain (cl  
42 35 62.5 107 2 S69906 Ig kappa chain (cl  
43 35 62.5 108 1 KVM5AR Ig kappa chain V r  
44 35 62.5 108 2 C26405 Ig kappa chain V r  
45 35 62.5 108 2 PL0282 Ig kappa chain V r

#### ALIGNMENTS

RESULT 1

PL0267  
Ig kappa chain V region (anti-DNA, Dp12VK) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
C:Accession: PL0267  
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990  
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat  
A:Reference number: PL0231; MUID:90111618  
A:Accession: PL0267  
A:Molecule type: mRNA  
A:Residues: 1-106 <SHL>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-23/Region: framework 1  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:24-34/Region: complementarity-determining 1  
F:35-49/Region: framework 2  
F:50-56/Region: complementarity-determining 2  
F:57-88/Region: framework 3  
F:89-97/Region: complementarity-determining 3  
F:98-106/Region: framework 4

Query Match 82.1%; Score 46; DB 2; Length 106;  
Best Local Similarity 81.8%; Pred No. 0.098;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSIHNLH 11  
:|||||||:  
DB 24 RASQSIHNLH 34

RESULT 2

S35479  
Ig kappa chain precursor V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: S35479  
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.  
Nucleic Acids Res. 20, 4099, 1992  
A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from  
A:Reference number: S35479; MUID:92375706  
A:Accession: S35479  
A>Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-123 <TAK>  
A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148  
C:Genetics:  
A:Map position: 6  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>  
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>  
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 46; DB 2; Length 123;  
Best Local Similarity 81.8%; Pred. No. 0.12; Indels 0; Gaps 0;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11  
:|||||:||  
Db 36 RASQSISNHLH 46

RESULT 3  
S26346  
Ig kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26346  
R:Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e  
A:Reference number: S26309; MUID:91341421  
A:Accession: S26346  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-102 <STA>  
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:g1334075  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 102;  
Best Local Similarity 81.8%; Pred. No. 0.15; Indels 0; Gaps 0;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11  
:|||||:||  
Db 22 RASQSISNHLH 32

RESULT 4  
B43413  
Ig kappa chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: B43413  
R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum  
J. Biol. Chem. 267, 18085-18092, 1992  
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific  
A:Reference number: A43413; MUID:92388177  
A:Accession: B43413  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-104 <TOM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 104;  
Best Local Similarity 81.8%; Pred. No. 0.15; Indels 0; Gaps 0;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11  
:|||||:||  
Db 21 RASQSISNHLH 31

RESULT 5  
B45722

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: B45722  
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va  
J. Virol. 67, 489-496, 1993  
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on  
A:Reference number: A45722; MUID:93100833  
A:Accession: B45722  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-107 <SIM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:120590)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.16; Indels 0; Gaps 0;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11  
:|||||:||  
Db 24 RASQSISNHLH 34

RESULT 6  
A45722

anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (C  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Mar-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: A45722  
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va  
J. Virol. 67, 489-496, 1993  
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on  
A:Reference number: A45722; MUID:93100833  
A:Accession: A45722  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-107 <SIM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 45; DB 2; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.16; Indels 0; Gaps 0;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11  
:|||||:||  
Db 24 RASQSISNHLH 34

RESULT 7  
A26471

Ig kappa chain precursor V region (MAK33) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 23-Jul-1999  
C:Accession: A26471  
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.  
Gene 51, 13-19, 1987  
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat  
A:Reference number: A91572; MUID:87248058  
A:Accession: A26471  
A:Molecule type: mRNA  
A:Residues: 1-138 <BUC>

A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 80.4%; Score 45; DB 2; Length 138;  
Best Local Similarity 81.8%; Pred. No. 0.21;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSIISNHLH 11  
:|||||::||  
DB 44 RASQSIISNHLH 54

## RESULT 8

C45722  
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: C45722  
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, J.; Virol, 67, 489-496, 1993  
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on human IgG1 heavy chain variable domain (Mab 115)  
A;Reference number: A45722; MUID:93100833  
A;Accession: C45722  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-107 <SIM>  
A;Note: sequence extracted from NCBI backbone (NCBI:P120591)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: glycoprotein  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 44; DB 2; Length 107;  
Best Local Similarity 72.7%; Pred. No. 0.24;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSIISNHLH 11  
:|||||::||  
DB 24 RASQSVSNHLH 34

## RESULT 9

S32188  
Ig kappa chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S32188  
R;Izui, S.  
submitted to the EMBL Data Library, February 1993  
A;Reference number: S32188  
A;Accession: S32188  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-107 <IZU>  
A;Cross-references: EMBL:X70090; NID:g288253; PIDN:CAA4695.1; PID:g288254  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 42; DB 2; Length 107;  
Best Local Similarity 72.7%; Pred. No. 0.59;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSIISNHLH 11  
:|||||::||  
DB 24 RASQSIISNHLH 34

## RESULT 10

G33730  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Ig kappa chain V region (23.32) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 21-Jan-2000  
C;Accession: G33730  
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.

A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u  
A;Reference number: A33730; MUID:89367325  
A;Accession: G33730  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-96 <LAW>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 96;  
Best Local Similarity 72.7%; Pred. No. 0.82;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSIISNHLH 11  
:|||||::||  
DB 24 RASQSIISNHLH 34

## RESULT 11

S19975  
Ig kappa chain V region (M-7408) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S19975  
R;Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A;Description: Structural characterization of CD4 mAb.  
A;Reference number: S19963  
A;Accession: S19975  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-103 <WEI>  
A;Cross-references: EMBL:X65097; NID:g52296; PIDN:CAA46225.1; PID:g52297  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F:11-85/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 41; DB 2; Length 103;  
Best Local Similarity 72.7%; Pred. No. 0.89;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSIISNHLH 11  
:|||||::||  
DB 19 RASQSIISNHLH 29

## RESULT 12

S42265  
Ig kappa chain V region (018) - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
C;Accession: S42265  
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; J. Immunol. 147, 4007-4013, 1991  
A;Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus  
A;Reference number: S42263; MUID:92043792  
A;Accession: S42265  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-62 <SCO>  
A;Cross-references: EMBL:M64856  
C;Genetics:  
A;Introns: 19/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 69.6%; Score 39; DB 2; Length 62;  
Best Local Similarity 72.7%; Pred. No. 1.2;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11  
|||||  
Db 24 QASQDISNYLN 34

## RESULT 13

Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
C:Accession: I52592  
R:Wagner, S.D.; Martinelli, V.; Luzzatto, L.  
Blood 83, 3647-3653, 1994  
A:Title: Similar patterns of V kappa gene usage but different degrees of somatic mutation  
A:Reference number: I52592; MUID:94264318  
A:Accession: I52592  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-87 <RES>  
A:Cross-references: GB:S71057; NID:G547053; PIDN:AAB30971.1; PID:G547054  
C:Genetics:  
A:Gene: IgKV  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 39; DB 2; Length 87;  
Best Local Similarity 72.7%; Pred. No. 1.8;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11  
|||||  
Db 17 QASQDISNYLN 27

## RESULT 14

Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S34088  
R:Wagner, S.D.; Luzzatto, L.  
Eur. J. Immunol. 23, 391-397, 1993  
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed  
A:Reference number: S34076; MUID:93170387  
A:Accession: S34088  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-88 <WAG>  
A:Cross-references: EMBL:X67172  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 39; DB 2; Length 88;  
Best Local Similarity 72.7%; Pred. No. 1.8;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11  
|||||  
Db 17 QASQDISNYLN 27

## RESULT 15

Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S34087  
R:Wagner, S.D.; Luzzatto, L.  
Eur. J. Immunol. 23, 391-397, 1993  
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed  
A:Reference number: S34076; MUID:93170387  
A:Accession: S34087  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-88 <WAG>  
A:Cross-references: EMBL:X67171  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:9-83/Domain: immunoglobulin homology <IMM>

Ig kappa chain V region - human

C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S34087  
R:Wagner, S.D.; Luzzatto, L.  
Eur. J. Immunol. 23, 391-397, 1993  
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed  
A:Reference number: S34076; MUID:93170387  
A:Accession: S34087  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-88 <WAG>  
A:Cross-references: EMBL:X67171  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 39; DB 2; Length 88;  
Best Local Similarity 72.7%; Pred. No. 1.8;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11  
|||||  
Db 17 QASQDISNYLN 27

Search completed: August 19, 2002, 06:36:07  
Job time: 1288 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:10 ; Search time 51.81 Seconds  
(without alignments)  
8.221 Million cell updates/sec

Title: US-09-339-922A-108

Perfect score: 56

Sequence: 1 QASQISNHLH 11

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	69.6	129	1 KVIW_HUMAN	P04431 homo sapien
2	36	64.3	129	1 KVI0_RABIT	P01691 oryctolagus
3	36	64.3	129	1 KV3H_HUMAN	P04207 homo sapien
4	35	62.5	92	1 KV09_RABIT	P01690 oryctolagus
5	35	62.5	108	1 KV5K_MOUSE	P01644 mus musculus
6	35	62.5	108	1 KV5L_MOUSE	P01645 mus musculus
7	35	62.5	108	1 KV5M_MOUSE	P01646 mus musculus
8	35	62.5	455	1 NH55_CAEEL	O16962 caenorhabdi
9	34	60.7	108	1 KV1B_HUMAN	P01594 homo sapien
10	34	60.7	108	1 KV1Q_HUMAN	P01609 homo sapien
11	34	60.7	108	1 KV5U_MOUSE	P04946 mus musculus
12	34	60.7	379	1 FLIP_BUCAI	P57184 buchnera ap
13	34	60.7	446	1 CLUS_PIG	Q29549 sus scrofa
14	34	60.7	746	1 YUV1_CAEEL	P54073 caenorhabdi
15	34	60.7	866	1 MYSP_SCHJA	Q05870 schistosoma
16	34	60.7	866	1 MYSP_SCHMA	P06198 schistosoma
17	33	58.9	108	1 KVIH_HUMAN	P01600 homo sapien
18	33	58.9	108	1 KV5J_MOUSE	P01643 mus musculus
19	33	58.9	111	1 KV12_RABIT	P01693 oryctolagus
20	33	58.9	157	1 HMAA_SCHGR	P29556 schistosom
21	33	58.9	447	1 CLUS_RABIT	Q9xsc5 oryctolagus
22	33	58.9	494	1 YPCL_CAEEL	Q11178 caenorhabdi
23	33	58.9	553	1 ASNB_ECOLI	P22106 escherichia
24	33	58.9	594	1 Y410_ARATH	P16128 arabidopsis
25	33	58.9	708	1 GIT2_MOUSE	Q9j1q2 mus musculus
26	33	58.9	759	1 GIT2_HUMAN	Q14161 homo sapien
27	33	58.9	886	1 ORCL_KLULA	P54788 kinuiveromyc
28	33	58.9	1581	1 ACC8_CRICR	Q09427 cricetus cr
29	33	58.9	1581	1 ACC8_RAT	Q09429 rattus norv
30	33	58.9	1900	1 STW4_YEAST	P37297 saccharomyc
31	32	57.1	108	1 KV5N_MOUSE	P01647 mus musculus
32	32	57.1	108	1 KV5O_MOUSE	P01648 mus musculus
33	32	57.1	109	1 KV3F_HUMAN	P01624 homo sapien

34 32 57.1 115 1 KV3I\_HUMAN P04433 homo sapien  
35 32 57.1 237 1 MINC\_NEIMA Q91x17 neisseria m  
36 32 57.1 237 1 MINC\_NEIMB Q9k110 neisseria m  
37 32 57.1 277 1 MCRA\_ECOLI P24200 escherichia  
38 32 57.1 308 1 RIBF\_HAEIN P44957 haemophilus  
39 32 57.1 308 1 YPER\_ECOLI P77500 escherichia  
40 32 57.1 349 1 PERM\_HAEIN P43969 haemophilus  
41 32 57.1 398 1 DAP3\_HUMAN P51398 homo sapien  
42 32 57.1 432 1 RMUC\_RICCN Q92gr5 rickettsia  
43 32 57.1 445 1 ML64\_HUMAN Q14849 homo sapien  
44 32 57.1 451 1 YOEV\_BACSU P54462 bacillus su  
45 32 57.1 471 1 HH\_DROME Q02936 drosophila

#### ALIGNMENTS

RESULT 1  
KVIW\_HUMAN  
ID KVIW\_HUMAN STANDARD; PRT; 129 AA.  
AC P04431;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Walker precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85014148; PubMed=6091049;  
RA Klobbeck H.G., Combratio G., Zachau H.G.;  
RT "Immunoglobulin genes of the kappa light chain type from two human  
RT lymphoid cell lines are closely related";  
RL Nucleic Acids Res. 12:6995-7006(1984).  
CC -----  
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; X00965; CAA25477.1; ALT\_TERM.  
CC PIR; A01883; KLHUKK.  
CC HSP; P01607; IREI.  
CC InterPro; IPR003006; Ig\_MHC.  
CC InterPro; IPR003596; Ig\_V.  
CC Pfam; PF00047; Ig; 1.  
CC SMART; SM00406; IGV; 1.  
CC Immunoglobulin V region; Signal.  
CC SIGNAL 1 22  
CC CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.  
CC DOMAIN 23 45 FRAMEWORK-1.  
CC DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.  
CC DOMAIN 57 71 FRAMEWORK-2.  
CC DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.  
CC DOMAIN 79 110 FRAMEWORK-3.  
CC DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.  
CC DOMAIN 120 129 FRAMEWORK-4.  
CC DISULFID 45 110 BY SIMILARITY.  
CC NON\_TER 129 129  
CC SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 69.6%; Score 39; DB 1; Length 129;  
Best Local Similarity 72.7%; Pred. No. 0.64;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QASQISNHLH 11  
:|||||||:



```

Db 46 RASQISISNYLN 56

RESULT 2
KV10_RABIT
ID KV10_RABIT STANDARD; PRT; 117 AA.
AC P01691;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region 12F2 precursor (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83273646; PubMed=6410392;
RA Dreher K.L., Emorine L., Kindt T.J., Max E.E.;
RT "cDNA clone encoding a complete rabbit immunoglobulin kappa light
chain of b4 allotype."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4489-4493(1983).
CC -1- MISCELLANEOUS: THIS CLONE WAS DERIVED FROM THE RABBIT-MOUSE
HYBRIDOMA 12F2: THE CHAIN PRODUCED IS A MONOCLONAL ANTIBODY
AGAINST STREPTOCOCCAL GROUP C VACCINE.
CC -----
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CC -----
DR EMBL; K01358; AAB59259.1; ALT_TERM.
DR PIR; A01954; K4RBF2.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma; Signal.
FT NON_TER 1
FT SIGNAL <1 6
FT CHAIN 7 117 IG KAPPA CHAIN V REGION 12F2.
FT DOMAIN 7 29 FRAMEWORK-1.
FT DOMAIN 30 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 29 86 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12288 MW; E24A7582389E4439 CRC64;

Query Match 64.3%; Score 36; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 2.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISISNHL 10
|||||:|
Db 30 QASQISISYLN 39

RESULT 3
KV3H_HUMAN
ID KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 15-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region 12F2 precursor (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=75176905; PubMed=1094456;
RA Margolies M.N., Cannon L.E. III, Strosberg A.D., Haber E.;
RT "Diversity of light chain variable region sequences among rabbit
antibodies elicited by the same antigens."
RL Proc. Natl. Acad. Sci. U.S.A. 72:2180-2184(1975).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III

```

```

DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
light-chain gene."
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC -----
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CC -----
DR EMBL; M12740; AAA58992.1; -.
DR PIR; A01898; K3HUC1.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 64.3%; Score 36; DB 1; Length 129;
Best Local Similarity 70.0%; Pred. No. 2.6;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISISNHL 10
|||||:|
Db 44 RASQSVSNL 53

RESULT 4
KV09_RABIT
ID KV09_RABIT STANDARD; PRT; 92 AA.
AC P01690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V region 3381 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=75176905; PubMed=1094456;
RA Margolies M.N., Cannon L.E. III, Strosberg A.D., Haber E.;
RT "Diversity of light chain variable region sequences among rabbit
antibodies elicited by the same antigens."
RL Proc. Natl. Acad. Sci. U.S.A. 72:2180-2184(1975).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III

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CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.

DR PIR: A01953; KVRB38.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 >92  
FT NON\_TER 92 92  
SQ SEQUENCE 92 AA; 9730 MW; 9A36B15913CB3BEE CRC64;

Query Match 62.5%; Score 35; DB 1; Length 92;  
Best Local Similarity 80.0%; Pred. No. 2.7;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSISNHL 10  
:|||||  
Db 24 QASESISNWL 33

RESULT 5  
KV5K\_MOUSE  
ID KV5K\_MOUSE STANDARD; PRT; 108 AA.  
AC P01644;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-V region HP R16.7.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.

RC STRAIN=A/J;  
RX MEDLINE=82150934; PubMed=6801658;  
RA Siegelman M., Capra J.D.;  
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

DR PIR: A01927; KVM5AR.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Antiarsonate antibody.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 108  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 62.5%; Score 35; DB 1; Length 108;  
Best Local Similarity 63.6%; Pred. No. 3.3;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSISNHL 11  
:|||||  
Db 24 RASQDISNYLN 34

RESULT 6  
KV5L\_MOUSE  
ID KV5L\_MOUSE STANDARD; PRT; 108 AA.  
AC P01645;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-V region HP 93G7.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=A/J;  
RX MEDLINE=82150934; PubMed=6801658;  
RA Siegelman M., Capra J.D.;  
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.  
DR PIR: A01927; KVM5AR.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Antiarsonate antibody.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 108  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;

Query Match 62.5%; Score 35; DB 1; Length 108;  
Best Local Similarity 63.6%; Pred. No. 3.3;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSISNHL 11  
:|||||  
Db 24 RASQDISNYLN 34

RESULT 7  
KV5M\_MOUSE  
ID KV5M\_MOUSE STANDARD; PRT; 108 AA.  
AC P01646;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-V region HP 123E6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=A/J;  
RX MEDLINE=82150934; PubMed=6801658;  
RA Siegelman M., Capra J.D.;  
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
CC -I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

```
DR PIR: A01927; KVMASR.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match 62.5%; Score 35; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 3.3;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11
DB 24 RASQDISNYLN 34
:::|::|:|:|

RESULT 8
NH55_CAEEL STANDARD; PRT; 455 AA.
AC O16962; Q9GTF8;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Nuclear hormone receptor family member nhr-55.
GN NHR-55 OR T01G6.7
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Jones K., Bradshaw H., Graves T.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
[2]
SQ SEQUENCE OF 103-455 FROM N.A.
RA Boran A., Maina C.V., Yamamoto K., Cohen F., Sluder A.E.;
RT "Caenorhabditis elegans nuclear receptor sequences exhibit biophysical
compatibility with the ligand-binding domain fold.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ORPHAN NUCLEAR RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
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DR EMBL; AF022978; AAG24179.1; -
DR EMBL; AF273801; AAG15150.1; -
DR EMBL; AF273802; AAG15151.1; -
DR WormPep; T01G6.7; CEL3002.
DR InterPro: IPR000536; Hormone_rec_lig.
DR InterPro: IPR001628; zf-C4.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; ZnF_C4; 1.

DR PIR: PS00031; NUCLEAR_RECEPTOR; FALSE_NEG.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger. 59 124 NUCLEAR RECEPTOR-TYPE.
FT ZN_BIND 59 86 C4-TYPE.
FT ZN_FING 59 86 C4-TYPE.
FT ZN_FING 95 119 C4-TYPE.
FT DOMAIN 34 40 POLY-SER.
FT DOMAIN 43 50 POLY-SER.
SQ SEQUENCE 455 AA; 52956 MW; B56CEFA00D6B1A3 CRC64;

Query Match 62.5%; Score 35; DB 1; Length 455;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 QSISNHLH 11
DB 389 ETLNHLH 396
:::|::|::|:|

RESULT 9
KV1B_HUMAN STANDARD; PRT; 108 AA.
ID KV1B_HUMAN
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT Immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlinhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
REGION OF THE KAPPA CHAIN REI.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01862; K1HUAV.
DR HSP; P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6FB9 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 108;
```

;

```
Best Local Similarity 63.6%; Pred. No. 5.3;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 QASQDISNYL 34

RESULT 10
KV1Q_HUMAN STANDARD; PRT; 108 AA.
AC KV1Q_HUMAN
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Scw.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059271; PubMed=4435756;
RA Eulitz M., Hilschmann N.;
RT "The primary structure of a human immunoglobulin L-chain of
kappa-type (Bence-Jones protein Scw.); II: The chymotryptic peptides
and the complete amino acid sequence.";
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01875; KIHUSW.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11764 MW; 32CECDDDF9644414 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 QASQDIRKHLN 34

RESULT 11
KV5U_MOUSE STANDARD; PRT; 108 AA.
AC KV5U_MOUSE
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region NQ5-89.4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC -----
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CC -----
CC EMBL; K00745; AAA38690.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DDD CRC64;

Query Match 60.7%; Score 34; DB 1; Length 108;
Best Local Similarity 70.0%; Pred. No. 5.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQISNHLH 11
Db 25 ASQDISNYL 34

RESULT 12
FLIP_BUCAI STANDARD; PRT; 379 AA.
AC P57184;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Flagellar biosynthetic protein flip.
GN FLIP OR BU082.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: PLAYS A ROLE IN THE FLAGELLUM-SPECIFIC TRANSPORT SYSTEM
(BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.
CC -----
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CC -----

DR EMBL; AP001118; BAB12802.1; -.  
DR InterPro: IPR002039; FlIP.  
DR Pfam; PF00813; FlIP; 1.  
DR PRINTS; PR01302; TYPE3IMPPROT.  
DR PRODOM; PD002586; FlIP; 1.  
DR PROSITE; PS01060; FlIP.1; FALSE\_NEG.  
DR PROSITE; PS01061; FlIP.2; 1.  
KW Flagella; Transmembrane; Complete proteome.  
FT TRANSMEM 23 43 POTENTIAL.  
FT TRANSMEM 140 160 POTENTIAL.  
FT TRANSMEM 178 198 POTENTIAL.  
FT TRANSMEM 222 242 POTENTIAL.  
FT TRANSMEM 319 339 POTENTIAL.  
FT TRANSMEM 357 377 POTENTIAL.  
SQ SEQUENCE 379 AA; 43192 MW; DE6E1F040DA825B0 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 379;  
Best Local Similarity 87.5%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QSISNHLH 11  
|||||

Db 8 QSISNSLH 15  
|||||

## RESULT 13

CLUS\_PIG  
ID CLUS\_PIG STANDARD; PRT; 446 AA.  
AC Q29549;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Clusterin precursor (Complement cytotoxicity inhibitor) (CLI).  
GN CLI.  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92184774; PubMed=1544909;  
RA Diemer V., Hoyle M., Baglioni C., Millis A.J.;  
RT "Expression of porcine complement cytotoxicity inhibitor mRNA in  
RT cultured aortic smooth muscle cells. Changes during differentiation  
RT in vitro.";  
RL J. Biol. Chem. 267:5257-5264(1992).  
CC -!- FUNCTION: NOT YET CLEAR, IT IS KNOWN TO BE EXPRESSED IN A VARIETY  
CC OF TISSUES AND IT SEEMS TO BE ABLE TO BIND TO CELLS, MEMBRANES,  
CC AND HYDROPHOBIC PROTEINS. IT HAS BEEN ASSOCIATED WITH PROGRAMMED  
CC CELL DEATH (BY SIMILARITY).  
CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED HETERODIMER (BY  
CC SIMILARITY).  
CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND LIVER; LOWER  
CC LEVELS ARE DETECTED IN OTHER TISSUES, INCLUDING THE AORTA.  
CC -!- SIMILARITY: BELONGS TO THE CLUSTERIN FAMILY.  
CC -----  
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CC -----  
DR EMBL; M84639; AAA31013.1; -.  
DR InterPro: IPR000753; Clusterin.  
DR Pfam; PF01093; Clusterin; 1.  
DR SMART; SM00035; CLa; 1.  
DR SMART; SM00030; CLb; 1.

DR PROSITE; PS00492; CLUSTERIN\_1; 1.  
DR PROSITE; PS00493; CLUSTERIN\_2; 1.  
KW Glycoprotein; Signal.  
FT SIGNAL 1 28 BY SIMILARITY.  
FT CHAIN 29 446 CLUSTERIN.  
FT CHAIN 29 446 BETA-CHAIN (A CHAIN).  
FT CHAIN 228 446 ALPHA-CHAIN (B CHAIN).  
FT DISULFID 102 312 INTERCHAIN (BY SIMILARITY).  
FT DISULFID 113 304 INTERCHAIN (BY SIMILARITY).  
FT DISULFID 116 301 INTERCHAIN (BY SIMILARITY).  
FT DISULFID 121 294 INTERCHAIN (BY SIMILARITY).  
FT DISULFID 129 284 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 86 86 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 103 103 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 145 145 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 290 290 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 316 316 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 353 353 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 373 373 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 446 AA; 51774 MW; BID5B434B668E3AA CRC64;

Query Match 60.7%; Score 34; DB 1; Length 446;  
Best Local Similarity 54.5%; Pred. No. 28;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11  
|||||

Db 253 QAQAMDAHLH 263  
|||||

## RESULT 14

YUY1-CAEEL  
ID YUY1-CAEEL STANDARD; PRT; 746 AA.  
AC P54073; Q20418;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Hypothetical 86.9 kDa protein F44G4.1 in chromosome II precursor.  
GN F44G4.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Sims M.;  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP REVISIONS.  
RP Durbin R.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: SOME, TO YEAST YHR088W AND IMP4.  
CC -----  
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CC -----  
DR EMBL; Z49910; CAA90124.2; -.  
DR EMBL; Z70034; CAA90124.2; JOINED.  
DR WormPep; F44G4.1; CE23730.  
DR InterPro; IPR003593; AAA.  
DR InterPro; IPR001270; CLP\_AB.  
DR InterPro; IPR002799; IMP4.  
DR Pfam; PF01945; IMP4; 1.  
DR PRINTS; PR00300; CLPPROTEASEA.  
DR SMART; SM00382; AAA; 1.  
KW Hypothetical protein; Signal.

```
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 746 HYPOTHETICAL 86.9 KDA PROTEIN F44G4.1.
SQ SEQUENCE 746 AA; 86929 MW; 84333162C34A70C6 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 746;
Best Local Similarity 70.0%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNHL 10
   I I I I I I I I
Db 254 QMSSELISNHL 263

RESULT 15
MYSIP_SCHJA STANDARD; PRT; 866 AA.
AC Q05870; Q26510; Q26518;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Paramyosin (Antigen S97).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
OC Rhabditophora; Eulecithophora; Revertospermata; Mediofusata;
OC Neodermata; Trematoda; Digenea; Strigoida; Schistosomatidae;
OC Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PHILIPPINE;
RX MEDLINE=95407380; PubMed=7676905;
RA Becker M.M., Kallina B.H., Yang W., Harrop S.A., Scott J.C.,
RA Wayne G.J., Kurtis J.D., McManus D.P.;
RT "Gene cloning and complete nucleotide sequence of Philippine
RT Schistosoma japonicum paramyosin."
RL Acta Trop. 59:143-147(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JAPANESE;
RX MEDLINE=95034466; PubMed=7947464;
RA Nara T., Matsumoto N., Janechart T., Matsuda H., Yamamoto K.,
RA Iimura T., Nakamura K.I., Aikawa M., Oswald I., Sher A., Kita K.,
RA Kojima S.;
RT "Demonstration of the target molecule of a protective IgE antibody in
RT secretory glands of Schistosoma japonicum larvae."
RL Int. Immunol. 6:963-971(1994).
RN [3]
RP SEQUENCE OF 171-559 FROM N.A.
RX MEDLINE=93138870; PubMed=1487380;
RA Yang W., Wayne G.J., Sculley D.G., Liu X., McManus D.P.;
RT "Cloning and partial nucleotide sequence of Schistosoma japonicum
RT paramyosin: a potential vaccine candidate against schistosomiasis."
RL Int. J. Parasitol. 22:1187-1191(1992).
CC -!- FUNCTION: PARAMYOSIN IS A MAJOR STRUCTURAL COMPONENT OF
CC MANY THICK FILAMENTS ISOLATED FROM INVERTEBRATE MUSCLES.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC -!- DEVELOPMENTAL STAGE: MAY BE INCORPORATED INTO THE TEGUMENT DURING
CC THE DEVELOPMENT OF SCHISTOSOMA, THUS BECOMING A TARGET FOR
CC PROTECTIVE IMMUNITY DURING THE MIGRATORY PHASE OF THE PARASITE.
CC -!- SIMILARITY: HIGH, TO MYOSIN HEAVY CHAINS.
-----
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EMBL; U11825; AAA81003.1; -.
EMBL; D28811; BAA05972.1; -.
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DR EMBL; M90492; -; NOT_ANNOTATED_CDS.
DR InterPro; IPR002928; Myosin_tail.
DR Pfam; PF01576; Myosin_tail; 1.
KW Coiled coil; Muscle protein; Thick filament; Myosin; Antigen.
FT DOMAIN 1 22 NONHELICAL REGION (POTENTIAL).
FT DOMAIN 23 839 COILED COIL (POTENTIAL).
FT DOMAIN 840 866 NONHELICAL REGION (POTENTIAL).
FT DISULFID 750 750 INTERCHAIN (POTENTIAL).
FT CONFLICT 371 371 E -> D (IN REF. 1).
FT CONFLICT 559 559 E -> K (IN REF. 3).
SQ SEQUENCE 866 AA; 100541 MW; 37D7BDF2CF32775D CRC64;
```

Query Match 60.7%; Score 34; DB 1; Length 866;  
Best Local Similarity 70.0%; Pred. No. 60;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNHL 10  
 I I I I I I I I  
Db 475 QASQAALNHL 484

Search completed: August 19, 2002, 06:59:11  
Job time: 1376 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:15 ; Search time 140.4 seconds  
(without alignments)  
13.554 Million cell updates/sec

Title: US-09-339-922A-108

Perfect score: 56

Sequence: 1 QASQISINHLH 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	42	75.0	116	4	Q96PF6	Q96pf6 homo sapien
2	42	75.0	431	5	Q966H7	Q966h7 caenorhabdi
3	41	73.2	414	5	Q966H8	Q966h8 caenorhabdi
4	39	69.6	107	4	Q9UL81	Q9ul81 homo sapien
5	38	67.9	401	5	Q9VM04	Q9vm04 drosophila
6	38	67.9	417	13	P79751	P79751 fugu rubrip
7	37	66.1	1085	16	Q9KNE5	Q9kne5 vibrio chol
8	37	66.1	1574	16	Q92M45	Q92m45 rhizobium m
9	37	66.1	1581	2	Q9ZFB9	Q9zfb9 rhizobium e
10	37	66.1	10797	3	Q94116	Q94116 aureobasidi
11	36	64.3	506	16	Q9KOS2	Q9kos2 neisseria m
12	36	64.3	833	2	Q9JPE1	Q9jpe1 neisseria m
13	36	64.3	833	16	Q9JQR5	Q9jqr5 neisseria m
14	35	62.5	38	13	Q9PV38	Q9pv38 channa sp.
15	35	62.5	234	11	Q91WF8	Q91wf8 mus musculu
16	35	62.5	293	10	O49020	O49020 gossypium h

17	35	62.5	293	10	Q94JN5	Q94jn5 gossypium h
18	35	62.5	293	10	Q94JN4	Q94jn4 gossypium h
19	35	62.5	388	5	Q9VMB3	Q9vmb3 drosophila
20	35	62.5	452	5	Q9U100	Q9u100 leishmania
21	35	62.5	464	16	Q99W16	Q99w16 staphylococ
22	35	62.5	2630	12	O55319	O55319 acyrthosiph
23	34	60.7	107	4	Q96SA9	Q96sa9 homo sapien
24	34	60.7	108	4	Q9UL77	Q9ul77 homo sapien
25	34	60.7	108	4	Q9UL70	Q9ul70 homo sapien
26	34	60.7	193	12	Q9YW53	Q9yhw53 melanoplus
27	34	60.7	200	17	Q9HHY3	Q9hh3 halobacteri
28	34	60.7	305	16	Q9KFT1	Q9kft1 bacillus ha
29	34	60.7	313	2	Q9RN71	Q9rn71 streptomyce
30	34	60.7	334	8	Q33795	Q33795 emericella
31	34	60.7	349	10	Q9SQL0	Q9sq10 lycopersico
32	34	60.7	350	5	Q95NY6	Q95ny6 caenorhabdi
33	34	60.7	356	5	Q95NU5	Q95nu5 caenorhabdi
34	34	60.7	375	8	Q9TL10	Q9tl10 nephroselmi
35	34	60.7	435	2	O86899	O86899 sphingomona
36	34	60.7	443	5	O26507	O26507 schistosoma
37	34	60.7	443	5	O26508	O26508 schistosoma
38	34	60.7	449	6	Q29482	Q29482 equus caball
39	34	60.7	458	10	Q9AY47	Q9ay47 oryza sativ
40	34	60.7	487	10	Q9S794	Q9s794 adiantum ca
41	34	60.7	527	5	Q93762	Q93762 caenorhabdi
42	34	60.7	560	10	O49896	O49896 arabidopsis
43	34	60.7	566	10	Q9ZQK5	Q9zqk5 arabidopsis
44	34	60.7	578	2	Q9ZG94	Q9z994 pseudomonas
45	34	60.7	866	5	Q9UAS3	Q9uas3 schistosoma

#### ALIGNMENTS

#### RESULT 1

Q96PF6 ID Q96PF6 PRELIMINARY; PRT; 116 AA.

AC Q96PF6; Q96PF6; PRELIMINARY; PRT; 116 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).

GN SDNK1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21361171; PubMed=11468171;

RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;

RT "The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell burden."

RT Burden."

RL Blood 98:714-720(2001).

DR EMBL; AF361758; AAK51465.1; -.

FT NON\_TER 1 116

FT NON\_TER 1 116

SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 75.0%; Score 42; DB 4; Length 116;

Best Local Similarity 72.7%; Pred. No. 1.3;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINHLH 11

|||||:

Db 24 QASQDIANHLN 34

#### RESULT 2

Q966H7 ID Q966H7 PRELIMINARY; PRT; 431 AA.

Q966H7;  
 AC 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL PROTEIN M02H5.3.  
 GN M02H5.3.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Bradshaw-Cordum H.;  
 RT "The sequence of C. elegans cosmid M02H5.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RT "Direct Submission.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC006675; AAK84553.1; --  
 SQ SEQUENCE 431 AA; 50490 MW; E026D36A14019BD2 CRC64;

Query Match 75.0%; Score 42; DB 5; Length 431;  
 Best Local Similarity 72.7%; Pred. No. 5;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QASQSISNHLH 11  
 | | | | | | | |  
 Db 361 QLQDSISNHLH 371

RESULT 3  
 Q966H8  
 ID Q966H8 PRELIMINARY; PRT; 414 AA.  
 AC Q966H8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL PROTEIN M02H5.4.  
 GN M02H5.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Bradshaw-Cordum H.;  
 RT "The sequence of C. elegans cosmid M02H5.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;

RA Waterston R.;  
 RT "Direct Submission.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC006675; AAK84554.1; --  
 SQ SEQUENCE 414 AA; 48113 MW; 34E312692E3B30A0 CRC64;

Query Match 73.2%; Score 41; DB 5; Length 414;  
 Best Local Similarity 72.7%; Pred. No. 7.5;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QASQSISNHLH 11  
 | | | | | | | |  
 Db 344 QFQDSISNHLH 354

RESULT 4  
 Q9UL81  
 ID Q9UL81 PRELIMINARY; PRT; 107 AA.  
 AC Q9UL81;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035033; AAD56269.1; --  
 DR HSSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR NON\_TER 1  
 FT NON\_TER 107  
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 69.6%; Score 39; DB 4; Length 107;  
 Best Local Similarity 72.7%; Pred. No. 4.4;  
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 QASQSISNHLH 11  
 | | | | | | | |  
 Db 24 RASQSISNHLN 34

RESULT 5  
 Q9VW04  
 ID Q9VW04 PRELIMINARY; PRT; 401 AA.  
 AC Q9VW04;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE CG9295 PROTEIN.  
 GN CG9295.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.



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RX STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Branton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balwle R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003516; AAF49151.1; -.
DR FlyBase; FBgn0036880; CG9295.
DR InterPro; IPR000618; Insect_cuticle.
DR Pfam; PF00379; Insect_cuticle; 1.
DR PRINTS; PR00947; CUTICLE.
DR PROSITE; PS00233; CUTICLE; 1.
SQ SEQUENCE 401 AA; 45863 MW; CD2341B6F9715308 CRC64;

Query Match 67.9%; Score 38; DB 5; Length 401;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 Q5ISNHLH 11
Db 277 ESISNHH 284

RESULT 6
P79751 PRELIMINARY; PRT; 417 AA.
AC
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IKAROS-LIKE.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OC NCBI_TaxID=31033;
RN [1]

SEQUENCE FROM N.A.
MEDLINE=99177347; PubMed=10077531;
Gellner K., Brenner S.;
"Analysis of 148 kb of genomic DNA around the wnt1 locus of Fugu
rubripes."
Genome Res. 9:251-258(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF056116; AAC34387.1; -.
DR HSP; P15822; IBB0.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00096; zf-C2H2; 5.
DR PRINTS; PR00048; ZINC_FINGER.
DR SMART; SM00355; Znf_C2H2; 6.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
SQ SEQUENCE 417 AA; 45664 MW; 8A4E4AA806946D74 CRC64;

Query Match 67.9%; Score 38; DB 13; Length 417;
Best Local Similarity 72.7%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QASOSISNHLH 11
Db 322 QISTSNHLH 332

RESULT 7
Q9KNE5 PRELIMINARY; PRT; 1085 AA.
AC
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN VCA0020.
GN VCA0020.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
[1]
RP SEQUENCE FROM N.A.
STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae."
RL Nature 406:477-483(2000).
DR EMBL; AE004345; AAF95934.1; -.
DR TIGR; VCA0020; -.
DR InterPro; IPR001917; AminoTransf_2.
DR PROSITE; PS00599; AA_TRANSFER_CLASS.2; UNKNOWN_1.
KW Hypothetical protein; Complete proteome
SQ SEQUENCE 1085 AA; 121042 MW; D176D85571729945 CRC64;

Query Match 66.1%; Score 37; DB 16; Length 1085;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASOSISNHLH 10
Db 497 QANQAINNH 506

RESULT 8
Q92M45

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ID Q92M45 PRELIMINARY; PRT; 1574 AA.
AC Q92M45;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PROBABLE GLUTAMATE SYNTHASE NADPH LARGE CHAIN PROTEIN (EC
DE 1.4.1.13).
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cloux A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
RA Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
RA Vorhoefer F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti."
RL Science 293:668-672(2001).
KW EMBL; AL591791; CAC47390.1; -.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 1574 AA; 172198 MW; 6D2EBBECE0BA0E29 CRC64;

Query Match 66.1%; Score 37; DB 16; Length 1574;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QSISNHLH 11
Db 1521 QLISNHLH 1528

RESULT 9
Q92FB9 PRELIMINARY; PRT; 1581 AA.
ID Q92FB9;
AC Q92FB9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GLUTAMATE SYNTHASE LARGE SUBUNIT (EC 1.4.1.13).
GN GLTB.
OS Rhizobium etli.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RX MEDLINE=20340966; PubMed=10878127;
RA Castillo A., Taboada H., Mendoza A., Valderrama B., Encarnacion S.,
RA Mora J.;
RT "Role of GOGAT in carbon and nitrogen partitioning in Rhizobium
RT etli."
RL Microbiology 146:1627-1637(2000).
DR EMBL; AF107264; AAC97376.1; -.
DR HSP; P00175; ILCO.
DR InterPro; IPR002489; DUF14.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR002932; Glu_synthase.
DR Pfam; PF01493; DUF14; 1.
DR Pfam; PF01645; Glu_synthase; 1.
KW Oxidoreductase.
SQ SEQUENCE 1581 AA; 171437 MW; 87AB88A9AB590F3C CRC64;

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Query Match 66.1%; Score 37; DB 2; Length 1581;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QSISNHLH 11
Db 1528 QLISNHLH 1535

RESULT 10
Q94116 PRELIMINARY; PRT; 10797 AA.
ID Q94116;
AC Q94116;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PEPTIDE SYNTHETASE.
OS Aureobasidium pullulans.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
OC Dothideomycetes et Chaetothyriomycetes incertae sedis; Dothioraceae;
OC mitosporic Dothioraceae; Aureobasidium.
OX NCBI_TaxID=5580;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R106;
RA Peery R.B., Thornevell S.J., Tobin M.B., Skatrud P.L.;
RT "Discovery of an MDR-like gene adjacent to a peptide synthetase in
RT Aureobasidium pullulans."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U85909; AAD00581.1; -.
DR HSP; P14687; IAMU.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001242; DUF4.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR003880; Phosphopant_attach.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00501; AMP-binding; 9.
DR Pfam; PF00668; Condensation; 11.
DR Pfam; PF00550; pp-binding; 12.
DR PROSITE; PS00075; ACP_DOMAIN; 12.
DR PROSITE; PS00455; AMP_BINDING; 4.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_10.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW Phosphopantetheine.
SQ SEQUENCE 10797 AA; 1190733 MW; 9EDB1A3E0A13A2D0 CRC64;

Query Match 66.1%; Score 37; DB 3; Length 10797;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASOSISNHLH 11
Db 8368 KASESVKNNLH 8278

RESULT 11
Q9K0S2 PRELIMINARY; PRT; 506 AA.
ID Q9K0S2;
AC Q9K0S2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN NMB0506.
GN NMB0506.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;

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RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citron H., Clark E.B.,
RA Cotton M.D., Uterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RA "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL: AE002407; AAF40938.1; -.
DR TIGR: NMB0506; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 506 AA; 52695 MW; A45ECDEA04046E5C CRC64;

Query Match 64.3%; Score 36; DB 16; Length 506;
Best Local Similarity 45.5%; Pred. No. 86;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11
Db 131 QAAEAVSKHFH 141
||:::| | |

RESULT 12
Q9JPE1 PRELIMINARY; PRT; 833 AA.
AC Q9JPE1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 88.4 KDA PROTEIN.
GN RTW4.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_taxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FAM18;
RX MEDLINE=20187481; PubMed=10722605;
RA Klee S.R., Nassif X., Kusecek B., Merker P., Beretti J.L., Achtman M.,
RA Tinsley C.R.;
RT "Molecular and biological analysis of eight genetic islands that
RT distinguish neisseria meningitidis from the closely related pathogen
RT neisseria gonorrhoeae."
RL Infect. Immun. 68:2082-2095(2000).
DR EMBL: AJ391284; CAB72083.1; -.
DR EMBL: AJ391284; CAB72083.1; -.
KW Hypothetical protein.
SQ SEQUENCE 833 AA; 88396 MW; B967C8422CD71A12 CRC64;

Query Match 64.3%; Score 36; DB 2; Length 833;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11
Db 458 QAAEAVSKHFH 468
||:::| | |

RESULT 13
Q9JQR5 PRELIMINARY; PRT; 833 AA.
AC Q9JQR5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN NMA0692.
GN NMA0692 OR RTW4.
OS Neisseria meningitidis (serogroup A), and

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OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_taxID=63699; 487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20187481; PubMed=10722605;
RA Klee S.R., Nassif X., Kusecek B., Merker P., Beretti J.L., Achtman M.,
RA Tinsley C.R.;
RT "Molecular and biological analysis of eight genetic islands that
RT distinguish neisseria meningitidis from the closely related pathogen
RT neisseria gonorrhoeae."
RL Infect. Immun. 68:2082-2095(2000).
DR EMBL: ALJ62753; CAB83978.1; -.
DR EMBL: AJ391255; CAB71949.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 833 AA; 88713 MW; DBC9914A375114C9 CRC64;

Query Match 64.3%; Score 36; DB 16; Length 833;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11
Db 458 QAAEAVSKHFH 468
||:::| | |

RESULT 14
Q9PV38 PRELIMINARY; PRT; 38 AA.
AC Q9PV38;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DYSTROPHIN (FRAGMENT).
GN DYST.
OS Channa sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Channoidae;
OC Channidae; Channa.
OX NCBI_taxID=94222;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL: AF137157; AAD53434.1; -.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA; 4342 MW; AAC53B3FF62C025C CRC64;

Query Match 62.5%; Score 35; DB 13; Length 38;
Best Local Similarity 70.0%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 QASQISNHL 10  
   |||  
Db 20 QAQPSISNHV 29

## RESULT 15

Q91WF8 PRELIMINARY; PRT; 234 AA.  
AC Q91WF8;  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE HYPOTHETICAL 25.9 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; BC015292; AAH15292.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 62.5%; Score 35; DB 11; Length 234;  
Best Local Similarity 63.6%; Pred. No. 60;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNHL 11  
   |||  
Db 44 RASQDISNYLN 54

Search completed: August 19, 2002, 06:58:18  
Job time: 1408 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:39:14 ; Search time 180.34 Seconds  
(without alignments)  
6.775 Million cell updates/sec

Title: US-09-339-922A-108

Perfect score: 56

Sequence: 1 QASQISNHLH 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	11	22 AAB61402	Enhanced 6H6LH lig
2	56	100.0	13	19 AAW76011	LM609 grafted anti
3	56	100.0	13	22 AAB61369	LM609 VL CDRI pept
4	56	100.0	107	19 AAW76006	LM609 grafted anti
5	56	100.0	107	19 AAW76002	Vitaxin antibody l
6	56	100.0	107	19 AAW76004	LM609 antibody lig
7	56	100.0	107	22 AAG63588	A light chain vari
8	56	100.0	107	22 AAG63590	A light chain vari
9	56	100.0	107	22 AAB61360	Vitaxin light chai
10	56	100.0	107	22 AAB61362	Antibody LM609 lig
11	56	100.0	107	22 AAB61364	Light chain variab

12	52	92.9	105	20 AAW87456	Jk gene product.
13	52	92.9	105	20 AAW87458	Humanised anti-alp
14	52	92.9	107	20 AAW84098	Humanised anti-alp
15	52	92.9	108	20 AAW84094	Murine vitronectin
16	52	92.9	109	20 AAY05380	Murine monoclonal
17	52	92.9	112	20 AAW84100	Vitronectin alpha-
18	47	83.9	11	22 AAB61403	Enhanced LM609 VH
19	47	83.9	13	19 AAW76031	LM609 grafted anti
20	47	83.9	13	22 AAB61389	Mutant VL CDRI pep
21	45	80.4	107	13 AAR25729	Humanised VL regio
22	45	80.4	107	15 AAR54319	Anti-HIV gp120 imm
23	45	80.4	107	17 AAW01287	VL region of HIV n
24	45	80.4	107	21 AAY95139	Anti-gp120 antibod
25	45	80.4	107	21 AAY98248	Anti-gp120 antibod
26	45	80.4	107	22 AAB69677	Murine CMV5 antibo
27	45	80.4	107	22 AAB69678	Humanised CMV5 ant
28	45	80.4	107	22 AAB69690	Human Wol antibody
29	45	80.4	108	12 AAR15438	Light chain variab
30	45	80.4	109	20 AAW89176	Anti-p53 monoclon
31	45	80.4	127	15 AAR54093	Sequence of mouse
32	45	80.4	127	22 AAB69687	Murine CMV5 antibo
33	45	80.4	240	12 AAR15443	Single chain Fv fr
34	43	76.8	108	17 AAW00241	EGF receptor chime
35	43	76.8	259	21 AAB09775	TMV 30K movement p
36	42	75.0	88	21 AAY56654	Partial peptide fr
37	42	75.0	124	21 AAY56719	Amino acid sequenc
38	42	75.0	127	21 AAY32405	Mouse anti-verotox
39	42	75.0	127	21 AAY32407	Mouse anti-verotox
40	41	73.2	11	15 AAR52526	306 light chain co
41	41	73.2	107	14 AAR38601	HVH light chain.
42	41	73.2	107	19 AAW58482	Murine HVH antibod
43	41	73.2	107	20 AAY30203	The variable light
44	41	73.2	107	20 AAY30205	The variable light
45	41	73.2	107	21 AAY71240	Humanised antibody

#### ALIGNMENTS

RESULT 1  
AAB61402  
ID AAB61402 standard; peptide; 11 AA.  
XX AAB61402;  
XX 03-APR-2001 (first entry)  
XX DT  
XX DE Enhanced 6H6LH light chain CDRI.  
XX LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.  
XX OS Unidentified.  
XX PN WO200078815-A1.  
XX PD 28-DEC-2000.  
XX PF 23-JUN-2000; 2000WO-US17454.  
XX PR 24-JUN-1999; 99US-0339922.  
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
XX osteoporosis--

PS Claim 4; Page 46; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX Sequence 11 AA;

Query Match 100.0%; Score 56; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00041;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSTSNHLH 11  
 ID | | | | | | | | | |  
 Db 1 qasqsishlh 11

RESULT 2

AAW76011  
 ID AAW76011 standard; Protein; 13 AA.

AC AAW76011;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-L region CDR1 protein fragment #1.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;  
 KW complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

PD 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR N-PSDB; AAV49848.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta<sub>3</sub>  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis

XX Disclosure; Page 40; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody  
 CC LM609 heavy and light chain variable region. LM609 and the antibody  
 CC vitaxin bind selectively to integrin alphaVbeta<sub>3</sub> and can be used to  
 CC inhibit binding of alphaVbeta<sub>3</sub> to a ligand and thus block  
 CC integrin-mediated signal transduction. This is useful in the treatment,  
 CC prevention and diagnosis of alphaVbeta<sub>3</sub>-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
 CC antibodies contain non-murine framework regions so are suitable for use  
 CC in humans. Enhanced types of LM609 have affinity more than 90 times  
 CC greater than that of parent the parent antibody.

SQ Sequence 13 AA;

Query Match 100.0%; Score 56; DB 19; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00049;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSTSNHLH 11  
 ID | | | | | | | | | |  
 Db 1 qasqsishlh 11

RESULT 3

AAB61369  
 ID AAB61369 standard; peptide; 13 AA.

XX AAB61369;

XX 03-APR-2001 (first entry)

XX LM609 VL CDR1 peptide.

DE LM609; grafted antibody; alphaVbeta<sub>3</sub> integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta<sub>3</sub> integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -

PS Disclosure; Page 39; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX Sequence 13 AA;

Query Match 100.0%; Score 56; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00049;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQTSISNHLH 11  
Db 1 qasqsisnhlh 11

RESULT 4  
AAW76006  
ID AAW76006 standard; Protein; 107 AA.  
XX  
AC AAW76006;  
XX  
DT 02-NOV-1998 (first entry)  
XX  
DE LM609 grafted antibody light chain variable region protein fragment.  
XX  
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 49 /label= Arg, Met  
FT  
XX WO9833919-A2.  
XX  
XX 06-AUG-1998.  
XX  
XX 30-JAN-1998; 98WO-US01826.  
XX  
XX 30-JAN-1997; 97US-0791391.  
XX  
XX (IXSY-) IXSYS INC.  
XX  
XX Glaser SM, Huse WD;  
XX WPI; 1998-437472/37.  
XX N-PSDB; AAV49843.  
XX  
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3  
XX integrin - and related grafted antibodies based on murine monoclonal  
XX LM609, also related nucleic acid, used to treat, prevent or diagnose  
XX angiogenesis or restenosis  
XX  
XX Claim 19; Fig 7; 129pp; English.  
XX  
XX This sequence represents a LM609 grafted antibody variable light chain  
XX region. LM609 and the antibody vitaxin bind selectively to integrin  
XX alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a ligand  
XX and thus block integrin-mediated signal transduction. This is useful in  
XX the treatment, prevention and diagnosis of alphaVbeta3-mediated disease,  
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune  
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
XX etc.). The antibodies contain non-murine framework regions so are  
XX suitable for use in humans. Enhanced types of LM609 have affinity  
XX more than 90 times greater than that of parent the parent antibody.  
XX  
SQ Sequence 107 AA;

Query Match 100.0%; Score 56; DB 19; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.0058;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQTSISNHLH 11  
Db 24 qasqsisnhlh 34

RESULT 5  
AAW76002  
ID AAW76002 standard; Protein; 107 AA.  
XX  
AC AAW76002;  
XX  
DT 02-NOV-1998 (first entry)  
XX  
DE Vitaxin antibody light chain variable region protein fragment.  
XX  
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis.  
XX  
OS Mus sp.  
XX  
PN WO9833919-A2.  
XX  
XX 06-AUG-1998.  
XX  
XX 30-JAN-1998; 98WO-US01826.  
XX  
XX 30-JAN-1997; 97US-0791391.  
XX  
XX (IXSY-) IXSYS INC.  
XX  
XX Glaser SM, Huse WD;  
XX WPI; 1998-437472/37.  
XX N-PSDB; AAV49821.  
XX  
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3  
XX integrin - and related grafted antibodies based on murine monoclonal  
XX LM609, also related nucleic acid, used to treat, prevent or diagnose  
XX angiogenesis or restenosis  
XX  
XX Claim 1; Fig 1b; 129pp; English.  
XX  
XX This sequence represents the vitaxin antibody variable light chain  
XX region. Vitaxin and the antibody LM609 bind selectively to integrin  
XX alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a  
XX ligand and thus block integrin-mediated signal transduction. This is  
XX useful in the treatment, prevention and diagnosis of alphaVbeta3-mediated  
XX disease, specifically angiogenesis and restenosis (but also e.g.  
XX (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,  
XX cancer, psoriasis, rheumatoid arthritis, macular degeneration,  
XX osteoporosis etc.). The antibodies contain non-murine framework regions  
XX so are suitable for use in humans. Enhanced types of LM609 have affinity  
XX more than 90 times greater than that of parent the parent antibody.  
XX  
SQ Sequence 107 AA;

Query Match 100.0%; Score 56; DB 19; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.0058;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQTSISNHLH 11  
Db 24 qasqsisnhlh 34

RESULT 6  
AAW76004  
ID AAW76004 standard; Protein; 107 AA.  
XX  
AC AAW76004;  
XX  
DT 02-NOV-1998 (first entry)  
XX

DE XX LM609 antibody light chain variable region protein fragment.  
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9833919-A2.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 30-JAN-1998; 98WO-US01826.  
 XX  
 PR 30-JAN-1997; 97US-0791391.  
 XX  
 PA (IXSY-) IXSYS INC.  
 XX  
 PI Glaser SM, Huse WD;  
 XX  
 XX WPI: 1998-437472/37.  
 DR N-PSDB; AAW76004.  
 XX  
 XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX  
 PS Claim 46; Fig 2b; 129pp; English.  
 XX  
 CC This sequence represents the LM609 antibody variable light chain region.  
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3  
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
 CC block integrin-mediated signal transduction. This is useful in the  
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
 CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.  
 XX  
 SQ Sequence 107 AA;  
  
 Query Match 100.0%; Score 56; DB 19; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.0058;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 QASQSISNHLH 11  
 Db 24 qasqsishlh 34  
 |||||||||  
  
 RESULT 7  
 AAG63588  
 ID AAG63588 standard; Protein; 107 AA.  
 XX  
 AC AAG63588;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX  
 DE A light chain variable region of LM609 grafted antibody.  
 XX  
 KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer.  
 XX  
 OS Synthetic.  
 OS Mus sp.

XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 49 /note= "unspecified residue encoded by MKK"  
 XX  
 XX US2001011125-A1.  
 PN  
 XX 02-AUG-2001.  
 PD  
 XX 30-JAN-1997; 97US-0790540.  
 XX  
 XX 30-JAN-1997; 97US-0790540.  
 PR  
 XX (HUSE/) HUSE W D.  
 PA  
 XX Huse WD;  
 PI  
 XX WPI: 2001-496171/54.  
 DR N-PSDB; AAH74624.  
 XX  
 XX New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer  
 XX  
 PS Claim 1; Fig 1B; 25pp; English.  
 XX  
 CC The present sequence represents the light chain variable region of the  
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which  
 CC specifically recognises the integrin alphavbeta3, and inhibits its  
 CC functional activity. The LM609 grafted antibody has the  
 CC complementarity determining regions (CDRs) substituted into a non-murine  
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain  
 CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis  
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
 CC disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 CC an alphavbeta3-mediated disease.  
 XX  
 SQ Sequence 107 AA;  
  
 Query Match 100.0%; Score 56; DB 22; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.0058;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 QASQSISNHLH 11  
 Db 24 qasqsishlh 34  
 |||||||||  
  
 RESULT 8  
 AAG63590  
 ID AAG63590 standard; Protein; 107 AA.  
 XX  
 AC AAG63590;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX  
 DE A light chain variable region of LM609 antibody.  
 XX  
 KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer.  
 XX  
 OS Mus sp.



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XX PN US2001011125-A1.
XX PD 02-AUG-2001.
XX XX
XX PF 30-JAN-1997; 97US-0790540.
XX PR 30-JAN-1997; 97US-0790540.
XX PA (HUSE/) HUSE W D.
XX PI Huse WD;
XX DR WPI; 2001-496171/54.
XX DR N-PSDB; AAH74626.
XX XX
XX PT New LM609 grafted antibody exhibiting selective binding affinity to
XX PT alphavbeta3, comprising at least one LM609 grafted heavy and light
XX PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
XX PT disorders or cancer -
XX XX
XX PS Disclosure; Fig 2B; 25pp; English.
XX CC
XX CC The present sequence represents the light chain variable region of the
XX CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
XX CC recognises the integrin alphavbeta3, and inhibits its functional activity.
XX CC The specification describes a LM609 grafted antibody which has the
XX CC complementarity determining regions (CDRs) substituted into a non-murine
XX CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
XX CC polypeptides and fragments are useful in diagnostic and therapeutic
XX CC purposes, such as in the production of LM609 grafted antibodies and
XX CC fragments having binding specificity and inhibitory activity against
XX CC the integrin alphavbeta3. The antibody can be used for the diagnosis
XX CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
XX CC disorders, chronic articular rheumatism, psoriasis, disorders
XX CC associated with inappropriate or inopportune invasion of vessels such
XX CC as diabetic retinopathy, neovascular glaucoma and capillary
XX CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
XX CC binding activity of alphavbeta3 that are necessary for progression of
XX CC an alphavbeta3-mediated disease.
XX XX
XX SQ Sequence 107 AA;

Query Match 100.0%; Score 56; DB 22; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNHLH 11
Db 24 qasqsishlh 34
|||||
|

RESULT 9
AAB61360
ID AAB61360 standard; protein; 107 AA.
XX AC
XX AC AAB61360;
XX XX
XX DT 03-APR-2001 (first entry)
XX XX
XX DE Vitaxin light chain variable region protein.
XX XX
XX KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;
XX KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX XX
XX OS Unidentified.
XX XX
XX PN WO200078815-A1.
XX AC
XX PD 28-DEC-2000.
XX XX
XX PF 23-JUN-2000; 2000WO-US17454.
XX XX
XX PR 24-JUN-1999; 99US-0339922.
XX XX
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX XX
XX DR WPI; 2001-050110/06.
XX XX
XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis -
XX PT

```

XX Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta<sub>3</sub> integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

XX osteoporosis.

XX Sequence 107 AA;

Query Match 100.0%; Score 56; DB 22; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.0058;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11

Db 24 qasqsishlh 34

RESULT 11

AAAB61364

ID AAB61364 standard; protein; 107 AA.

AC AAB61364;

XX 03-APR-2001 (first entry)

XX Light chain variable region of LM609.

DE LM609; grafted antibody; alphavbeta<sub>3</sub> integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis.

KW Unidentified.

OS WO200078815-A1.

PN 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

FA Huse WD, Wu H;

XX WPI; 2001-050110/06.

DR Enhanced LM609 grafted antibodies exhibiting selective binding affinity

XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX Disclosure; Fig 7; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta<sub>3</sub> integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

XX osteoporosis.

SQ Sequence 107 AA;

Query Match 100.0%; Score 56; DB 22; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.0058;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11

Db 24 qasqsishlh 34

RESULT 12

AAW87456

ID AAW87456 standard; Protein; 105 AA.

XX AAW87456;

XX 15-MAR-1999 (first entry)

XX Jk gene product.

XX Humanised antibody; monoclonal antibody; MAB; antibody engineering;

KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;

KW angiogenesis; diabetic retinopathy; inflammation;

KW macular degeneration; osteoporosis; Paget's disease;

KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;

KW D12HZREI; Jk protein.

XX Mus sp.

OS WO9840488-A1.

PN 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04987.

PF 12-MAR-1997; 97US-0039609.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA Johanson KO, Jonak ZL, Taylor AH;

XX WPI; 1999-034590/03.

DR N-PSDB; AAV71803.

XX New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for

PT immunotherapeutic treatment of e.g. diabetic retinopathy,

PT inflammatory disorders, atherosclerosis, restenosis, cancers or

PT osteoporosis

XX Example 14; Page 66; 97pp; English.

PS This polypeptide is encoded by a Jk synthetic gene segment (see

XX AAV71803). It was utilising in novel D12HZREI humanised light chain

CC variable region (see AAW87456), which comprises a human REI framework

CC and complementarity determining regions from the anti-human alpha-v

CC beta-3 vitronectin receptor monoclonal antibody D12. Humanised D12

CC antibodies can be used for passive immunotherapy of disorders

CC mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis

CC and angiogenic associated diseases.

XX Sequence 105 AA;

Query Match 92.9%; Score 52; DB 20; Length 105;

Best Local Similarity 90.9%; Pred. No. 0.031;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11

Db 24 rasqsishlh 34  
:|||||

## RESULT 13

AAW87458  
ID AAW87458 standard; Protein; 105 AA.

XX  
AC AAW87458;

XX  
DT 15-MAR-1999 (first entry)

XX  
DE Humanised anti-alpha-v beta-3 MAB D12HZLCREI VL.

XX  
KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;  
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
KW angiogenesis; diabetic retinopathy; inflammation;  
KW macular degeneration; osteoporosis; Paget's disease;  
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;  
KW D12HZLCREI.

XX  
OS Homo sapiens.

OS  
Synthetic.

XX  
PN WO9840488-A1.

XX  
PD 17-SEP-1998.

XX  
PF 12-MAR-1998; 98WO-US04987.

XX  
PR 12-MAR-1997; 97US-0039609.

XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX  
PI Johanson KO, Jonak ZL, Taylor AH;

XX  
DR WPI; 1999-034590/03.

XX  
DR N-PSDB; AAV71805.

XX  
PT New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
PT osteoporosis

XX  
PS Example 14; Page 68-69; 97pp; English.

XX  
CC This is the amino acid sequence of the light chain variable region  
CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor  
CC monoclonal antibody D12HZLCREI. It is based on a synthetic  
CC humanised kappa chain based on a modified human REI kappa  
CC framework and complementarity determining regions from the murine  
CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody  
CC D12 (see AAW84094). Humanised antibodies of the invention can be used  
CC for passive immunotherapy of a disorder mediated by the alpha-v  
CC beta-3 receptor, e.g. cardiovascular disorders or angiogenic-  
CC related disorders, such as angiogenesis associated with diabetic  
CC retinopathy, atherosclerosis and restenosis, chronic inflammatory  
CC disorders, macular degeneration, rheumatoid arthritis and cancer.  
CC e.g. solid tumour metastasis, and diseases where bone resorption is  
CC associated with pathology such as osteoporosis, hyperparathyroidism,  
CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions  
CC produced by bone metastasis, bone loss due to immobilisation or sex  
CC hormone deficiency. They can also be used for targeted drug  
CC therapy, and for detection and diagnosis.

XX  
SQ Sequence 105 AA;

Query Match 92.9%; Score 52; DB 20; Length 105;  
Best Local Similarity 90.9%; Pred. No. 0.031;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNHLH 11  
Db :|||||  
24 rasqsishlh 34

## RESULT 14

AAW84098

ID AAW84098 standard; Protein; 107 AA.

XX  
AC AAW84098;

XX  
DT 15-MAR-1999 (first entry)

XX  
DE Humanised anti-alpha-v beta-3 MAB D12HZHC 1-0 VL.

XX  
KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;  
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
KW angiogenesis; diabetic retinopathy; inflammation;  
KW macular degeneration; osteoporosis; Paget's disease;  
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;  
KW D12HZHC-10.

XX  
OS Homo sapiens.

OS  
Synthetic.

XX  
FH Key Location/Qualifiers

FT Region 24..34

FT /label= CDR1

FT Region 50..56

FT /label= CDR2

FT Region 89..97

FT /label= CDR3

XX  
PN WO9840488-A1.

XX  
PD 17-SEP-1998.

XX  
PF 12-MAR-1998; 98WO-US04987.

XX  
PR 12-MAR-1997; 97US-0039609.

XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX  
PI Johanson KO, Jonak ZL, Taylor AH;

XX  
DR WPI; 1999-034590/03.

XX  
DR N-PSDB; AAV71800.

XX  
PT New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
PT osteoporosis

XX  
PS Claim 2; Page 61-62; 97pp; English.

XX  
CC This is the amino acid sequence of the light chain variable region  
CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor  
CC monoclonal antibody D12HZHC 1-0. It is based on the VL sequence  
CC (see AAW84096) of human Kabat subgroup III kappa chain, with  
CC complementarity determining regions (CDRs) from the murine  
CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody  
CC D12 (see AAW84093). 3 Murine framework residues (1, 49 and 60)  
CC are retained. The humanised light chain can be expressed in host  
CC cells using nucleic acid molecules (see AAV71800) of the invention.  
CC Humanised D12 VH is also provided (see AAW84097). The humanised  
CC antibodies can be used for passive immunotherapy of disorders  
CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or  
CC angiogenic-related disorders, such as angiogenesis associated  
CC with diabetic retinopathy, atherosclerosis and restenosis, chronic  
CC inflammatory disorders, macular degeneration, rheumatoid arthritis  
CC and cancer, e.g. solid tumour metastasis, and diseases where bone  
CC resorption is associated with pathology such as osteoporosis,

CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,  
 CC osteolytic lesions produced by bone metastasis, bone loss due to  
 CC immobilisation or sex hormone deficiency. They can also be used for  
 CC targeted drug therapy, and for detection and diagnosis.  
 XX  
 SQ Sequence 107 AA;

Query Match 92.9%; Score 52; DB 20; Length 107;  
 Best Local Similarity 90.9%; Pred. No. 0.032;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11  
 :|||||  
 Db 24 rasqsisnhlh 34

RESULT 15  
 AAW84094  
 ID AAW84094 standard; Protein: 108 AA.  
 XX  
 AC AAW84094;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE Murine vitronectin alpha-v beta-3 receptor MAB VL region.  
 XX  
 KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;  
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
 KW angiogenesis; diabetic retinopathy; inflammation;  
 KW macular degeneration; osteoporosis; Paget's disease;  
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.  
 XX  
 OS Mus sp.  
 XX

Key Location/Qualifiers  
 Region 24..34  
 FT /label= CDR1  
 FT Region 50..56  
 FT /label= CDR2  
 FT Region 89..97  
 FT /label= CDR3

WO9840488-A1.  
 XX  
 XX  
 PD 17-SEP-1998.  
 XX  
 XX 12-MAR-1998; 98WO-US04987.  
 XX  
 XX 12-MAR-1997; 97US-0039609.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 XX Johanson KO, Jonak ZL, Taylor AH;  
 XX  
 XX WPI: 1999-034590/03.  
 DR N-PSDB: AAV71798.  
 XX

New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
 PT osteoporosis  
 XX  
 PS Example 13; Page 59-60; 97pp; English.  
 XX

This is the amino acid sequence of the light chain variable region  
 CC (VL) of the anti-human alpha-v beta-3 vitronectin receptor murine  
 CC monoclonal antibody D12, as deduced from isolated cDNA (see  
 CC AAV71798). D12 VH (see AAW84093) and VL show sequence similarity to  
 CC Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see  
 CC AAW84096), respectively. Humanised VH (see AAW84097) and VL (see  
 CC AAW84098) were constructed by combining the framework regions of the

CC human V region consensus sequences with complementarity determining  
 CC regions of D12 (keeping some preferred murine framework residues).  
 CC The humanised antibodies are specifically reactive with the human  
 CC alpha-v beta-3 protein receptor and capable of neutralising the  
 CC receptor. They can be used for passive immunotherapy of a disorder  
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular  
 CC disorders or angiogenic-related disorders, such as angiogenesis  
 CC associated with diabetic retinopathy, atherosclerosis and  
 CC restenosis, chronic inflammatory disorders, macular degeneration,  
 CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and  
 CC diseases where bone resorption is associated with pathology such as  
 CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia  
 CC of malignancy, osteolytic lesions produced by bone metastasis, bone  
 CC loss due to immobilisation or sex hormone deficiency. They can also  
 CC be used for targeted drug therapy, and for detection and diagnosis.  
 XX  
 SQ Sequence 108 AA;

Query Match 92.9%; Score 52; DB 20; Length 108;  
 Best Local Similarity 90.9%; Pred. No. 0.032;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNHLH 11  
 :|||||  
 Db 24 rasqsisnhlh 34

Search completed: August 19, 2002, 06:39:14  
 Job time: 1475 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:42 ; Search time 61.75 seconds  
(without alignments)  
4.351 Million cell updates/sec

Title: US-09-339-922a-108

Perfect score: 56

Sequence: 1 QASQISNHLH 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PTCUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	80.4	100	1	US-08-436-463-19
2	45	80.4	103	1	US-08-436-463-21
3	45	80.4	107	1	US-07-634-278-62
4	45	80.4	107	1	US-07-634-278-63
5	45	80.4	107	1	US-07-634-278-87
6	45	80.4	107	1	US-08-477-728-62
7	45	80.4	107	1	US-08-477-728-63
8	45	80.4	107	1	US-08-477-728-87
9	45	80.4	107	1	US-08-276-852-108
10	45	80.4	107	1	US-08-474-040-62
11	45	80.4	107	1	US-08-474-040-63
12	45	80.4	107	1	US-08-474-040-87
13	45	80.4	107	1	US-08-487-200-62
14	45	80.4	107	1	US-08-487-200-63
15	45	80.4	107	1	US-08-487-200-87
16	45	80.4	107	1	US-08-899-575-108
17	45	80.4	107	1	US-08-899-575-108
18	45	80.4	107	4	US-08-484-537-62
19	45	80.4	107	4	US-08-484-537-63
20	45	80.4	107	4	US-08-484-537-87
21	45	80.4	107	5	PTC-US95-08743-108
22	45	80.4	127	1	US-07-634-278-83
23	45	80.4	127	1	US-08-477-728-83
24	45	80.4	127	1	US-08-474-040-83
25	45	80.4	127	1	US-08-487-200-83
26	45	80.4	127	1	US-08-436-463-4
27	45	80.4	127	1	US-08-436-463-18

28 45 80.4 127 4 US-08-484-537-83 Sequence 83, Appl  
29 41 73.2 11 1 US-07-942-245-497 Sequence 497, App  
30 41 73.2 31 4 US-08-525-539A-3 Sequence 3, Appli  
31 41 73.2 96 2 US-08-737-560A-9 Sequence 9, Appli  
32 41 73.2 107 1 US-08-436-463-20 Sequence 20, Appl  
33 41 73.2 107 1 US-08-107-669D-1 Sequence 1, Appli  
34 41 73.2 107 1 US-08-472-788A-1 Sequence 1, Appli  
35 41 73.2 107 2 US-08-477-531B-1 Sequence 1, Appli  
36 41 73.2 107 2 US-08-082-842A-1 Sequence 1, Appli  
37 41 73.2 107 4 US-09-247-352-8 Sequence 8, Appli  
38 41 73.2 107 4 US-09-247-352-12 Sequence 12, Appl  
39 41 73.2 108 2 US-08-378-939-20 Sequence 20, Appl  
40 41 73.2 108 4 US-09-247-352-1 Sequence 1, Appli  
41 41 73.2 109 1 US-07-942-245-4 Sequence 4, Appli  
42 41 73.2 214 4 US-09-247-352-4 Sequence 4, Appli  
43 40 71.4 108 4 US-09-157-370-4 Sequence 4, Appli  
44 39 69.6 76 4 US-08-851-362D-20 Sequence 20, Appl  
45 39 69.6 105 4 US-08-851-362D-28 Sequence 28, Appl

#### ALIGNMENTS

RESULT 1  
US-08-436-463-19  
; Sequence 19, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoto  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,463  
; FILING DATE: 26-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 341255/1992  
; FILING DATE: 28-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: KIMACHI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 100 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-436-463-19

Query Match 80.4%; Score 45; DB 1; Length 100;  
Best Local Similarity 81.8%; Pred. No. 0.35;

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Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 RASQISNNLH 34

RESULT 2
US-08-436-463-21
; Sequence 21, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-463-21

Query Match 80.4%; Score 45; DB 1; Length 103;
Best Local Similarity 81.8%; Pred. No. 0.36;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 22 RASQISNNLH 32

RESULT 3
US-07-634-278-62
; Sequence 62, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.

Qy 1 QASQISNHLH 11
Db 24 RASQISNNLH 34

Query Match 80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11
Db 24 RASQISNNLH 34

RESULT 4
US-07-634-278-63
; Sequence 63, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
```

COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-634-278-63

Query Match 80.4%; Score 45; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.38;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11  
Db 24 RASQISNHLH 34

RESULT 5  
US-07-634-278-87  
Sequence 87, Application US/07634278  
Patent No. 5530101  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourlie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-634-278-87

Query Match 80.4%; Score 45; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.38;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNHLH 11  
Db 24 RASQISNHLH 34

RESULT 6  
US-08-477-728-62  
Sequence 62, Application US/08477728  
Patent No. 5585089  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,728  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-477-728-62

Query Match 80.4%; Score 45; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.38;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSTSNHLH 11  
Db 24 RASQSTSNHLH 34

## RESULT 7

US-08-477-728-63  
; Sequence 63, Application US/08477728  
; Patent No. 5385089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-477-728-63

Query Match 80.4%; Score 45; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.38;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSTSNHLH 11  
Db 24 RASQSTSNHLH 34

## RESULT 8

US-08-477-728-87  
; Sequence 87, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-477-728-87



Query Match 80.4%; Score 45; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.38;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISSNHLH 11  
Db 24 RASQSISSNHLH 34

RESULT 9  
US-08-276-852-108  
; Sequence 108, Application US/08276852  
; Patent No. 5652138  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,852  
FILING DATE: 18-JUL-1994

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SC1452P  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-108

Query Match 80.4%; Score 45; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.38;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISSNHLH 11  
Db 22 QASQSISSNHLH 32

RESULT 10  
US-08-474-040-62  
; Sequence 62, Application US/08474040

; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Kathleen F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,040  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-474-040-62

Query Match 80.4%; Score 45; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.38;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISSNHLH 11  
Db 24 RASQSISSNHLH 34

RESULT 11  
US-08-474-040-63  
; Sequence 63, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Kathleen F.  
; APPLICANT: COELINGH, Kathleen L.

```

; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 63:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-63

```

```

Query Match      80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 QASQISNHLH 11
Db      24 RASQISNHLH 34

```

```

RESULT 12
US-08-474-040-87

```

```

; Sequence 87, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto

```

```

; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 87:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-474-040-87

```

```

Query Match      80.4%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 QASQISNHLH 11
Db      24 RASQISNHLH 34

```

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RESULT 13
US-08-487-200-62

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```

; Sequence 62, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,200  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002610  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-487-200-62

Query Match 80.4%; Score 45; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.38;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNHLH 11  
Db 24 RASQSISNHLH 34

RESULT 14  
US-08-487-200-63  
Sequence 63, Application US/08487200  
Patent No. 5693762  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,200  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002610  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-487-200-63

Query Match 80.4%; Score 45; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.38;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNHLH 11  
Db 24 RASQSISNHLH 34

RESULT 15  
US-08-487-200-87  
Sequence 87, Application US/08487200  
Patent No. 5693762  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,200  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-487-200-87

Query Match 80.4%; Score 45; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.38;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISNLH 11  
Db 24 RASQISNLH 34

Search completed: August 19, 2002, 06:34:42  
Job time: 1203 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:07 ; Search time 78.53 Seconds  
(without alignments)  
13.460 Million cell updates/sec

Title: US-09-339-922a-110

Perfect score: 54

Sequence: 1 QASQSISNFLH 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_71:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	87.0	106	2	PL0267
2	47	87.0	123	2	S35479
3	44	81.5	122	2	S40370
4	43	79.6	107	2	S32188
5	42	77.8	96	2	G33730
6	42	77.8	103	2	S19975
7	41	75.9	95	2	PH0867
8	41	75.9	102	2	S26346
9	41	75.9	104	2	B43413
10	41	75.9	107	2	B45722
11	41	75.9	107	2	A45722
12	41	75.9	138	2	A26471
13	40	74.1	62	2	S42265
14	40	74.1	87	2	I52592
15	40	74.1	88	2	S34088
16	40	74.1	88	2	S34087
17	40	74.1	95	2	PH0862
18	40	74.1	107	2	A45722
19	40	74.1	108	2	S19674
20	40	74.1	110	2	S44118
21	40	74.1	117	2	S33528
22	40	74.1	117	2	S42263
23	40	74.1	127	2	S40367
24	40	74.1	129	1	K1HUWK
25	40	74.1	129	2	S52789
26	38	70.4	92	1	KVRB38
27	38	70.4	106	2	PC4282
28	38	70.4	162	2	T18855
29	37	68.5	103	2	S44121

```

30 37 68.5 117 1 K4RBF2      Ig kappa chain pre
31 37 68.5 122 2 S40314      Ig kappa chain - h
32 37 68.5 334 2 B72033      conserved hypotet
33 37 68.5 334 2 C86593      C1S66 hypothetical
34 36 66.7 93 2 S38564      Ig kappa chain V r
35 36 66.7 107 2 B28044      Ig kappa chain V r
36 36 66.7 107 2 A28044      Ig kappa chain V r
37 36 66.7 107 2 D48677      Ig kappa chain V-J
38 36 66.7 107 2 B49026      Ig kappa chain (cl
39 36 66.7 107 2 S69901      Ig kappa chain (cl
40 36 66.7 107 2 S69906      Ig kappa chain V r
41 36 66.7 108 1 KVM5AR      Ig kappa chain V r
42 36 66.7 108 2 C26405      Ig kappa chain V r
43 36 66.7 108 2 B30551      Ig kappa chain V r
44 36 66.7 108 2 PL0282      Ig kappa chain V r
45 36 66.7 108 2 S38862      Ig kappa chain V r

```

#### ALIGNMENTS

RESULT 1

PL0267

Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000

C:Accession: PL0267

R:Shlomchik, M.; Mascellli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A:Reference number: PL0231; MUID:90111618

A:Accession: PL0267

A:Molecule type: mRNA

A:Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3

F:98-106/Region: framework 4

Query Match

Best Local Similarity 87.0%; Score 47; DB 2; Length 106;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNFLH 11

Db 24 RASQSISNYLH 34

RESULT 2

S35479

Ig kappa chain precursor V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: S35479

R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.

Nucleic Acids Res. 20, 4099, 1992

A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from A:Reference number: S35479; MUID:92375706

A:Accession: S35479

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-123 <TAK>

A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148

C:Genetics:

A:Map position: 6

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin  
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>  
F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>  
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 47; DB 2; Length 123;  
Best Local Similarity 81.8%; Pred. No. 0.03;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11  
:|||||:|  
Db 36 RASQISNYLH 46

RESULT 3  
S40370  
Ig kappa chain - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40370  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:9408091  
A;Accession: S40370  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-122 <KLE>  
A;Cross-references: EMBL:X72480; NID:g441428; PIDN:CRA51148.1; PID:g441429  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 44; DB 2; Length 122;  
Best Local Similarity 81.8%; Pred. No. 0.12;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11  
:|||||:|  
Db 38 RASQISNYLH 48

RESULT 4  
S32188  
Ig kappa chain V region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S32188  
R;Izui, S.  
submitted to the EMBL Data Library, February 1993  
A;Reference number: S32185  
A;Accession: S32188  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-107 <IZU>  
A;Cross-references: EMBL:X70900; NID:g288253; PIDN:CAA49695.1; PID:g288254  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 43; DB 2; Length 107;  
Best Local Similarity 72.7%; Pred. No. 0.17;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11  
:|||||:|  
Db 24 RASQISNYLH 34

RESULT 5  
S40370  
Ig kappa chain V region (23.32) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 21-Jan-2000  
C;Accession: G33730  
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.  
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989  
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u  
A;Reference number: A33730; MUID:89367325  
A;Accession: G33730  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-96 <LAW>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 42; DB 2; Length 96;  
Best Local Similarity 72.7%; Pred. No. 0.24;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11  
:|||||:|  
Db 24 RASQISNYLH 34

RESULT 6  
S1975  
Ig kappa chain V region (M-T408) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S1975  
R;Weissenhorn, W.; Rietmueller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A;Description: Structural characterization of CD4 mAb.  
A;Reference number: S19963  
A;Accession: S1975  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-103 <WEI>  
A;Cross-references: EMBL:X65097; NID:g52296; PIDN:CAA46225.1; PID:g52297  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F:11-85/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 42; DB 2; Length 103;  
Best Local Similarity 72.7%; Pred. No. 0.26;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11  
:|||||:|  
Db 19 RASQISNYLH 29

RESULT 7  
PH0867  
Ig kappa chain V region (anti-DNA, R3.5H5G) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 21-Jan-2000  
C;Accession: PH0867  
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.  
J. Exp. Med. 174, 1639-1652, 1991  
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot  
A;Reference number: PH0862; MUID:92078875  
A;Accession: PH0867  
A;Molecule type: DNA  
A;Residues: 1-95 <MAN>  
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that be  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>  
 F:24-34/Region: complementarity-determining 1  
 F:35-49/Region: framework 2  
 F:50-56/Region: complementarity-determining 2  
 F:57-88/Region: framework 3  
 F:89-95/Region: complementarity-determining 3

Query Match 75.9%; Score 41; DB 2; Length 95;  
 Best Local Similarity 72.7%; Pred. No. 0.38;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFH 11  
 Db 24 RASQISNLFH 34

## RESULT 8

S26346  
 Ig kappa chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
 C:Accession: S26346  
 R:Stark, S.E.; Caton, A.J.  
 J. Exp. Med. 174, 613-624, 1991  
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e  
 A:Reference number: S26309; MUID:91341421  
 A:Accession: S26346  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-102 <STA>  
 A:Cross-references: EMBL:X59211; NID:952338; PIDN:CAA41921.1; PID:g1334075  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 41; DB 2; Length 102;  
 Best Local Similarity 81.8%; Pred. No. 0.41;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFH 11  
 Db 22 RASQISNLFH 32

## RESULT 9

B43413  
 Ig kappa chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: B43413  
 R:Tomiya, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum  
 J. Biol. Chem. 267, 18085-18092, 1992  
 A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specif  
 A:Reference number: A43413; MUID:92388177  
 A:Accession: B43413  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-104 <TOM>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:112818)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 41; DB 2; Length 104;  
 Best Local Similarity 81.8%; Pred. No. 0.42;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFH 11  
 Db 21 RASQISNLFH 31

## RESULT 10

B45722  
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: B45722  
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va  
 J. Virol. 67, 489-496, 1993  
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on  
 A:Reference number: A45722; MUID:93100833  
 A:Accession: B45722  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-107 <SIM>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:120590)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: glycoprotein  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 41; DB 2; Length 107;  
 Best Local Similarity 81.8%; Pred. No. 0.43;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFH 11  
 Db 24 RASQISNLFH 34

## RESULT 11

A45722  
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 03-Mar-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: A45722  
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va  
 J. Virol. 67, 489-496, 1993  
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on  
 A:Reference number: A45722; MUID:93100833  
 A:Accession: A45722  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <SIM>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:120589)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: glycoprotein  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 41; DB 2; Length 107;  
 Best Local Similarity 81.8%; Pred. No. 0.43;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISNLFH 11  
 Db 24 RASQISNLFH 34

## RESULT 12

A26471  
 Ig kappa chain precursor V region (MAK33) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 23-Jul-1999  
 C:Accession: A26471  
 R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.  
 Gene 51, 13-19, 1987  
 A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat  
 A:Reference number: A91572; MUID:87248058  
 A:Accession: A26471  
 A:Molecule type: mRNA  
 A:Residues: 1-138 <BUC>

A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 75.9%; Score 41; DB 2; Length 138;  
Best Local Similarity 81.8%; Pred. No. 0.57;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11  
:|||||:|  
Db 44 RASQISNNLH 54

## RESULT 13

Ig kappa chain V region (018) - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
C:Accession: S42265  
R:Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que  
J. Immunol. 147, 4007-4013, 1991  
A:Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf  
A:Reference number: S42263; MUID:92043792  
A:Accession: S42265

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-62 <SCO>  
A:Cross-references: EMBL:M64856  
C:Genetics:

A:Introns: 19/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 74.1%; Score 40; DB 2; Length 62;  
Best Local Similarity 72.7%; Pred. No. 0.38;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11  
:|||||:|  
Db 24 QASQISNNLH 34

## RESULT 14

Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
C:Accession: I52592  
R:Wagner, S.D.; Martinelli, V.; Luzzatto, L.  
Blood 83, 3647-3653, 1994  
A:Title: Similar patterns of V kappa gene usage but different degrees of somatic mutatio  
A:Reference number: I52592; MUID:94264318  
A:Accession: I52592

A:Status: preliminary; translated from GB/EMBL/DBBJ  
A:Molecule type: DNA  
A:Residues: 1-87 <RES>  
A:Cross-references: GB:S71057; NID:g547053; PIDN:AAB30971.1; PID:g547054

C:Gene: IgKV

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 87;  
Best Local Similarity 72.7%; Pred. No. 0.55;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11  
:|||||:|

Db 17 QASQISNNLH 27

## RESULT 15

Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S34088  
R:Wagner, S.D.; Luzzatto, L.  
Eur. J. Immunol. 23, 391-397, 1993  
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distrib  
A:Reference number: S34076; MUID:93170387  
A:Accession: S34088

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-88 <WAG>

A:Cross-references: EMBL:X67172  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 88;  
Best Local Similarity 72.7%; Pred. No. 0.56;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11  
:|||||:|  
Db 17 QASQISNNLH 27

Search completed: August 19, 2002, 06:36:07  
Job time: 1288 sec



{

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:11 ; Search time 51.81 Seconds  
(without alignments)  
8.221 Million cell updates/sec

Title: US-09-339-922A-110  
Perfect score: 54  
Sequence: 1 QASQSISNLFH 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	74.1	129	1 KVIW_HUMAN	P04431 homo sapien
2	38	70.4	92	1 KV09_RABIT	P01690 oryctolagus
3	37	68.5	117	1 KVI0_RABIT	P01891 oryctolagus
4	36	66.7	108	1 KV5K_MOUSE	P01844 mus musculus
5	36	66.7	108	1 KV5L_MOUSE	P01645 mus musculus
6	36	66.7	108	1 KV5M_MOUSE	P01646 mus musculus
7	36	66.7	2345	1 COAL_RAT	P11497 rattus norv
8	36	66.7	2346	1 COAL_BOVIN	Q91583 bos taurus
9	36	66.7	2346	1 COAL_SHEEP	Q28559 ovis aries
10	35	64.8	108	1 KVI1_HUMAN	P01594 homo sapien
11	35	64.8	108	1 KV5U_MOUSE	P04946 mus musculus
12	35	64.8	2324	1 COAC_CHICK	P11029 gallus gall
13	35	64.8	2346	1 COAL_HUMAN	Q13085 homo sapien
14	34	63.0	108	1 KVIH_HUMAN	P01600 homo sapien
15	34	63.0	108	1 KVIJ_HUMAN	P01608 homo sapien
16	34	63.0	108	1 KV5J_MOUSE	P01643 mus musculus
17	34	63.0	187	1 PABA_ECOLI	P09303 escherichia
18	34	63.0	3083	1 POLG_ZYMRV	Q89330 z genome po
19	33	61.1	108	1 KV5N_MOUSE	P01647 mus musculus
20	33	61.1	108	1 KV5O_MOUSE	P01648 mus musculus
21	33	61.1	115	1 KV3I_HUMAN	P04433 homo sapien
22	33	61.1	329	1 YDA8_SCHPO	Q10350 schizosacch
23	33	61.1	349	1 PERM_HAEIN	P43969 haemophilus
24	33	61.1	379	1 FLIP_BUCAL	P57184 buchnera ap
25	32	59.3	108	1 KVI1_HUMAN	P01593 homo sapien
26	32	59.3	109	1 KV3F_HUMAN	P01624 homo sapien
27	32	59.3	117	1 KVIJ_HUMAN	P01602 homo sapien
28	32	59.3	129	1 KV3H_HUMAN	P04207 homo sapien
29	32	59.3	412	1 YL57_YEAST	Q12358 saccharomyc
30	32	59.3	459	1 NU4M_CHICK	P18939 gallus gall
31	32	59.3	485	1 Y44E_CAEEL	Q18411 caenorhabdi
32	32	59.3	509	1 CPT7_BOVIN	P05185 bos taurus
33	32	59.3	523	1 C9B1_GLYEC	P93149 glycyrrhiza

34	32	59.3	644	1 VEL_HPV58	P26543 human papil
35	32	59.3	724	1 EF2K_MOUSE	C08796 mus musculu
36	32	59.3	724	1 EF2K_RAT	P70531 rattus norv
37	32	59.3	725	1 EF2K_HUMAN	O00418 homo sapien
38	32	59.3	1310	1 ACN1_HUMAN	O14525 homo sapien
39	32	59.3	1581	1 ACC8_CRICR	Q09427 cricetus cr
40	32	59.3	1581	1 ACC8_RAT	Q09429 rattus norv
41	32	59.3	1629	1 RRPO_SHMV	P89202 sunn-hemp m
42	32	59.3	2037	1 FAS1_CANAL	P34731 c fatty aci
43	31	57.4	109	1 KV3B_HUMAN	P01620 homo sapien
44	31	57.4	109	1 KV3D_HUMAN	P01622 homo sapien
45	31	57.4	153	1 PEN3_ADEB2	Q96623 bovine aden

ALIGNMENTS

RESULT 1					
KVIW_HUMAN					
ID	KVIW_HUMAN	STANDARD;	PRT;	129 AA.	
AC	P04431;				
DT	13-AUG-1987 (Rel. 05, Created)				
DT	13-AUG-1987 (Rel. 05, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-I region Walker precursor.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85014148; PubMed=6091049;				
RA	Klobeck H.G.; Combratio G.; Zachau H.G.;				
RT	"Immunoglobulin genes of the kappa light chain type from two human				
RT	lymphoid cell lines are closely related.";				
RL	Nucleic Acids Res. 12:6995-7006(1984)				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; X00965; CAA25477.1; ALT_TERM.				
DR	PIR; A01883; KIHUWK.				
DR	HSSP; P01607; IREI.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL 1 22				
FT	CHAIN 23 129				
FT	DOMAIN 23 45				
FT	DOMAIN 46 56				
FT	DOMAIN 57 71				
FT	DOMAIN 72 78				
FT	DOMAIN 79 110				
FT	DOMAIN 111 119				
FT	DOMAIN 120 129				
FT	DISULFID 45 110				
FT	NON_TER 129 129				
FT	SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;				

Query Match 74.1%; Score 40; DB 1; Length 129;  
Best Local Similarity 72.7%; Pred. No. 0.25;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QASQSISNLFH 11  
:|||||:

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Db      46 RASQISISNYLN 56

RESULT 2
KV09_RABIT
ID   KV09_RABIT      STANDARD;          PRT;          92 AA.
AC   P01690;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V region 3381 (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75176905; PubMed=1094456;
RA   Margolies M.N., Cannon L.E. III, Strosberg A.D., Haber E.;
RT   "Diversity of light chain variable region sequences among rabbit
RT   antibodies elicited by the same antigens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 72:2180-2184(1975).
CC   -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM THE SERUM OF A SINGLE RABBIT.
CC   PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.
CC   PIR; A01953; KVR38.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; Igv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN          1 23
FT   DOMAIN          24 34
FT   DOMAIN          35 49
FT   DOMAIN          50 56
FT   DOMAIN          57 88
FT   DOMAIN          89 >92
FT   NON_TER         92
FT   SEQUENCE        92 AA; 9730 MW; 9A36B15913CB3BEE CRC64;

Query Match      70.4%; Score 38; DB 1; Length 92;
Best Local Similarity 80.0%; Pred. No. 0.45;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QASQISISNPL 10
      |||:||||:|
Db      24 QASESISNWL 33

RESULT 3
KV10_RABIT
ID   KV10_RABIT      STANDARD;          PRT;          117 AA.
AC   P01691;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V region 12f2 precursor (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83273646; PubMed=6410392;
RA   Dreher K.L., Emorine L., Kindt T.J., Max E.E.;
RT   "CDNA clone encoding a complete rabbit immunoglobulin kappa light
RT   chain of b4 allotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4489-4493(1983).
CC   -1- MISCELLANEOUS: THIS CLONE WAS DERIVED FROM THE RABBIT-MOUSE
CC   HYBRIDOMA 12f2; THE CHAIN PRODUCED IS A MONOCLONAL ANTIBODY
CC   AGAINST STREPTOCOCCAL GROUP C VACCINE.
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; K01358; AAB59259.1; ALT_TERM.
DR   PIR; A01954; K4RBF2.
DR   HSP; P01789; IMCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; Igv; 1.
KW   Immunoglobulin V region; Monoclonal antibody; Hybridoma; Signal.
FT   NON_TER         1 1
FT   SIGNAL          <1 6
FT   CHAIN           7 117
FT   DOMAIN          7 29
FT   DOMAIN          30 40
FT   DOMAIN          41 55
FT   DOMAIN          56 62
FT   DOMAIN          63 94
FT   DOMAIN          95 106
FT   DOMAIN          107 116
FT   DISULFID        29 86
FT   NON_TER         117 117
SQ   SEQUENCE        117 AA; 12288 MW; E24A7582389E4439 CRC64;

Query Match      68.5%; Score 37; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.95;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 QASQISISNPL 10
      |||:||||:|
Db      30 QASQISISNPL 39

RESULT 4
KV5K_MOUSE
ID   KV5K_MOUSE      STANDARD;          PRT;          108 AA.
AC   P01644;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region Hp R16.7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsenate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; Igv; 1.
KW   Immunoglobulin V region; Antiarsenate antibody.
FT   DOMAIN          1 23
FT   DOMAIN          24 34
FT   DOMAIN          35 49
FT   DOMAIN          50 56
FT   DOMAIN          57 88
FT   DOMAIN          89 97

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FT DOMAIN 98 108 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 108;  
 Best Local Similarity 63.6%; Pred. No. 1.4;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINFLH 11  
 :||| |||:|:  
 Db 24 RASQDISNYLN 34

RESULT 5  
 KV5L\_MOUSE STANDARD; PRT; 108 AA.  
 AC P01645;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-V region HP 93G7.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=A/J;  
 RX MEDLINE=82150934; PubMed=6801658;  
 RA Siegelman M., Capra J.D.;  
 RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype."  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
 CC -I- MISCELLANEOUS; ANTI-ARSONATE HYBRIDOMA PROTEIN.  
 DR PIR; A01927; KVMASR.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Antiarsonate antibody.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 108 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;

Query Match 66.7%; Score 36; DB 1; Length 108;  
 Best Local Similarity 63.6%; Pred. No. 1.4;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINFLH 11  
 :||| |||:|:  
 Db 24 RASQDISNYLN 34

RESULT 6  
 KV5L\_MOUSE STANDARD; PRT; 108 AA.  
 AC P01646;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-V region HP 123E6.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=A/J;  
 RX MEDLINE=82150934; PubMed=6801658;  
 RA Siegelman M., Capra J.D.;  
 RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype."  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).  
 CC -I- MISCELLANEOUS; ANTI-ARSONATE HYBRIDOMA PROTEIN.  
 DR PIR; A01927; KVMASR.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Antiarsonate antibody.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 108 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match 66.7%; Score 36; DB 1; Length 108;  
 Best Local Similarity 63.6%; Pred. No. 1.4;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQISINFLH 11  
 :||| |||:|:  
 Db 24 RASQDISNYLN 34

RESULT 7  
 COAL\_RAT STANDARD; PRT; 2345 AA.  
 ID COAL\_RAT P11497; P97902;  
 AC P11497; P97902;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Acetyl-CoA carboxylase 1 [EC 6.4.1.2] (ACC-alpha) [Includes: Biotin carboxylase (EC 6.3.4.14)].  
 GN ACACA OR ACAC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88320328; PubMed=2901088;  
 RA Lopez-Casillas F., Bai D.-H., Luo X., Kong I.-S., Hermodson M.A., Kim K.-H.;  
 RT "Structure of the coding sequence and primary amino acid sequence of acetyl-coenzyme A carboxylase."  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:5784-5788(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89264558; PubMed=2566999;  
 RA Luo X.N., Park K., Lopez-Casillas F., Kim K.-H.;  
 RT "Structural features of the acetyl-CoA carboxylase gene: mechanisms for the generation of mRNAs with 5' end heterogeneity."  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4042-4046(1989).  
 RN [3]  
 RP SEQUENCE OF 1-33 FROM N.A.  
 RX MEDLINE=89214151; PubMed=2565337;  
 RA Lopez-Casillas F., Kim K.-H.;



DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00866; CPSASE\_1; 1.  
 DR PROSITE; PS00867; CPSASE\_2; 1.  
 KW Fatty acid biosynthesis; Biotin; Ligase; Multifunctional enzyme;  
 KW ATP-binding; Phosphorylation.  
 FT NP\_BIND 315 320 ATP (POTENTIAL).  
 FT ACT\_SITE 441 441 BY SIMILARITY.  
 FT BINDING 786 786 BIOTIN (BY SIMILARITY).  
 FT DOMAIN 1959 1988 COENZYME A-BINDING (BY SIMILARITY).  
 FT MOD\_RES 78 78 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 80 80 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 1201 1201 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 2346 AA; 265301 MW; 32886C5D03EEAE0E CRC64;

Query Match 66.7%; Score 36; DB 1; Length 2346;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SISNFLH 11  
 |||||  
 Db 647 SISNFLH 653

RESULT 9  
 COAL\_SHEEP STANDARD; PRT; 2346 AA.  
 ID COAL\_SHEEP STANDARD; PRT; 2346 AA.  
 AC Q28559;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin  
 carboxylase (EC 6.3.4.14)].  
 GN ACACA OR ACAC.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FINN-DORSET; TISSUE=Adipose tissue;  
 RX MEDLINE=95197015; PubMed=7890176;  
 RA Barber M.C., Travers M.T.;  
 RT "Cloning and characterisation of multiple acetyl-CoA carboxylase  
 transcripts in ovine adipose tissue.";  
 RL Gene 154:271-275(1995).  
 CC -!- FUNCTION: CATALYZES THE RATE-LIMITING REACTION IN THE BIOGENESIS  
 OF LONG-CHAIN FATTY ACIDS. THIS PROTEIN CARRIES THREE FUNCTIONS:  
 BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE, AND  
 CARBOXYLTRANSFERASE.  
 CC -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate  
 + malonyl-CoA.  
 CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)  
 = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.  
 CC -!- COFACTOR: BIOTIN.  
 CC -!- ENZYME REGULATION: BY PHOSPHORYLATION (BY SIMILARITY).  
 CC -!- PATHWAY: FIRST STEP (RATE LIMITING) IN LONG-CHAIN FATTY ACID  
 SYNTHESIS.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: PARTIAL TO CARBAMOYL PHOSPHATE SYNTHETASES.  
 CC -----  
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 CC -----  
 DR EMBL; X80045; CAA56352.1; -.  
 DR HSP; P24182; IDV1.  
 DR InterPro; IPR001882; Biotin.

DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR000901; CPSase.  
 DR InterPro; IPR000022; Carboxyl\_trans.  
 DR Pfam; PF02785; Biotin\_carb\_C; 1.  
 DR Pfam; PF00364; Biotin\_lipoyl; 1.  
 DR Pfam; PF01039; Carboxyl\_trans; 1.  
 DR Pfam; PF00289; CPSase\_L\_chain; 1.  
 DR Pfam; PF02786; CPSase\_L\_D2; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00866; CPSASE\_1; 1.  
 DR PROSITE; PS00867; CPSASE\_2; 1.  
 KW Fatty acid biosynthesis; Biotin; Ligase; Multifunctional enzyme;  
 KW ATP-binding; Phosphorylation.  
 FT NP\_BIND 315 320 ATP (POTENTIAL).  
 FT ACT\_SITE 441 441 BY SIMILARITY.  
 FT BINDING 786 786 BIOTIN (BY SIMILARITY).  
 FT DOMAIN 1959 1988 COENZYME A-BINDING (BY SIMILARITY).  
 FT MOD\_RES 78 78 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 80 80 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 1201 1201 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 2346 AA; 265249 MW; BCA010ADF6CD24EF CRC64;

Query Match 66.7%; Score 36; DB 1; Length 2346;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SISNFLH 11  
 |||||  
 Db 647 SISNFLH 653

RESULT 10  
 KV1B\_HUMAN STANDARD; PRT; 108 AA.  
 ID KV1B\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01594;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region AU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72189444; PubMed=5028201;  
 RA Schiechl H., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
 protein Au).";  
 RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=77022433; PubMed=1234024;  
 RA Feilhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
 RA Schwager P., Steigemann W., Schramm H.J.;  
 RT "The structure determination of the variable portion of the  
 Bence-Jones protein Au.";  
 RT Biophys. Struct. Mech. 1:139-146(1975).  
 CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
 MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
 REGION OF THE KAPPA CHAIN REI.  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC PIR; A01862; KIHU4U.  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW immunoglobulin\_v region; Bence-Jones protein.  
 DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11939 MW; E8011187E6F6FB9 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 108;  
 Best Local Similarity 63.6%; Pred. No. 2.3;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QASQISNPLH 11  
 |||||  
 Db 24 QASQDISDYLN 34

RESULT 11  
 KV5U\_MOUSE  
 ID KV5U\_MOUSE STANDARD; PRT; 108 AA.  
 AC P04946;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-V region NQ5-89.4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83271467; PubMed=6877353;  
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;  
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone and its early diversification";  
 RL Nature 304:320-324(1983).  
 CC -1- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.  
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 CC

DR EMBL; K00745; AAA38690.1; -;  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; Ig; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DDD CRC64;

Query Match 64.8%; Score 35; DB 1; Length 108;  
 Best Local Similarity 70.0%; Pred. No. 2.3;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 ASQDISNPLH 11  
 |||||

Db 25 ASQDISNPLN 34

RESULT 12  
 COAC\_CHICK  
 ID COAC\_CHICK STANDARD; PRT; 2324 AA.  
 AC P11029;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Includes: Biotin  
 DE carboxylase (EC 6.3.4.14)].  
 GN ACAC.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=88139305; PubMed=2893793;  
 RA Takai T., Yokoyama C., Wada K., Tanabe T.;  
 RT "Primary structure of chicken liver acetyl-CoA carboxylase deduced  
 RT from cDNA sequence";  
 RL J. Biol. Chem. 263:2651-2657(1988).  
 RN [2]  
 RP SEQUENCE OF 493-820 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=87106011; PubMed=2879745;  
 RA Takai T., Wada K., Tanabe T.;  
 RT "Primary structure of the biotin-binding site of chicken liver  
 RT acetyl-CoA carboxylase";  
 RL FEBS Lett. 212:98-102(1987).  
 CC -1- FUNCTION: CATALYZES THE RATE-LIMITING REACTION IN THE BIOGENESIS  
 CC OF LONG-CHAIN FATTY ACIDS. THIS PROTEIN CARRIES THREE FUNCTIONS:  
 CC BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE, AND  
 CC CARBOXYLTRANSFERASE.  
 CC -1- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate  
 CC + malonyl-CoA.  
 CC -1- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)  
 CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.  
 CC -1- COFACTOR: BIOTIN.  
 CC -1- ENZYME REGULATION: BY PHOSPHORYLATION.  
 CC -1- PATHWAY: FIRST STEP (RATE LIMITING) IN LONG-CHAIN FATTY ACID  
 CC SYNTHESIS.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: PARTIAL TO CARBAMOYL PHOSPHATE SYNTHETASES.  
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 CC EMBL; J03541; AAA48701.1; -;  
 DR EMBL; X05019; CAA28675.1; -;  
 DR PIR; A27903; A27903.  
 DR PIR; A29337; A29337.  
 DR PIR; A29924; A29924.  
 DR HSSP; P24182; 1DV1.  
 DR InterPro; IPR001882; Biotin.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR000901; CPSase.  
 DR InterPro; IPR000022; Carboxyl\_trans.  
 DR Pfam; PF02785; Biotin\_carb\_C; 1.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF01039; Carboxyl\_trans; 1.  
 DR Pfam; PF00289; CPSase\_L\_chain; 1.  
 DR Pfam; PF02786; CPSase\_L\_D2; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.

DR PROSITE; PS00866; CPSASE\_1; 1.  
 DR PROSITE; PS00867; CPSASE\_2; 1.  
 KW Fatty acid biosynthesis; Biotin; Ligase; Multifunctional enzyme;  
 KW ATP-binding; Phosphorylation.  
 FT NP\_BIND 315 320 ATP (POTENTIAL).  
 FT ACT\_SITE 441 441 BY SIMILARITY.  
 FT BINDING 786 786 BIOTIN.  
 FT MOD\_RES 78 78 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 80 80 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 1193 1193 PHOSPHORYLATION (BY SIMILARITY).  
 FT DOMAIN 1936 1965 COENZYME A-BINDING (BY SIMILARITY).  
 SQ SEQUENCE 2324 AA; 262717 MW; 3F1C541F01BBBF6 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 2324;  
 Best Local Similarity 85.7%; Pred. No. 73;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SISNFLH 11  
 I:|||||  
 DB 647 SVSNFLH 653

## RESULT 13

COAL\_HUMAN  
 ID COAL\_HUMAN STANDARD; PRT; 2346 AA.  
 AC Q13085;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin  
 carboxylase (EC 6.3.4.14)].  
 GN ACACA OR ACAC OR ACC1 OR ACCA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=95249602; PubMed=7732023;  
 RA Abu-Elheiga L., Jayakumar A., Baldini A., Chirala S.S., Wakil S.J.;  
 RT "Human acetyl-CoA carboxylase: characterization, molecular cloning,  
 and evidence for two isoforms.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:4011-4015(1995).  
 CC -1- FUNCTION: CATALYZES THE RATE-LIMITING REACTION IN THE BIOGENESIS  
 OF LONG-CHAIN FATTY ACIDS. THIS PROTEIN CARRIES THREE FUNCTIONS:  
 BIOTIN CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE, AND  
 CARBOXYLTRANSFERASE.  
 CC -1- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate  
 + malonyl-CoA.  
 CC -1- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)  
 = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.  
 CC -1- COFACTOR: BIOTIN.  
 CC -1- ENZYME REGULATION: BY PHOSPHORYLATION (BY SIMILARITY).  
 CC -1- PATHWAY: FIRST STEP (RATE LIMITING) IN LONG-CHAIN FATTY ACID  
 SYNTHESIS.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PLACENTAL, SKELETAL  
 MUSCLE, RENAL, PANCREATIC AND ADIPOSE TISSUES; EXPRESSED AT LOW  
 LEVEL IN PULMONARY TISSUE; NOT DETECTED IN THE LIVER.  
 CC -1- SIMILARITY: PARTIAL TO CARBAMOYL PHOSPHATE SYNTHETASES.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U19822; AAC50139.1; -;  
 DR HSSP; P24182; 1DV1.

DR MIM; 200350; -;  
 DR InterPro; IPR001882; Biotin.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR000901; CPSase.  
 DR InterPro; IPR000022; Carboxyl\_trans.  
 DR Pfam; PF02785; Biotin\_carb\_C; 1.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF01039; Carboxyl\_trans; 1.  
 DR Pfam; PF00289; CPSase\_L\_chain; 1.  
 DR Pfam; PF02786; CPSase\_L\_D2; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00866; CPSASE\_1; 1.  
 DR PROSITE; PS00867; CPSASE\_2; 1.  
 KW Fatty acid biosynthesis; Biotin; Ligase; Multifunctional enzyme;  
 KW ATP-binding; Phosphorylation.  
 FT NP\_BIND 315 320 ATP (POTENTIAL).  
 FT ACT\_SITE 441 441 BY SIMILARITY.  
 FT BINDING 786 786 BIOTIN (BY SIMILARITY).  
 FT DOMAIN 1959 1988 COENZYME A-BINDING (POTENTIAL).  
 FT MOD\_RES 78 78 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 80 80 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 1201 1201 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 2346 AA; 265038 MW; 9519190D40190D14 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 2346;  
 Best Local Similarity 85.7%; Pred. No. 74;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SISNFLH 11  
 I:|||||  
 DB 647 SVSNFLH 653

## RESULT 14

KVIH\_HUMAN  
 ID KVIH\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01600;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Hau.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71032830; PubMed=4097974;  
 RA Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
 chain of subgroup I (Bence-Jones Protein Hau): subdivision within  
 subgroups.";  
 RT subgroups.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01868; KIHUHU.  
 DR HSSP; P80362; 1WTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 108;  
 Best Local Similarity 70.0%; Pred. No. 3.7;  
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLF 10  
 DB 24 RASQSISSYL 33

RESULT 15  
 KVIP\_HUMAN STANDARD; PRT; 108 AA.  
 AC PO1608;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Roy.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=68362076; PubMed=5595110;  
 RA Hilschmann N.;  
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and  
 Cum.)";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).  
 RN [2]  
 RP REVISIONS TO 39 AND 41.  
 RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,  
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;  
 RL (In) Franek F., Shugar D. (eds.);  
 RL Gamma globulins: structure and function, pp.57-74, Academic Press,  
 RL New York (1969).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01874; K1HURY.  
 DR HSSP; P80362; 1WTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Igv; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 63.0%; Score 34; DB 1; Length 108;  
 Best Local Similarity 72.7%; Pred. No. 3.7;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNLFH 11  
 DB 24 QASQDISIFLN 34

Search completed: August 19, 2002, 06:59:12  
 Job time: 1377 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:18 ; Search time 140.4 Seconds  
(without alignments)  
13.554 Million cell updates/sec

Title: US-09-339-922A-110

Perfect score: 54

Sequence: 1 QASQSISNFLH 11

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPREMBL19.\*
- 2: sp\_archaea.\*
- 3: sp\_bacteria.\*
- 4: sp\_fungi.\*
- 5: sp\_human.\*
- 6: sp\_invertebrate.\*
- 7: sp\_mammal.\*
- 8: sp\_mhc.\*
- 9: sp\_organelle.\*
- 10: sp\_phase.\*
- 11: sp\_plant.\*
- 12: sp\_rodent.\*
- 13: sp\_virus.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	74.1	107	4 Q9UL81	Q9ul81 homo sapien
2	38	70.4	162	5 Q17590	Q17590 caenorhabdi
3	37	68.5	334	16 Q9Z785	Q9Z785 chlamydia p
4	36	66.7	234	11 Q91WF8	Q91wf8 mus musculu
5	36	66.7	256	6 Q06980	Q06980 capra hircu
6	36	66.7	293	10 Q49020	Q49020 gossypium h
7	36	66.7	293	10 Q94JN5	Q94jn5 gossypium h
8	36	66.7	293	10 Q94JN4	Q94jn4 gossypium h
9	36	66.7	307	3 Q59680	Q59680 schizosacch
10	36	66.7	336	10 Q9LM02	Q9lm02 arabidopsis
11	36	66.7	340	2 Q9ZIT2	Q9zit2 escherichia
12	36	66.7	340	2 Q9R9D5	Q9r9d5 escherichia
13	36	66.7	340	2 Q9R9C9	Q9r9c9 escherichia
14	36	66.7	572	16 Q9KSL6	Q9ksl6 vibrio chol
15	36	66.7	573	5 Q95PR8	Q95pr8 leishmania
16	36	66.7	816	5 Q9N9P7	Q9n9p7 leishmania

17	35	64.8	107	4 Q96SA9	Q96sa9 homo sapien
18	35	64.8	108	4 Q9UL77	Q9ul77 homo sapien
19	35	64.8	108	4 Q9UL70	Q9ul70 homo sapien
20	35	64.8	267	13 Q98909	Q98909 gallus gall
21	35	64.8	375	8 Q9TL10	Q9tl10 nephroselmi
22	35	64.8	395	10 Q9LU60	Q9lu60 arabidopsis
23	35	64.8	698	16 Q92RJ4	Q92rj4 rhizobium m
24	35	64.8	707	2 Q9FSN1	Q9fsn1 rhizobium m
25	35	64.8	1360	2 Q9RFK6	Q9rfk6 stigmatella
26	34	63.0	534	5 Q9XUR9	Q9xur9 caenorhabdi
27	34	63.0	536	16 Q99SK4	Q99sk4 staphylococ
28	34	63.0	592	4 Q9NU33	Q9nu33 homo sapien
29	34	63.0	605	3 Q74207	Q74207 candida alb
30	34	63.0	605	3 Q9UNF6	Q9unf6 candida alb
31	34	63.0	753	13 Q9DE07	Q9de07 gallus gall
32	34	63.0	800	12 Q9WA54	Q9wa54 zucchini ye
33	34	63.0	803	11 Q9DC20	Q9dc20 mus musculu
34	34	63.0	889	3 Q9USQ6	Q9usq6 schizosacch
35	34	63.0	929	5 Q18759	Q18759 caenorhabdi
36	34	63.0	996	5 Q95XN3	Q95xn3 caenorhabdi
37	34	63.0	1416	5 Q9XZ34	Q9xz34 drosophila
38	34	63.0	2553	5 Q22860	Q22860 caenorhabdi
39	34	63.0	3944	5 Q18667	Q18667 caenorhabdi
40	33	61.1	116	4 Q96PF6	Q96pf6 homo sapien
41	33	61.1	184	11 Q9CTM3	Q9ctm3 mus musculu
42	33	61.1	219	4 Q9NT75	Q9nt75 homo sapien
43	33	61.1	292	16 Q97J05	Q97j05 clostridium
44	33	61.1	312	11 Q9DIP6	Q9dip6 mus musculu
45	33	61.1	323	10 Q9AWW7	Q9aww7 oryza sativ

#### ALIGNMENTS

RESULT 1

Q9UL81 ID Q9UL81 PRELIMINARY; PRT; 107 AA.  
AC Q9UL81;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035033; AAD56269.1; -;  
DR HSSP; P01607; IREI.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF000047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 74.1%; Score 40; DB 4; Length 107;  
Best Local Similarity 72.7%; Pred. No. 1.4;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNFLH 11

:|||||:

DB 24 RASQSISNYLN 34

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RESULT 2
ID Q17590 PRELIMINARY; PRT; 162 AA.
AC Q17590;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE C02B4.3 PROTEIN.
GN C02B4.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pezodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z50004; CAA90292.1; -.
SQ SEQUENCE 162 AA; 19034 MW; B9731BD4E3A37B18 CRC64;

Query Match 70.4%; Score 38; DB 5; Length 162;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASQSISNFLH 11
:|:|||||
Db 107 SSEDVSNFLH 116

RESULT 3
ID Q92785 PRELIMINARY; PRT; 334 AA.
AC Q92785;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE C7566 HYPOTHETICAL PROTEIN.
GN CPN0821 OR CPJ0821 OR CPJ050.
OS Chlamydia pneumoniae (Chlamydothilla pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydothilla.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA HIRAKAWA H., SHIRAI M., KUHARA S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=J138;
RN [4]
RP SEQUENCE FROM N.A.
RA SHIRAI M.;
RT "Genomic sequence comparison of two unrelated isolates of chlamydia
RT pneumoniae from Japan and U.S.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.

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RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AE001662; AAD18959.1; -.
DR EMBL; AB035931; BAA8639.1; -.
DR EMBL; AP002548; BAA99029.1; -.
DR EMBL; AE002261; AAF38823.1; -.
DR TIGR; CP1050; -.
KW Complete proteome.
SQ SEQUENCE 334 AA; 38106 MW; C4D557A9464EAEF9 CRC64;

Query Match 68.5%; Score 37; DB 16; Length 334;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQSISNFLH 11
|||:||||
Db 197 SQSLLNFLH 205

RESULT 4
Q91WF8
ID Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 25.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 66.7%; Score 36; DB 11; Length 234;
Best Local Similarity 63.6%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFLH 11
:|||||:|
Db 44 RASQDISNYLN 54

RESULT 5
Q06980
ID Q06980 PRELIMINARY; PRT; 256 AA.
AC Q06980;
DT 01-NOV-1996 (TReMBLrel. 01, Created)

```

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)  
 DE ACETYL-COA CARBOXYLASE (FRAGMENT).  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MAMMARY GLAND;  
 RX MEDLINE=93278985; PubMed=8099321;  
 RA Travers M.T., Barber M.C.;  
 RT "Isolation of a goat acetyl-CoA carboxylase complementary DNA and  
 RT effect of milking frequency on the expression of the acetyl-CoA  
 RT carboxylase and fatty acid synthase genes in goat mammary gland.";  
 RL Comp. Biochem. Physiol. 105B:123-128(1993).  
 DR EMBL: Z17803; CAA79077.1; -.  
 DR InterPro: IPR000901; CPSase.  
 DR Pfam: PF02785; Biotin\_carb\_C; 1.  
 FT NON\_TER 1  
 FT NON\_TER 256  
 SQ SEQUENCE 256 AA; 28454 MW; 3BC340D409C43B9D CRC64;

Query Match 66.7%; Score 36; DB 6; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SISNLFH 11  
 DB 125 SISNLFH 131

## RESULT 6

ID 049020 PRELIMINARY; PRT; 293 AA.  
 AC 049020;  
 DT 01-JUN-1998 (TReMBLrel. 06, Created)  
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE MYB-LIKE DNA-BINDING DOMAIN PROTEIN.  
 GN CMY-N.  
 OS Gossypium hirsutum (Upland cotton).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Malvales; Malvaceae; Gossypium.  
 OX NCBI\_TaxID=3635;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. ACALA SJ-2; TISSUE=OVULE;  
 RA Loquerio L.L., Zhang J., Wilkins T.A.;  
 RT "Structure and expression of six classes of myb-domain genes in  
 RT allotetraploid cotton (Gossypium hirsutum L.);"  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF034133; AAC04719.1; -.  
 DR HSP; P06876; IMSE.  
 DR InterPro: IPR001005; Myb\_DNA\_bind.  
 DR Pfam: PF00249; myb\_DNA-binding; 2.  
 DR SMART; SM00395; SANT; 2.  
 DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.  
 DR PROSITE; PS00334; MYB\_2; 1.  
 DR PROSITE; PS00090; MYB\_3; 2.  
 KW DNA-binding.  
 SQ SEQUENCE 293 AA; 33746 MW; 06901890BD174772 CRC64;

Query Match 66.7%; Score 36; DB 10; Length 293;  
 Best Local Similarity 75.0%; Pred. No. 27;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 QSISNLFH 11  
 DB 125 SISNLFH 131

Db 227 QSLSNYLH 234  
 RESULT 7  
 Q94JN5  
 ID 094JN5 PRELIMINARY; PRT; 293 AA.  
 AC 094JN5;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE MYB-LIKE TRANSCRIPTION FACTOR MYB 5.  
 OS Gossypium hirsutum (Upland cotton).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Malvales; Malvaceae; Gossypium.  
 OX NCBI\_TaxID=3635;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. LANDRACE 'PALMERI';  
 RA Cronn R., Cedroni M., Haselkorn T., Osborne C., Wendel J.F.;  
 RT "PCR-mediated recombination in a polyploid plant";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF377316; AAK57698.1; -.  
 SQ SEQUENCE 293 AA; 33557 MW; 4F8912A79659F53E CRC64;

Query Match 66.7%; Score 36; DB 10; Length 293;  
 Best Local Similarity 75.0%; Pred. No. 27;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 QSISNLFH 11  
 DB 228 QSLSNYLH 235

## RESULT 8

ID 094JN4 PRELIMINARY; PRT; 293 AA.  
 AC 094JN4;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE MYB-LIKE TRANSCRIPTION FACTOR MYB 5.  
 OS Gossypium hirsutum (Upland cotton).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Malvales; Malvaceae; Gossypium.  
 OX NCBI\_TaxID=3635;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. LANDRACE 'PALMERI';  
 RA Cronn R., Cedroni M., Haselkorn T., Osborne C., Wendel J.F.;  
 RT "PCR-mediated recombination in a polyploid plant.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF377317; AAK57699.1; -.  
 SQ SEQUENCE 293 AA; 33407 MW; C1F1ADBA5966401A CRC64;

Query Match 66.7%; Score 36; DB 10; Length 293;  
 Best Local Similarity 75.0%; Pred. No. 27;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 QSISNLFH 11  
 DB 228 QSLSNYLH 235

RESULT 9  
 O59680 PRELIMINARY; PRT; 307 AA.  
 ID O59680  
 AC O59680;  
 DT 01-JAN-1999 (TReMBLrel. 09, Created)  
 DT 01-JAN-1999 (TReMBLrel. 09, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE PROBABLE CYTOCHROME C1, HEME PROTEIN PRECURSOR.  
GN SPBC29A3.18.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RA Lyne M., Rajandream M.A., Barrell B.G., Volckaert G.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: THIS IS THE HEME-CONTAINING COMPONENT OF THE CYTOCHROME  
CC B-C1 COMPLEX, WHICH ACCEPTS ELECTRONS FROM RIESKE PROTEIN AND  
CC TRANSFERS ELECTRONS TO CYTOCHROME C IN THE MITOCHONDRIAL  
CC RESPIRATORY CHAIN.  
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.  
CC -!- SUBCELLULAR LOCATION: ANCHORED IN THE INNER MITOCHONDRIAL MEMBRANE  
CC WITH ITS N-TERMINUS PROTRUDING INTO THE MITOCHONDRIAL  
CC INTERMEMBRANE SPACE (BY SIMILARITY).  
DR EMBL; AL022299; CAA18395.1; -.  
DR InterPro; IPR000345; CytC\_heme\_bind.  
DR InterPro; IPR002326; Cyt\_C1.  
DR Pfam; PF02167; Cytochrome\_C1; 1.  
DR PRINTS; PR00603; CYTOCHROME\_C1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
KW Electron transport; Respiratory chain; Oxidative phosphorylation;  
KW Heme; Mitochondrion; Transmembrane; Transist peptide.  
FT TRANSIT 1 62 MITOCHDRION (BY SIMILARITY).  
FT CHAIN 63 307 PROBABLE CYTOCHROME C1, HEME PROTEIN.  
FT BINDING 102 102 HEME (COVALENT) (BY SIMILARITY).  
FT BINDING 105 105 HEME (COVALENT) (BY SIMILARITY).  
FT METAL 106 106 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
FT METAL 225 225 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
FT TRANSMEM 273 287 ANCHORS TO THE MEMBRANE (BY SIMILARITY).  
SQ SEQUENCE 307 AA; 34340 MW; FAD8B9D3A9A3C1B3 CRC64;

Query Match 66.7%; Score 36; DB 3; Length 307;  
Best Local Similarity 54.5%; Pred. No. 29;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11  
II::: |||||  
DB 246 QAAKDVVNFH 256

RESULT 10  
Q9LM02 PRELIMINARY; PRT; 336 AA.  
AC Q9LM02;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE SAM:CYCLOARTENOL-C24-METHYLTRANSFERASE (24-STEROL C-METHYLTRANSFERASE)  
DE (STEROL METHYLTRANSFERASE SMT1).  
GN SMT1.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Schaeffer A., Schaller H., Benveniste P.;  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RX MEDLINE=98069011; PubMed=9405937;

RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,  
RA Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.  
RT Sequence features of the regions of 1,044,062 bp covered by thirteen  
RT physically assigned P1 clones.";  
RL DNA Res. 4:291-300(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Diener A.C., Li H., Zhou W.-X., Whoriskey W.J., Nes W.D., Fink G.R.;  
RT "Effects of reduced C-24 sterol alkylation on plant growth due to a  
RT deficiency in sterol methyltransferase 1.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF090372; AAF78847.1; -.  
DR EMBL; AB006704; BAB08698.1; -.  
DR EMBL; AF195648; AAG28462.1; -.  
DR InterPro; IPR00051; SAM\_bind.  
KW Transferase; Methyltransferase.  
SQ SEQUENCE 336 AA; 38268 MW; 4649BB3868DE1CE9 CRC64;

Query Match 66.7%; Score 36; DB 10; Length 336;  
Best Local Similarity 70.0%; Pred. No. 32;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNLF 10  
II::: |||||  
DB 299 QGSQSVSNFL 308

RESULT 11  
Q9ZIT2 PRELIMINARY; PRT; 340 AA.  
AC Q9ZIT2;  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE WAAQ.  
GN WAAQ.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F653;  
RX MEDLINE=99009352; PubMed=9791168;  
RA Heinrichs D.E., Yethon J.A., Whitfield C.;  
RT "Molecular basis for structural diversity in the core regions of the  
RT lipopolysaccharides of Escherichia coli and salmonella enterica.";  
RL Mol. Microbiol. 30:221-232(1998).  
DR EMBL; AF019745; AAC69668.1; -.  
DR InterPro; IPR002201; Glyco\_transf\_9.  
DR Pfam; PF01075; Glyco\_transf\_9; 1\_  
SQ SEQUENCE 340 AA; 37934 MW; FF3818CF4A687D24 CRC64;

Query Match 66.7%; Score 36; DB 2; Length 340;  
Best Local Similarity 54.5%; Pred. No. 32;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11  
II::: |||||  
DB 56 KASEKIANFFH 66

RESULT 12  
Q9R9D5 PRELIMINARY; PRT; 340 AA.  
AC Q9R9D5;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE WAAQ.  
GN WAAQ.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
ON NCBI\_TaxID=562;  
RX [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F470;  
RX MEDLINE=99009352; PubMed=9791168;  
RA Heinrichs D.E., Yethon J.A., Whitfield C.;  
RT "Molecular basis for structural diversity in the core regions of the  
RT lipopolysaccharides of *Escherichia coli* and *salmonella enterica*.";  
RL Mol. Microbiol. 30:221-232(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F470;  
RX MEDLINE=98434532; PubMed=9756860;  
RA Yethon J.A., Heinrichs D.E., Monteiro M.A., Perry M.B., Whitfield C.;  
RT "Involvement of waaY, waaQ, and waaP in the modification of  
RT *Escherichia coli* lipopolysaccharide and their role in the formation of  
RT a stable outer membrane.";  
RL J. Biol. Chem. 273:26310-26316(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F470;  
RX MEDLINE=99009057; PubMed=9792656;  
RA Heinrichs D.E., Yethon J.A., Amor P.A., Whitfield C.;  
RT "The assembly system for the outer core portion of R1- and R4-type  
RT lipopolysaccharides of *Escherichia coli*. The R1 core-specific beta-  
RT glucosyltransferase provides a novel attachment site for O-  
RT polysaccharides.";  
RL J. Biol. Chem. 273:29497-29505(1998).  
DR EMBL; AF019746; AAC69679.1; -.  
DR InterPro; IPR002201; Glyco\_transf\_9.  
DR Pfam; PF01075; Glyco\_transf\_9; 1.  
SQ SEQUENCE 340 AA; 37920 MW; FBA620791EFA61DF CRC64;  
  
Query Match 66.7%; Score 36; DB 2; Length 340;  
Best Local Similarity 54.5%; Pred. No. 32;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 QASQISNLFH 11  
Db :||: ||| |  
56 KASEKIANFFH 66  
  
RESULT 13  
Q9R9C9 PRELIMINARY; PRT; 340 AA.  
ID Q9R9C9;  
AC Q9R9C9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE WAAQ.  
GN WAAQ.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
ON NCBI\_TaxID=562;  
RX [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F2513;  
RX MEDLINE=99009352; PubMed=9791168;  
RA Heinrichs D.E., Yethon J.A., Whitfield C.;  
RT "Molecular basis for structural diversity in the core regions of the  
RT lipopolysaccharides of *Escherichia coli* and *salmonella enterica*.";  
RL Mol. Microbiol. 30:221-232(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=F2513;  
RX MEDLINE=99009057; PubMed=9792656;

RA Heinrichs D.E., Yethon J.A., Amor P.A., Whitfield C.;  
RT "The assembly system for the outer core portion of R1- and R4-type  
RT lipopolysaccharides of *Escherichia coli*. The R1 core-specific beta-  
RT glucosyltransferase provides a novel attachment site for O-  
RT polysaccharides.";  
RL J. Biol. Chem. 273:29497-29505(1998).  
DR EMBL; AF019747; AAC69690.1; -.  
DR InterPro; IPR002201; Glyco\_transf\_9.  
DR Pfam; PF01075; Glyco\_transf\_9; 1.  
SQ SEQUENCE 340 AA; 37948 MW; AE76AB57B3A792E4 CRC64;  
  
Query Match 66.7%; Score 36; DB 2; Length 340;  
Best Local Similarity 54.5%; Pred. No. 32;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 QASQISNLFH 11  
Db :||: ||| |  
56 KASEKIANFFH 66  
  
RESULT 14  
Q9KS16 PRELIMINARY; PRT; 572 AA.  
ID Q9KS16;  
AC Q9KS16;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE SENSOR HISTIDINE KINASE/RESPONSE REGULATOR.  
GN VC1445.  
OS *Vibrio cholerae*.  
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*.  
ON NCBI\_TaxID=666;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EL TOR N16961 / SEROTYPE O1;  
RX MEDLINE=20406833; PubMed=10952301;  
RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,  
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
RA Fraser C.M.;  
RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*  
RT *cholerae*.";  
RL Nature 406:477-483(2000).  
CC -!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER  
CC REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.  
CC -!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.  
DR EMBL; AE004223; AAF94602.1; -.  
DR HSP; P06628; 1SRR.  
DR TIGR; VC1445; -.  
DR InterPro; IPR003594; HATPase\_c.  
DR InterPro; IPR003661; HIS\_kinA.  
DR InterPro; IPR004359; HIS\_kinA.  
DR InterPro; IPR001789; Response\_reg.  
DR Pfam; PF02518; HATPase\_c; 1.  
DR Pfam; PF00072; response\_reg; 1.  
DR Pfam; PF00512; signal; 1.  
DR SMART; SM00387; HATPase\_c; 1.  
DR SMART; SM00388; HSKA; 1.  
DR SMART; SM00448; REC; 1.  
KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;  
KW Transferase.  
SQ SEQUENCE 572 AA; 64561 MW; 8769513FFC8EDFED CRC64;  
  
Query Match 66.7%; Score 36; DB 16; Length 572;  
Best Local Similarity 80.0%; Pred. No. 55;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 QASQISNLFH 10

Db 207 QANQSKSNFL 216  
 !!:!! !!!!!

RESULT 15  
 Q95PR8 PRELIMINARY; PRT; 573 AA.  
 AC Q95PR8;  
 DT 01-DEC-2001 (TREMELrel. 19, Created)  
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
 DE POSSIBLE HYPOTHETICAL 88.2 KDA PROTEIN.  
 GN P1046.14  
 OS Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-FRIEDLIN;  
 RA Aert R., Robben J., Volckaert G., Ivens A.C., Quail M.,  
 RA Rajandream M.A., Barrell B.G.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-FRIEDLIN;  
 RX MEDLINE=98146435; PubMed=9477341;  
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
 RA Smith D.F.;  
 RT "A physical map of the Leishmania major Friedlin genome."  
 RL Genome Res. 8:135-145(1998).  
 DR EMBL; AL359683; CAC69084.1; -. 2573CCB7AE6476B6 CRC64;  
 SQ SEQUENCE 573 AA; 62853 MW; 2573CCB7AE6476B6 CRC64;

Query Match 66.7%; Score 36; DB 5; Length 573;  
 Best Local Similarity 77.8%; Pred. No. 55;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQISNFL 10  
 !:!!:!!  
 Db 320 ANQSLSNFL 328

Search completed: August 19, 2002, 06:58:19  
 Job time: 1409 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:39:14 ; Search time 180.34 Seconds  
(without alignments)  
6.775 Million cell updates/sec

Title: US-09-339-922A-110

Perfect score: 54

Sequence: 1 QASQISINFLH 11

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
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19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
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21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	11	22	AA661403
2	54	100.0	13	19	AAW76031
3	54	100.0	13	22	AA661389
4	50	92.6	259	21	AA609775
5	47	87.0	11	22	AA661402
6	47	87.0	13	19	AAW76011
7	47	87.0	13	22	AA661369
8	47	87.0	107	19	AAW76006
9	47	87.0	107	19	AAW76002
10	47	87.0	107	19	AAW76004
11	47	87.0	107	22	AA663588
					Enhanced LM609 VH
					LM609 grafted anti
					Mutant VL CDR1 pep
					TMV 30K movement p
					Enhanced 6H6LH lig
					LM609 grafted anti
					LM609 VL CDR1 pep
					LM609 grafted anti
					Vitaxin antibody 1
					LM609 antibody lig
					A light chain vari

12	47	87.0	107	22	AA663590	A light chain vari
13	47	87.0	107	22	AA661360	Vitaxin light chai
14	47	87.0	107	22	AA661362	Antibody LM609 lig
15	47	87.0	107	22	AA661364	Light chain variab
16	43	79.6	88	21	AA556654	Partial peptide fr
17	43	79.6	105	20	AAW87456	JK gene product.
18	43	79.6	105	20	AAW87458	Humanised anti-alp
19	43	79.6	107	20	AAW84098	Humanised anti-alp
20	43	79.6	108	20	AAW84094	Murine vitronectin
21	43	79.6	109	20	AAW06380	Murine monoclonal
22	43	79.6	111	22	AA663629	Vitronectin alpha-
23	43	79.6	112	20	AAW84100	Amino acid sequenc
24	43	79.6	124	21	AA556719	Amino acid sequenc
25	43	79.6	299	22	AA663633	Amino acid sequenc
26	43	79.6	299	22	AA663638	The variable light
27	42	77.8	107	20	AA530203	The variable light
28	42	77.8	107	20	AA530205	Humanised antibody
29	42	77.8	107	21	AAW71240	Murine antiCD40 re
30	42	77.8	107	22	AA680987	EGF receptor chime
31	42	77.8	108	17	AAW00241	Light chain variab
32	42	77.8	128	20	AA530199	Light chain sequen
33	42	77.8	214	20	AA530202	Humanised VL regio
34	41	75.9	107	13	AA25729	Murine CMV5 antibo
35	41	75.9	107	22	AA669677	Humanised CMV5 ant
36	41	75.9	107	22	AA669678	Human WOL antibody
37	41	75.9	107	22	AA669690	Light chain variab
38	41	75.9	108	12	AA615438	Anti-p53 monoclonal
39	41	75.9	109	20	AAW89176	Sequence of mouse
40	41	75.9	127	15	AA654093	Murine CMV5 antibo
41	41	75.9	127	22	AA669687	Single chain Fv fr
42	41	75.9	240	12	AA615443	CDR #1 of rB087 l1
43	40	74.1	11	18	AAW24543	Complementarity de
44	40	74.1	11	22	AA663614	Amino acid sequenc
45	40	74.1	75	19	AAW62818	

#### ALIGNMENTS

RESULT 1  
AA661403  
ID AA661403 standard; peptide; 11 AA.  
XX AA661403;  
AC AA661403  
DT 03-APR-2001 (first entry)  
XX  
XX Enhanced LM609 VH CDR1 peptide.  
DE  
XX LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis.  
XX Unidentified.  
OS  
XX WO200078815-A1.  
FN  
XX 28-DEC-2000.  
PD  
XX 23-JUN-2000; 2000WO-US17454.  
PF  
XX 24-JUN-1999; 99US-0339922.  
PR  
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
PA  
XX Huse WD, Wu H;  
PI  
XX WPI; 2001-050110/06.  
DR  
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis -  
XX

PS Claim 1; Page 46; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta<sub>3</sub> integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX Sequence 11 AA;

SQ

Query Match 100.0%; Score 54; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.00057;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISINFLH 11

Db 1 qasqsisnflh 11

RESULT 2

AAW76031

ID AAW76031 standard; Protein; 13 AA.

XX

AC AAW76031;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-L region CDR1 protein fragment #2.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-L region; CDR;

KW complementarity determining region.

XX

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI; 1998-437472/37.

XX

DR N-PSDB; AAV49868.

XX

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta<sub>3</sub>

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Claim 62; Page 41; 129pp; English.

XX

AAW76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta<sub>3</sub> and can be used to

CC inhibit binding of alphavbeta<sub>3</sub> to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta<sub>3</sub>-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX Sequence 13 AA;

SQ

Query Match 100.0%; Score 54; DB 19; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00068;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISINFLH 11

Db 1 qasqsisnflh 11

RESULT 3

AAB61389

ID AAB61389 standard; peptide; 13 AA.

XX

AC AAB61389;

XX

DT 03-APR-2001 (first entry)

XX

DE Mutant VL CDR1 peptide.

XX

KW LM609; grafted antibody; alphavbeta<sub>3</sub> integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX

OS Unidentified.

XX

PN WO200078815-A1.

XX

PD 28-DEC-2000.

XX

PF 23-JUN-2000; 2000WO-US17454.

XX

PR 24-JUN-1999; 99US-0339922.

XX

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX

PI Huse WD, Wu H;

XX

DR WPI; 2001-050110/06.

XX

PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta<sub>3</sub> integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX

PS Disclosure; Page 41; 132pp; English.

XX

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta<sub>3</sub> integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 54; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00068;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 QASQSISNFLH 11  
:|||||  
Db 1 qasqsisnflh 11

## RESULT 4

AAB09775  
ID AAB09775 standard; Protein; 259 AA.

XX AC AAB09775;

XX DT 06-SEP-2000 (first entry)

XX DE TMV 30K movement protein and scFv fusion protein scFv 30-1 SEQ ID NO:29.

XX KW Molecular pathogenicide; plant disease; resistance; antibody; scFv;  
KW gene construct; pathogen; toxin; fusion protein; antimicrobial;  
KW deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.

XX OS Tobacco mosaic virus.

XX PN WO200023593-A2.

XX PD 27-APR-2000.

XX PF 15-OCT-1999; 99WO-EF07844.

XX PR 16-OCT-1998; 98EP-0119630.

XX PR 16-OCT-1998; 98IN-0000666.

XX PA (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX PI Fischer R, Schillberg S, Naehring J, Sack M, Monecke M, Liao Y;  
PI Spiegel H, Zimmerman S, Emans N, Holzem A;

XX DR WPI: 2000-339692/29.

XX PT New fusion proteins and gene constructs for expressing agents  
PT (antibodies, enzymes, vectors or molecular pathogenicides), useful for  
PT protecting plants against pathogens and increasing resistance to  
PT disease

XX PS Example 5; Page 149-150; 193pp; English.

XX CC The present invention describes a fusion protein (I) comprising at least  
CC one binding domain specifically recognising an epitope of a plant  
CC pathogen and at least one further domain comprising a protein or peptide  
CC sequence which is toxic to the pathogen or detrimental to its  
CC replication, transmission or life cycle. Also described is a  
CC pathogenicide (II) comprising (I) and a cellular targeting sequence  
CC and/or membrane localisation sequence and/or motif that leads to  
CC membrane anchoring; or at least one binding domain that specifically  
CC recognises a viral movement and/or replicase protein. The fusion  
CC protein, pathogenicide, polynucleotide, vectors, and compositions from  
CC the present invention are useful for the protection of a plant against  
CC the action of a pathogen. The kit from the present invention is useful  
CC for carrying out the methods and may be employed in different  
CC applications, for example in the diagnostic field or as research tools.  
CC The kit or its components, such as the fusion protein, pathogenicide,  
CC polynucleotides, vectors or compositions are useful in plant cell and  
CC plant tissue culture, in agriculture. They are extremely useful for  
CC breeding new varieties of plants that display improved properties such as  
CC resistance to pathogens. AA56587 to AAA56702 and AAB09774 to B097820  
CC represent sequences used in the exemplification of the present  
CC invention.

XX SQ Sequence 259 AA;

Query Match 92.6%; Score 50; DB 21; Length 259;  
Best Local Similarity 90.9%; Pred. No. 0.1;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQSISNFLH 11  
:|||||  
Db 155 rasqsisnflh 165

## RESULT 5

AAB61402  
ID AAB61402 standard; peptide; 11 AA.

XX AC AAB61402;

XX DT 03-APR-2001 (first entry)

XX DE Enhanced 6H6LH light chain CDR1.

XX KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI: 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis

XX PS Claim 4; Page 46; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies  
CC exhibiting selective binding affinity to alphaVbeta3 integrin or  
CC their functional fragments. The antibodies or their functional  
CC fragments can be used in the diagnosis and treatment of  
CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory  
CC diseases (such as psoriasis and chronic articular rheumatism),  
CC disorders associated with inappropriate or inopportune invasion of  
CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
CC diseases (such as macular degeneration), restenosis and  
CC osteoporosis.

XX SQ Sequence 11 AA;

Query Match 87.0%; Score 47; DB 22; Length 11;  
Best Local Similarity 90.9%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQSISNFLH 11  
:|||||  
Db 1 qasqsishlh 11

## RESULT 6

AAW76011  
ID AAW76011 standard; Protein; 13 AA.

XX AC AAW76011;

XX DT 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-L region CDR1 protein fragment #1.  
 DE  
 XX  
 KW Vitamin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;  
 KW complementarity determining region.  
 XX  
 OS Mus sp.  
 XX  
 XX WO9833919-A2.  
 PN  
 XX  
 PD 06-AUG-1998.  
 XX  
 XX 30-JAN-1998; 98WO-US01826.  
 PF  
 XX 30-JAN-1997; 97US-0791391.  
 PR  
 XX (IXSY-) IXSYS INC.  
 PA  
 XX Glaser SM, Huse WD;  
 PI  
 XX WPI: 1998-437472/37.  
 DR  
 DR N-PSDB; AAV49848.  
 XX  
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX  
 PS Disclosure: Page 40; 129pp; English.  
 XX  
 CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody  
 CC LM609 heavy and light chain variable region. LM609 and the antibody  
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to  
 CC inhibit binding of alphavbeta3 to a ligand and thus block  
 CC integrin-mediated signal transduction. This is useful in the treatment,  
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically  
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
 CC antibodies contain non-murine framework regions so are suitable for use  
 CC in humans. Enhanced types of LM609 have affinity more than 90 times  
 CC greater than that of parent the parent antibody.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 87.0%; Score 47; DB 19; Length 13;  
 Best Local Similarity 90.9%; Pred. No. 0.015;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QASQISINFLH 11  
 Db | | | | | | | |  
 1 gasqsishnh 11  
 RESULT 7  
 AAB61369  
 ID AAB61369 standard; peptide; 13 AA.  
 XX  
 AC AAB61369;  
 XX  
 XX 03-APR-2001 (first entry)  
 DT  
 XX LM609 VL CDR1 peptide.  
 DE  
 XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 KW  
 XX Unidentified.

XX WO200078815-A1.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 23-JUN-2000; 2000WO-US17454.  
 PF  
 XX 24-JUN-1999; 99US-0339922.  
 PR  
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 PA  
 XX Huse WD, Wu H;  
 PI  
 XX WPI: 2001-050110/06.  
 DR  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure: Page 39; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 87.0%; Score 47; DB 22; Length 13;  
 Best Local Similarity 90.9%; Pred. No. 0.015;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QASQISINFLH 11  
 Db | | | | | | | |  
 1 gasqsishnh 11  
 RESULT 8  
 AAW76006  
 ID AAW76006 standard; Protein; 107 AA.  
 XX  
 AC AAW76006;  
 XX  
 DT 02-NOV-1998 (first entry)  
 DT  
 XX LM609 grafted antibody light chain variable region protein fragment.  
 DE  
 XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis.  
 KW  
 OS Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 49  
 FT /label= Arg, Met  
 XX  
 PN WO9833919-A2.  
 XX  
 PD 06-AUG-1998.  
 PD  
 XX 30-JAN-1998; 98WO-US01826.  
 PF

```

XX 30-JAN-1997; 97US-0791391.
XX (IXSY-) IXSYS INC.
XX Glaser SM, Huse WD;
XX WPI: 1998-437472/37.
XX N-PSDB; AAV49843.
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX Claim 19; Fig 7; 129pp; English.
XX This sequence represents a LM609 grafted antibody variable light chain
XX region. LM609 and the antibody vitaxin bind selectively to integrin
XX alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
XX and thus block integrin-mediated signal transduction. This is useful in
XX the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX etc.). The antibodies contain non-murine framework regions so are
XX suitable for use in humans. Enhanced types of LM609 have affinity more
XX than 90 times greater than that of parent the parent antibody.
XX Sequence 107 AA;

Query Match 87.0%; Score 47; DB 19; Length 107;
Best Local Similarity 90.9%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINFLH 11
DB 24 gasqsisnhlh 34

RESULT 9
AAW76002
ID AAW76002 standard; Protein; 107 AA.
XX AC AAW76002;
XX DT 02-NOV-1998 (first entry)
XX DE Vitaxin antibody light chain variable region protein fragment.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis.
XX OS Mus sp.
XX PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX DR WPI: 1998-437472/37.
XX DR N-PSDB; AAV49821.

```

```

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX Claim 1; Fig 1b; 129pp; English.
XX This sequence represents the vitaxin antibody variable light chain
XX region. Vitaxin and the antibody LM609 bind selectively to integrin
XX alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
XX ligand and thus block integrin-mediated signal transduction. This is
XX useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
XX disease, specifically angiogenesis and restenosis (but also e.g.
XX (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
XX cancer, psoriasis, rheumatoid arthritis, macular degeneration,
XX osteoporosis etc.). The antibodies contain non-murine framework regions
XX so are suitable for use in humans. Enhanced types of LM609 have affinity
XX more than 90 times greater than that of parent the parent antibody.
XX Sequence 107 AA;

Query Match 87.0%; Score 47; DB 19; Length 107;
Best Local Similarity 90.9%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINFLH 11
DB 24 gasqsisnhlh 34

RESULT 10
AAW76004
ID AAW76004 standard; Protein; 107 AA.
XX AC AAW76004;
XX DT 02-NOV-1998 (first entry)
XX DE LM609 antibody light chain variable region protein fragment.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis.
XX OS Mus sp.
XX PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX DR WPI: 1998-437472/37.
XX DR N-PSDB; AAW76004.
XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX PT integrin - and related grafted antibodies based on murine monoclonal
XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX Claim 46; Fig 2b; 129pp; English.
XX This sequence represents the LM609 antibody variable light chain region.

```

CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3  
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
 CC block integrin-mediated signal transduction. This is useful in the  
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
 CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.  
 XX  
 SQ Sequence 107 AA;

Query Match 87.0%; Score 47; DB 19; Length 107;  
 Best Local Similarity 90.9%; Pred. No. 0.15;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFLH 11  
 Db |||||| ||  
 24 qasqsishh 34

RESULT 11  
 AAG63588  
 ID AAG63588 standard; Protein; 107 AA.  
 XX  
 AC AAG63588;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX  
 DE A light chain variable region of LM609 grafted antibody.  
 XX  
 KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 49  
 FT /note= "unspecified residue encoded by MKK"  
 XX  
 PN US2001011125-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 30-JAN-1997; 97US-0790540.  
 XX  
 PR 30-JAN-1997; 97US-0790540.  
 XX  
 PA (HUSE/) HUSE W D.  
 XX  
 PI Huse WD;  
 XX  
 DR WPI: 2001-496171/54.  
 DR N-PSDB; AAH74624.  
 XX  
 PT New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer -  
 XX  
 PS Claim 1; Fig 1B; 25pp; English.  
 XX  
 CC The present sequence represents the light chain variable region of the  
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which  
 CC specifically recognises the integrin alphavbeta3, and inhibits its  
 CC functional activity. The LM609 grafted antibody has the  
 CC complementarity determining regions (CDRs) substituted into a non-murine  
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain  
 CC

CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis  
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
 CC disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 CC an alphavbeta3-mediated disease.  
 XX  
 SQ Sequence 107 AA;

Query Match 87.0%; Score 47; DB 22; Length 107;  
 Best Local Similarity 90.9%; Pred. No. 0.15;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFLH 11  
 Db |||||| ||  
 24 qasqsishh 34

RESULT 12  
 AAG63590  
 ID AAG63590 standard; Protein; 107 AA.  
 XX  
 AC AAG63590;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX  
 DE A light chain variable region of LM609 antibody.  
 XX  
 KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer.  
 XX  
 OS Mus sp.  
 XX  
 PN US2001011125-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 30-JAN-1997; 97US-0790540.  
 XX  
 PR 30-JAN-1997; 97US-0790540.  
 XX  
 PA (HUSE/) HUSE W D.  
 XX  
 PI Huse WD;  
 XX  
 DR WPI: 2001-496171/54.  
 DR N-PSDB; AAH74626.  
 XX  
 PT New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer -  
 XX  
 PS Disclosure; Fig 2B; 25pp; English.  
 XX  
 CC The present sequence represents the light chain variable region of the  
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically  
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.  
 CC The specification describes a LM609 grafted antibody which has the  
 CC complementarity determining regions (CDRs) substituted into a non-murine  
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain  
 CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis

CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
 CC disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 CC an alphavbeta3-mediated disease.

XX Sequence 107 AA;

Query Match 87.0%; Score 47; DB 22; Length 107;

Best Local Similarity 90.9%; Pred. No. 0.15;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQTSNPLH 11  
 Db 24 qasqsisnhlh 34

RESULT 13

AAB61360

ID AAB61360 standard; protein; 107 AA.

XX AC AAB61360;

XX DT 03-APR-2001 (first entry)

XX DE Vitaxin light chain variable region protein.

XX KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 XX KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI; 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -

XX PS Disclosure; Fig 1; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX SQ Sequence 107 AA;

Query Match

87.0%; Score 47; DB 22; Length 107;

Best Local Similarity 90.9%; Pred. No. 0.15;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQTSNPLH 11  
 Db 24 qasqsisnhlh 34

RESULT 14

AAB61362  
 ID AAB61362 standard; protein; 107 AA.

XX AC AAB61362;

XX DT 03-APR-2001 (first entry)

XX DE Antibody LM609 light chain variable region protein.

XX KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 XX KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI; 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -

XX PS Disclosure; Fig 2; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX SQ Sequence 107 AA;

Query Match

87.0%; Score 47; DB 22; Length 107;

Best Local Similarity 90.9%; Pred. No. 0.15;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QASQTSNPLH 11  
 Db 24 qasqsisnhlh 34

RESULT 15

AAB61364  
 ID AAB61364 standard; protein; 107 AA.

XX AC AAB61364;

XX XX

DT 03-APR-2001 (first entry)  
 XX  
 DE Light chain variable region of LM609.  
 XX  
 KW LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retins; restenosis; osteoporosis.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 DR WPI; 2001-050110/06.  
 XX  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Fig 7; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 107 AA;

Query Match 87.0%; Score 47; DB 22; Length 107;  
 Best Local Similarity 90.9%; Pred. No. 0.15;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFIH 11  
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 Db 24 gasqsisnlh 34

Search completed: August 19, 2002, 06:39:14  
 Job time: 1475 sec

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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:42 ; Search time 61.75 Seconds  
(without alignments)  
4.351 Million cell updates/sec

Title: US-09-339-922A-110  
Perfect score: 54  
Sequence: 1 QASQISNPLH 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	77.8	96	2	US-08-737-560A-9
2	42	77.8	107	4	US-09-247-352-8
3	42	77.8	107	4	US-09-247-352-12
4	42	77.8	108	2	US-08-378-939-20
5	42	77.8	108	4	US-09-247-352-1
6	42	77.8	214	4	US-09-247-352-4
7	41	75.9	100	1	US-08-436-463-19
8	41	75.9	103	1	US-08-436-463-21
9	41	75.9	107	1	US-07-634-278-62
10	41	75.9	107	1	US-07-634-278-63
11	41	75.9	107	1	US-07-634-278-87
12	41	75.9	107	1	US-08-477-728-62
13	41	75.9	107	1	US-08-477-728-63
14	41	75.9	107	1	US-08-477-728-87
15	41	75.9	107	1	US-08-474-040-62
16	41	75.9	107	1	US-08-474-040-63
17	41	75.9	107	1	US-08-474-040-87
18	41	75.9	107	1	US-08-487-200-62
19	41	75.9	107	1	US-08-487-200-63
20	41	75.9	107	1	US-08-487-200-87
21	41	75.9	107	4	US-08-484-537-62
22	41	75.9	107	4	US-08-484-537-63
23	41	75.9	107	4	US-08-484-537-87
24	41	75.9	108	4	US-09-157-370-4
25	41	75.9	127	1	US-07-634-278-83
26	41	75.9	127	1	US-08-477-728-83
27	41	75.9	127	1	US-08-474-040-83

28	41	75.9	127	1	US-08-487-200-83	Sequence 83, Appl
29	41	75.9	127	1	US-08-436-463-4	Sequence 4, Appl
30	41	75.9	127	1	US-08-436-463-18	Sequence 18, Appl
31	41	75.9	127	4	US-08-484-537-83	Sequence 83, Appl
32	40	74.1	76	4	US-08-851-362D-20	Sequence 20, Appl
33	40	74.1	105	4	US-08-851-362D-28	Sequence 28, Appl
34	40	74.1	105	4	US-08-851-362D-34	Sequence 34, Appl
35	40	74.1	105	4	US-08-851-362D-38	Sequence 38, Appl
36	40	74.1	107	2	US-08-652-558-36	Sequence 36, Appl
37	40	74.1	107	2	US-08-378-939-14	Sequence 14, Appl
38	40	74.1	107	4	US-09-240-274-173	Sequence 173, App
39	40	74.1	108	1	US-08-276-852-102	Sequence 102, App
40	40	74.1	108	1	US-08-899-575-102	Sequence 102, App
41	40	74.1	108	1	US-08-899-575-102	Sequence 102, App
42	40	74.1	108	2	US-08-378-939-30	Sequence 30, Appl
43	40	74.1	108	4	US-09-025-769B-14	Sequence 14, Appl
44	40	74.1	108	5	PCT-US95-08743-102	Sequence 102, App
45	39	72.2	56	1	US-08-162-102C-40	Sequence 40, Appl

#### ALIGNMENTS

RESULT 1  
US-08-737-560A-9  
; Sequence 9, Application US/08737560A  
; Patent No. 5928893  
; GENERAL INFORMATION:  
; APPLICANT: KANG, Chang-Yuill  
; APPLICANT: KIM, Joong-Gon  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN  
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KANG, Chang-Yuill  
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,  
; STREET: Kwanak-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 151-057  
; ADDRESSEE: KIM, Joong-Gon  
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 135-110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage  
; COMPUTER: IBM PC/AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,560A  
; FILING DATE: 13-NOV-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: KR 95-8176  
; FILING DATE: 08-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 96 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:

OTHER INFORMATION: VK23.32'CL  
US-08-737-560A-9

Query Match 77.8%; Score 42; DB 2; Length 96;  
Best Local Similarity 72.7%; Pred. No. 0.46;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11  
Db 24 RASQSISDYLH 34

## RESULT 2

US-09-247-352-8  
; Sequence 8, Application US/09247352  
; Patent No. 6312693  
; GENERAL INFORMATION:  
; APPLICANT: Aruffo, Alejandro A.  
; APPLICANT: Siadak, Anthony W.  
; APPLICANT: Berry, Karen K.  
; APPLICANT: Harris, Linda  
; APPLICANT: Thorne, Barbara A.  
; APPLICANT: Bajorath, Jurgen  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffery D.  
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40  
; FILE REFERENCE: DB2a SEQUENCE  
; CURRENT APPLICATION NUMBER: US/09/247,352  
; CURRENT FILING DATE: 1999-02-10  
; EARLIER APPLICATION NUMBER: 09/026,291  
; EARLIER FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Human and Mouse  
US-09-247-352-8

Query Match 77.8%; Score 42; DB 4; Length 107;  
Best Local Similarity 72.7%; Pred. No. 0.46;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11  
Db 24 RASQSISDYLH 34

## RESULT 3

US-09-247-352-12  
; Sequence 12, Application US/09247352  
; Patent No. 6312693  
; GENERAL INFORMATION:  
; APPLICANT: Aruffo, Alejandro A.  
; APPLICANT: Siadak, Anthony W.  
; APPLICANT: Berry, Karen K.  
; APPLICANT: Harris, Linda  
; APPLICANT: Thorne, Barbara A.  
; APPLICANT: Bajorath, Jurgen  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffery D.  
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40  
; FILE REFERENCE: DB2a SEQUENCE  
; CURRENT APPLICATION NUMBER: US/09/247,352  
; CURRENT FILING DATE: 1999-02-10  
; EARLIER APPLICATION NUMBER: 09/026,291  
; EARLIER FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Human and Mouse  
US-09-247-352-12

Query Match 77.8%; Score 42; DB 4; Length 107;  
Best Local Similarity 72.7%; Pred. No. 0.46;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11  
Db 24 RASQSISDYLH 34

## RESULT 4

US-08-378-939-20  
; Sequence 20, Application US/08378939  
; Patent No. 5876961  
; GENERAL INFORMATION:  
; APPLICANT: CROME, JAMES SCOTT  
; APPLICANT: LEWIS, ALAN PETER  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
; STREET: 555 THIRTEENTH ST. N.W.  
; CITY: WASHINGTON  
; STATE: D. C.  
; COUNTRY: U.S.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378,939  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952640  
; FILING DATE: 01-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1808-118  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-378-939-20

Query Match 77.8%; Score 42; DB 2; Length 108;  
Best Local Similarity 72.7%; Pred. No. 0.46;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNLFH 11  
Db 24 QASQSLSNLYN 34

## RESULT 5

US-09-247-352-1  
; Sequence 1, Application US/09247352  
; Patent No. 6312693



GENERAL INFORMATION:  
; APPLICANT: Aruffo, Alejandro A.  
; APPLICANT: Sladak, Anthony W.  
; APPLICANT: Berry, Karen K.  
; APPLICANT: Harris, Linda  
; APPLICANT: Thorne, Barbara A.  
; APPLICANT: Bajorath, Jurgen  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40  
; FILE REFERENCE: DB2a SEQUENCE  
; CURRENT APPLICATION NUMBER: US/09/247,352  
; CURRENT FILING DATE: 1999-02-10  
; EARLIER APPLICATION NUMBER: 09/026,291  
; EARLIER FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Human and Mouse  
US-09-247-352-1

Query Match 77.8%; Score 42; DB 4; Length 108;  
Best Local Similarity 72.7%; Pred. No. 0.46;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QASQSISNLFH 11  
Db 24 RASQSISDYH 34  
:|||||:|

RESULT 6  
US-09-247-352-4  
; Sequence 4, Application US/09247352  
; Patent No. 6312693  
; GENERAL INFORMATION:  
; APPLICANT: Aruffo, Alejandro A.  
; APPLICANT: Sladak, Anthony W.  
; APPLICANT: Berry, Karen K.  
; APPLICANT: Harris, Linda  
; APPLICANT: Thorne, Barbara A.  
; APPLICANT: Bajorath, Jurgen  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40  
; FILE REFERENCE: DB2a SEQUENCE  
; CURRENT APPLICATION NUMBER: US/09/247,352  
; CURRENT FILING DATE: 1999-02-10  
; EARLIER APPLICATION NUMBER: 09/026,291  
; EARLIER FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Human and Mouse  
US-09-247-352-4

Query Match 77.8%; Score 42; DB 4; Length 214;  
Best Local Similarity 72.7%; Pred. No. 0.96;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QASQSISNLFH 11  
Db 24 RASQSISDYH 34  
:|||||:|

RESULT 7

US-08-436-463-19  
; Sequence 19, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoto  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,463  
; FILING DATE: 26-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 341255/1992  
; FILING DATE: 28-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: KIMACHI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 100 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-436-463-19  
Query Match 75.9%; Score 41; DB 1; Length 100;  
Best Local Similarity 81.8%; Pred. No. 0.66;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 QASQSISNLFH 11  
Db 24 RASQSISNHLH 34  
:|||||:|  
RESULT 8  
US-08-436-463-21  
; Sequence 21, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoto  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.

; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,463  
; FILING DATE: 26-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 341255/1992  
; FILING DATE: 28-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: KIMACHI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 103 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-436-463-21

Query Match 75.9%; Score 41; DB 1; Length 103;  
Best Local Similarity 81.8%; Pred. No. 0.68;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNPLH 11  
:||||| ||  
Db 22 RASQISNNLH 32

RESULT 9  
US-07-634-278-62  
; Sequence 62, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-07-634-278-62

Query Match 75.9%; Score 41; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.71;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNPLH 11  
:||||| ||  
Db 24 RASQISNNLH 34

RESULT 10  
US-07-634-278-63  
; Sequence 63, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-634-278-63

Query Match 75.9%; Score 41; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.71;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINFLH 11  
:|||||  
Db 24 RASQISINLH 34

## RESULT 11

US-07-634-278-87  
Sequence 87, Application US/07634278  
Patent No. 5530101

GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLEI, Nicholas F.  
APPLICANT: COELLINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-07-634-278-87

Query Match 75.9%; Score 41; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.71;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINFLH 11  
:|||||  
Db 24 RASQISINLH 34

## RESULT 12

US-08-477-728-62  
Sequence 62, Application US/08477728  
Patent No. 5585089

GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,728  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-728-62

Query Match 75.9%; Score 41; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.71;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISINFLH 11



ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,040  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-474-040-62

Query Match 75.9%; Score 41; DB 1; Length 107;  
Best Local Similarity 81.8%; Pred. No. 0.71;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSSISNLFH 11  
Db 24 RASQSSISNNLH 34

Search completed: August 19, 2002, 06:34:43  
Job time: 1204 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:36:07 ; Search time 78.53 seconds  
(without alignments)  
8.565 Million cell updates/sec

Title: US-09-339-922A-112

Perfect score: 33

Sequence: 1 YRSQIS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	30	90.9	629	2 T31626	hypothetical prote
2	29	87.9	406	2 B96982	probable membrane
3	29	87.9	409	2 T29517	hypothetical prote
4	29	87.9	944	2 F90600	exonuclease ABC s
5	28	84.8	191	2 T43737	heat shock protein
6	28	84.8	191	2 AB1259	heat shock protein
7	28	84.8	191	2 AF1621	heat shock protein
8	28	84.8	206	2 T47433	hypothetical prote
9	28	84.8	250	2 G83283	precorrin-2 methyl
10	28	84.8	345	2 AB1813	hypothetical prote
11	28	84.8	368	1 HLBECH	membrane glycoprot
12	28	84.8	2028	2 T08025	DNA-directed RNA p
13	27	81.8	69	2 PH1080	ig light chain v r
14	27	81.8	96	2 G33730	ig kappa chain v r
15	27	81.8	104	2 B43413	ig kappa chain v r
16	27	81.8	106	2 PL0267	ig kappa chain v r
17	27	81.8	107	2 B45722	anti-glycoprotein
18	27	81.8	107	2 C45722	anti-glycoprotein
19	27	81.8	107	2 A45722	anti-glycoprotein
20	27	81.8	115	2 S10146	ig kappa chain pre
21	27	81.8	138	2 A26471	ig kappa chain pre
22	27	81.8	144	2 S34150	ig mu chain - axol
23	27	81.8	291	2 A81662	UDP-3-O-(3-hydroxy
24	27	81.8	367	2 T24298	hypothetical prote
25	27	81.8	423	2 E97165	flagellar hook pro
26	27	81.8	438	2 G64513	hypothetical prote
27	27	81.8	490	2 T43149	probable beta-fruc
28	27	81.8	493	2 T01495	hypothetical prote
29	27	81.8	504	2 I53868	alpha-internexin -

#### ALIGNMENTS

##### RESULT 1

T31626

hypothetical protein Y57A10A.d - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 20-Jun-2000

C:Accession: T31626

R:Smyle, R.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z21048

A:Accession: T31626

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-629 <WIL>

A:Cross-references: EMBL:AL117195; PIDN:CAB55009.1; CESP:Y57A10A.d

A:Experimental source: clone Y57A10A

C:Genetics:

A:Gene: CESP:Y57A10A.d

A:Introns: 51/2; 89/2; 183/2; 221/2; 284/2; 318/2; 399/2; 611/1

C:Superfamily: Caenorhabditis elegans hypothetical protein Y57A10A.d

Query Match 90.9%; Score 30; DB 2; Length 629;  
Best Local Similarity 85.7%; Pred. No. 26;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7

Db 466 YRNQIS 472

##### RESULT 2

B96982

probable membrane protein [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001

C:Accession: B96982

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.;

; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: B96982

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-406 <KUP>

A:Cross-references: GB:AB001437; PIDN:AAK78645.1; PID:gl5023544; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC0668

Query Match 87.9%; Score 29; DB 2; Length 406;

Best Local Similarity 85.7%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSI 7

|||||

DB 193 YRSQSI 199

RESULT 3

T29517

hypothetical protein T25F10.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T29517

R:Pauley, A.; Gattung, S.

submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid T25F10.

A:Reference number: Z20634

A:Accession: T29517

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-409 <PAU>

A:Cross-references: EMBL:U64856; PIDN:AAB04985.1; GSPDB:GN00023; CESP:T25F10.3

A:Experimental source: strain Bristol N2; clone T25F10

C:Genetics:

A:Gene: CESP:T25F10.3

A:Map position: 5

A:Introns: 86/3; 112/1; 233/3; 268/3; 291/1; 348/2

Query Match

Best Local Similarity 87.9%; Score 29; DB 2; Length 409;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 6

|||||

DB 133 YRSQSI 138

RESULT 4

F90600

excinuclease ABC subunit a [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C:Species: Mycoplasma pulmonis

C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001

C:Accession: F90600

R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A:Reference number: A95512; MUID:21267165; PMID:11353084

A:Accession: F90600

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-944 <KUR>

A:Cross-references: GB:A445566; PID:gl4090125; PIDN:CAC13883.1; GSPDB:GN00153

A:Experimental source: strain UAB CTIP

C:Genetics:

A:Gene: MYPu\_7100

C:Superfamily: excinuclease ABC chain A; ATP-binding cassette homology

Query Match

Best Local Similarity 87.9%; Score 29; DB 2; Length 944;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 7

|||||

DB 784 YRSQSI 790

RESULT 5

T43737

heat shock-protein grpE [imported] - Listeria monocytogenes

C:Species: Listeria monocytogenes  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000  
C:Accession: T43737

R:Hanawa, T.; Kai, M.; Kamiya, S.; Yamamoto, T.

submitted to the EMBL Data Library, February 1999

A:Description: Cloning, sequencing, and transcriptional analysis of the dnaK heat sho

A:Reference number: Z22656

A:Accession: T43737

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-191 <HAN>

A:Cross-references: EMBL:AB023064; PIDN:BAA82788.1

A:Experimental source: strain 10403S

C:Genetics:

A:Note: grpE

C:Superfamily: heat shock protein grpE

C:Keywords: stress-induced protein

Query Match

Best Local Similarity 84.8%; Score 28; DB 2; Length 191;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 7

|||||

DB 84 YRSQSLA 90

RESULT 6

AB1259

heat shock protein GrpE [imported] - Listeria monocytogenes (strain EGD-e)

C:Species: Listeria monocytogenes

C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001

C:Accession: AB1259

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AB1259

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-191 <GLA>

A:Cross-references: GB:NC\_003210; PIDN:CAC99552.1; PID:gl16410903; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: grpE

C:Superfamily: heat shock protein grpE

Query Match

Best Local Similarity 84.8%; Score 28; DB 2; Length 191;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 7

|||||

DB 84 YRSQSLA 90

RESULT 7

AF1621

heat shock protein GrpE [imported] - Listeria innocua (strain Clip11262)

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001

C:Accession: AF1621

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;

OK, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AF1621

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-191 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC96742.1; PID:g16413984; GSPDB:GN00178

A:Experimental source: strain Clp11262

C:Genetics:

A:Gene: grpE

C:Superfamily: heat shock protein grpE

Query Match 84.8%; Score 28; DB 2; Length 191;  
Best Local Similarity 71.4%; Pred. No. 24;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQSIS 7

|||||:

Db 84 YRSQSIA 90

RESULT 8

T47433

hypothetical protein T22K7.110 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C:Accession: T47433

R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24459

A:Accession: T47433

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-206 <RIE>

A:Cross-references: EMBL:AL138641

A:Experimental source: cultivar Columbia; BAC clone T22K7

C:Genetics:

A:Map position: 3

A:Note: T22K7.110

Query Match 84.8%; Score 28; DB 2; Length 206;  
Best Local Similarity 71.4%; Pred. No. 26;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQSIS 7

|||||:

Db 107 YRSRSVS 113

RESULT 9

G83283

precorin-2 methyltransferase Cobi PA2904 [imported] - Pseudomonas aeruginosa (strain PA

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: G83283

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: AB2950; MUID:20437337

A:Accession: G83283

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-250 <STO>

A:Cross-references: GB:AE004716; GB:AE004091; NID:g9948986; PIDN:AAG06292.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: cobI; PA2904

Query Match 84.8%; Score 28; DB 2; Length 250;  
Best Local Similarity 71.4%; Pred. No. 32;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQSIS 7

|||||:

Db 154 YRQSLS 160

RESULT 10

AB1813

hypothetical protein all0050 [imported] - *Anabaena* sp. (strain PCC 7120)

C:Species: *Anabaena* sp.

A:Note: *Anabaena* sp. (strain PCC 7120) is a synonym of *Nostoc* sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 11-Jan-2002

C:Accession: AB1813

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriqu

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing *Cyanobacterium*

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AB1813

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-345 <KUR>

A:Cross-references: GB:BA000019; PIDN:BAW77574.1; PID:g17135028; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all0050

Query Match 84.8%; Score 28; DB 2; Length 345;  
Best Local Similarity 85.7%; Pred. No. 45;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YRSQSIS 7

|||||:

Db 178 YRSNSIS 184

RESULT 11

HLBECM

membrane glycoprotein H301 alpha chain precursor - human cytomegalovirus

C:Alternate names: class I histocompatibility antigen homolog; UL18 glycoprotein prec

C:Species: human cytomegalovirus, human herpesvirus 5

A:Note: host *Homo sapiens* (man)

C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 22-Jun-1999

C:Accession: S09781; S00661

R:Chee, W.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T

M.; Barrell, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovi

A:Reference number: S09749; MUID:90269039

A:Accession: S09781

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-368 <CHE>

A:Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35417.1; PID:g59623

A:Experimental source: strain Ad169

A:Note: possible protein-coding frames are given

A:Note: the DNA sequence was submitted to EMBL, December 1989

R:Beck, S.; Barrell, B.G.

Nature 331, 269-272, 1988

A:Title: Human cytomegalovirus encodes a glycoprotein homologous to MHC class-I anti

A:Reference number: S00661; MUID:88094735

A:Accession: S00661

A:Molecule type: DNA

A:Residues: 1-368 <BEC>

A:Cross-references: EMBL:Y00293; NID:g59456; PIDN:CAA68399.1; PID:g59457

C:Genetics:

A:Gene: H301

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology



C;Keywords: glycoprotein; heterodimer; transmembrane protein  
F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-368/Product: membrane glycoprotein H301 alpha chain #status predicted <MAT>  
F;321-349/Domain: transmembrane #status predicted <TMW>

F;56-66-95,123,127,150,167,177,193,240,282,291/Binding site: carbohydrate (Asn) (covalent)

Query Match 84.8%; Score 28; DB 1; Length 368;

Best Local Similarity 83.3%; Pred. No. 48;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 6

Db 110 YRSQSV 115

RESULT 12

T08025 DNA-directed RNA polymerase beta' chain homolog - Chlamydomonas reinhardtii chloroplast

N;Alternate names: rpoC2 protein

C;Species: chloroplast Chlamydomonas reinhardtii

C;Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 08-Oct-1999

C;Accession: T08025

R;Nucleo, S.: Purton, S.

submitted to the EMBL Data Library, May 1996

A;Description: The chloroplast rpoC2 gene of Chlamydomonas reinhardtii.

A;Reference number: Z16298

A;Accession: T08025

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2028 <NUO>

A;Cross-references: EMBL:U57326; NID:g1354831; PIDN:AB01997.1; PID:g1354832

C;Genetics:

A;Gene: rpoC2

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 84.8%; Score 28; DB 2; Length 2028;

Best Local Similarity 71.4%; Pred. No. 2.8e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSI 7

Db 1734 YRSQSV 1740

RESULT 13

PH1080

Ig light chain V region (clone 165.60) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Jun-1996

C;Accession: PH1080

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell

A;Reference number: PH0971; MUID:92381444

A;Accession: PH1080

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-69 <TIL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

Query Match 81.8%; Score 27; DB 2; Length 69;

Best Local Similarity 85.7%; Pred. No. 15;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSI 7

Db 21 YRSQSI 27

RESULT 14

G33730

Ig kappa chain V region (23.32) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 21-Jan-2000

C;Accession: G33730

R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989

A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u

A;Reference number: A33730; MUID:89367325

A;Accession: G33730

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-96 <LAW>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 27; DB 2; Length 96;

Best Local Similarity 85.7%; Pred. No. 21;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSI 7

Db 50 YRSQSI 56

RESULT 15

B43413

Ig kappa chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000

C;Accession: B43413

R;Tomiyama, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.;

J. Biol. Chem. 267, 18085-18092, 1992

A;Title: A molecular model of RGD ligands. Antibody D gene segments that direct speci

A;Reference number: A43413; MUID:92388177

A;Accession: B43413

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-104 <TOM>

A;Note: sequence extracted from NCBI backbone (NCBIP:112818)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;13-87/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 27; DB 2; Length 104;

Best Local Similarity 85.7%; Pred. No. 23;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSI 7

Db 47 YRSQSI 53

Search completed: August 19, 2002, 06:36:09  
Job time: 1290 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:59:12 ; Search time 51.81 Seconds  
(without alignments)  
5.231 Million cell updates/sec

Title: US-09-339-922A-112  
Perfect score: 33  
Sequence: 1 YRSQIS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	84.8	191	GRPE_LISIN	Q92bn7 listeria in
2	28	84.8	191	GRPE_LISMO	Q9s5a5 listeria mo
3	28	84.8	368	VGH3_HCMVA	P08560 human cytom
4	27	81.8	208	TRAI_RHISN	P55394 rhizobium s
5	27	81.8	286	LPXC_CHLMU	Q9pjK9 chlamydia m
6	27	81.8	438	Y232_METJA	Q60289 methanococc
7	27	81.8	499	AINX_HUMAN	Q16352 homo sapien
8	27	81.8	504	AINX_MOUSE	P46650 mus musculu
9	27	81.8	505	AINX_RAT	P23565 rattus norv
10	27	81.8	581	INVL_SCHPO	O59852 schizosacch
11	27	81.8	3097	CADN_DROME	Q15943 drosophila
12	26	78.8	186	GRPE_BACSU	P15874 bacillus su
13	26	78.8	494	VE2_HPV12	P36782 human papil
14	26	78.8	542	CBPY_CANAL	P30574 candida alb
15	26	78.8	1080	NRK1_YEAST	P38692 saccharomyc
16	26	78.8	1093	SWR4_YEAST	P25302 saccharomyc
17	26	78.8	1807	TSC2_HUMAN	P49815 homo sapien
18	26	78.8	1809	TSC2_RAT	P49816 rattus norv
19	26	78.8	1814	TSC2_MOUSE	O61037 mus musculu
20	25	75.8	216	YH21_HAEIN	O05086 haemophilus
21	25	75.8	222	Y364_MYCLE	O69601 mycobacteri
22	25	75.8	264	MOVPE_CGMVW	P19522 cucumber gr
23	25	75.8	330	GRP2_HUMAN	Q75791 h grb2-rela
24	25	75.8	351	COLF_ARATH	Q9fh88 arabidopsis
25	25	75.8	410	ODBA_PSEPU	P09060 pseudomonas
26	25	75.8	418	HEM1_SALTY	P13581 salmonella
27	25	75.8	451	YPVE_METTF	P29578 methanobact
28	25	75.8	507	SEPA_STAEF	P43148 staphylococ
29	25	75.8	525	ACUB_NEUCR	P15937 neurospora
30	25	75.8	532	P72_MYCWM	P55801 mycoplasma
31	25	75.8	555	VGLF_PILHC	P12605 human parai
32	25	75.8	951	SPF8_HUMAN	Q12872 homo sapien
33	25	75.8	1081	ULS2_HSVEB	P28962 equine herp

34	25	75.8	1089	1	Y553_HUMAN	Q9ukj3 homo sapien
35	25	75.8	1283	1	PEX1_HUMAN	O43933 homo sapien
36	25	75.8	1316	1	RPOC_MYCLE	P30761 mycobacteri
37	25	75.8	1316	1	RPOC_MYCTU	P47769 mycobacteri
38	25	75.8	1369	1	YAZG_SCHPO	Q09706 schizosacch
39	25	75.8	1403	1	YGN1_YEAST	P53127 saccharomyc
40	25	75.8	1447	1	DCC_HUMAN	P43146 homo sapien
41	25	75.8	1481	1	RPOD_ODOSI	P49468 odontella s
42	25	75.8	1572	1	BAI2_HUMAN	O60241 homo sapien
43	25	75.8	1629	1	ATS9_HUMAN	Q9p2n4 homo sapien
44	25	75.8	2517	1	NCR2_HUMAN	Q9Y618 h nuclear r
45	24	72.7	38	1	TRPD_SERMA	P12321 serratia ma

ALIGNMENTS

RESULT 1						
GRPE_LISIN						
ID GRPE_LISIN	STANDARD;	PRT;	191 AA.			
AC	Q92BN7;					
DT	01-MAR-2002 (Rel. 41, Created)					
DT	01-MAR-2002 (Rel. 41, Last sequence update)					
DT	01-MAR-2002 (Rel. 41, Last annotation update)					
DE	GRPE protein (HSP-70 cofactor).					
GN	GRPE OR LIN1511.					
OS	Listeria innocua.					
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;					
OC	Bacillus/Staphylococcus group; Listeria.					
OX	NCBI_TaxID=1642;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=CLIP 11262 / Serovar 6a;					
RX	MEDLINE=21537279; PubMed=11679669;					
RA	Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,					
RA	Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,					
RA	Charbit A., Chetouani F., Couve E., de Daruvar A., Deloux P.,					
RA	Dammann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,					
RA	Entian K.-D., Fathi H., Garcia-del Portillo F., Garrido P.,					
RA	Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,					
RA	Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapkat G.,					
RA	Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,					
RA	Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,					
RA	Rommel B., Rose M., Schlueter T., Simoes N., Tierrez A.,					
RA	Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;					
RL	Science 294:849-852(2001).					
CC	-!- FUNCTION: STIMULATES, JOINTLY WITH DNAJ, THE ATPASE ACTIVITY OF					
CC	DNAK HELPS TO RELEASE ADP FROM DNAK THUS ALLOWING DNAK TO RECYCLE					
CC	MORE EFFICIENTLY (BY SIMILARITY).					
CC	-!- SIMILARITY: BELONGS TO THE GRPE FAMILY.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
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CC	or send an email to license@isb-sib.ch).					
CC	-----					
DR	EMBL; AL596168; CAC96742.1; -.					
DR	Listlist; LIN01511; -.					
DR	PROSITE; PS01071; GRPE; 1.					
KW	Chaperone; Heat shock; Complete proteome.					
SQ	SEQUENCE 191 AA; 21952 MW; 853F11392E126981 CRC64;					

Query Match 84.8%; Score 28; DB 1; Length 191;  
Best Local Similarity 71.4%; Pred. No. 8;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YRSQIS 7  
|||||:

Db 84 YRSQSLA 90

## RESULT 2

GRPE\_LISMO  
ID GRPE\_LISMO STANDARD; PRT; 191 AA.  
AC Q955A5;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE GRPE protein (HSP-70 cofactor).  
GN GRPE OR LM01474.  
OS Listeria monocytogenes.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.  
OX NCBI\_TaxID=1639;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=10403S;  
RX MEDLINE=20163771; PubMed=10701836;  
RA Hanawa T., Kai M., Kamiya S., Yamamoto T.;  
RT "Cloning, sequencing, and transcriptional analysis of the dnaK heat  
RT shock operon of Listeria monocytogenes.";  
RL Cell Stress Chaperones 5:21-29(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=EGD-e / Serovar 1/2a;  
RX MEDLINE=21537279; PubMed=11679669;  
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,  
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,  
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,  
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,  
RA Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,  
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
RA Jones L.-M., Kaerst U., Krest J., Kuhn M., Kunz F., Kurapkat G.,  
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,  
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,  
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,  
RA Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.;  
RT "Comparative genomics of Listeria species.";  
RL Science 294:849-852(2001).  
CC -!- FUNCTION: STIMULATES, JOINTLY WITH DNAJ, THE ATPASE ACTIVITY OF  
CC DNAK. HELPS TO RELEASE ADP FROM DNAK THUS ALLOWING DNAK TO RECYCLE  
CC MORE EFFICIENTLY (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE GRPE FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AB023064; BAB2788.1; -;  
CC EMBL; AL591979; CAC9552.1; -;  
CC ListList; LM01474; -;  
CC HSSP; P09372; 1DKG.  
CC InterPro: IPR000740; GRPE.  
CC Pfam: PF01025; GRPE; 1.  
CC PRINTS; PR00773; GRPEPROTEIN.  
CC PROSITE; PS01071; GRPE; 1.  
KW Chaperone; Heat shock; Complete proteome.  
SQ SEQUENCE 191 AA; 21918 MW; D93CFA0EB86CF0C8 CRC64;

Query Match 84.8%; Score 28; DB 1; Length 191;  
Best Local Similarity 71.4%; Pred. No. 8;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSLA 7

|||||

Db 84 YRSQSLA 90

## RESULT 3

VGH3\_HCMVA  
ID VGH3\_HCMVA STANDARD; PRT; 368 AA.  
AC P08560;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Glycoprotein H301 precursor.  
GN H301 OR ULI18.  
OS Human cytomegalovirus (strain AD169).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Cytomegalovirus.  
OX NCBI\_TaxID=10360;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88094735; PubMed=2827039;  
RA Beck S., Barrell B.G.;  
RT "Human cytomegalovirus encodes a glycoprotein homologous to MHC  
RL class-I antigens.";  
RL Nature 331:269-272(1988).  
RN [2]  
RP COMPLETE GENOME.  
RX MEDLINE=90269039; PubMed=2161319;  
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,  
RA Horsnell T., Hutchison C.A. III, Kourzaries T., Martignetti J.A.,  
RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;  
RT "Analysis of the protein-coding content of the sequence of human  
RT cytomegalovirus strain AD169.";  
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).  
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY RESPONSIBLE FOR BINDING TO  
CC BETA-2-MICROGLOBULIN.  
CC -!- SIMILARITY: STRONG TO THE MHC CLASS-I ANTIGENS.  
CC -----  
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CC -----  
CC EMBL; X17403; CAA35417.1; -;  
CC EMBL; Y00293; CAA68399.1; -;  
CC PIR; S09781; HLBECH.  
CC PIR; S00661; S00661.  
CC InterPro: IPR003006; Ig\_MHC.  
CC InterPro: IPR003600; Ig\_Like.  
CC InterPro: IPR001039; MHC\_I.  
CC ProDom; PD000050; MHC\_I; 1.  
CC SMART; SM00410; IG\_Like; 1.  
CC PROSITE; PS00290; IG\_MHC; 1.  
KW Glycoprotein; MHC I; Transmembrane; Signal.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 368 GLYCOPROTEIN H301.  
FT DOMAIN 19 114 ALPHA-1 LIKE.  
FT DOMAIN 115 208 ALPHA-2 LIKE.  
FT DOMAIN 209 303 ALPHA-3 LIKE.  
FT TRANSMEM 321 342 POTENTIAL.  
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 66 66 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 123 123 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 193 193 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 240 240 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 282 282 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 291 291 N-LINKED (GLCNAC. .) (POTENTIAL).

```

SQ SEQUENCE 368 AA; 41735 MW; 48AE7EFB4DDCCBAE CRC64;

Query Match 84.8%; Score 28; DB 1; Length 368;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 6
| | | | |
Db 110 YRSQSV 115

RESULT 4
ID TRAI_RHSN STANDARD; PRT; 208 AA.
AC P55394;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable autoinducer synthesis protein trai.
GN TRAI OR Y4CL.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret A.; basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF OHHL (N-(3-OXOOCTANOYL)-L-
CC HOMOSERINE LACTONE), AN AUTOINDUCER MOLECULE WHICH BINDS TO TRAI
CC AND THUS ACTS IN THE CONTROL OF CONJUGAL TRANSFER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AUTOINDUCER SYNTHETASE FAMILY.
CC STRONGEST, TO A.TUMEFACIENS TI PLASMID TRAI.
CC -----
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CC -----
CC EMBL: AE000068; AAB92427.1; -
CC InterPro: IPR001690; Autoinducers_synth.
CC Pfam: PF00765; Autoind_synth; 1.
CC PRINTS: PR01549; AUTOINDCRSYN.
CC ProDom: PD002752; Autoinducers_synth; 1.
CC PROSITE: PS00949; AUTOINDUCERS_SYNTH; 1.
KW Quorum sensing; Autoinducer synthesis; Conjugation; Plasmid.
SQ SEQUENCE 208 AA; 22826 MW; DF2F053C7A20D28E CRC64;

Query Match 81.8%; Score 27; DB 1; Length 208;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSI 7
| | | | |
Db 196 YRSQIS 202

RESULT 5
ID LPXC_CHLMU STANDARD; PRT; 286 AA.
AC Q9PKN9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)

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DE DE UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase
DE (EC 3.5.1.-) (UDP-3-O-acyl-GlcNAc deacetylase).
DN LPXC OR TC0820.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Winn M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF LIPID A, A
CC PHOSPHORYLATED GLYCOLIPID THAT ANCHORS THE LIPOPOLYSACCHARIDE TO
CC THE OUTER MEMBRANE OF THE CELL (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: UDP-3-O-(3-HYDROXYTETRADECANOYL)-N-
CC ACETYLGLUCOSAMINE + H(2)O = UDP-3-O-(3-HYDROXYTETRADECANOYL)-
CC GLUCOSAMINE + ACETATE.
CC -1- PATHWAY: LIPID A BIOSYNTHESIS; SECOND STEP.
CC -1- SIMILARITY: BELONGS TO THE LPXC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE002347; AAF39622.1; ALT_INIT.
CC TIGR: TC0820; -
CC Hydrolase; Lipid A biosynthesis; Lipid synthesis; Complete proteome.
SQ SEQUENCE 286 AA; 31149 MW; ICF81B900979D2A1 CRC64;

Query Match 81.8%; Score 27; DB 1; Length 286;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSI 7
| | | | |
Db 171 YRSQVIS 177

RESULT 6
Y232_METJA
ID Y232_METJA STANDARD; PRT; 438 AA.
AC Q60289;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJEC132.
GN MJEC132.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

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RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 RL Jannaschii.";  
 CC Science 273:1058-1073(1996).  
 CC -----  
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 CC -----  
 CC EMBL; L77118; AAC37101.1; -;  
 DR TIGR; MJEC32; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 438 AA; 50925 MW; DC8FB11505F5DEE3 CRC64;  
 Query Match 81.8%; Score 27; DB 1; Length 438;  
 Best Local Similarity 85.7%; Pred. No. 36;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YRSQSIS 7  
 Db |||||  
 359 YRSTSI 365  
 RESULT 7  
 AINX\_HUMAN  
 ID AINX\_HUMAN STANDARD; PRT; 499 AA.  
 AC Q16352; Q9BRC5;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Alpha-interneixin (Alpha-Inx) (66 kDa neurofilament protein)  
 DE (Neurofilament-66) (NF-66).  
 GN INA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal brain;  
 RX MEDLINE=95287809; PubMed=7769995;  
 RA Chan S.-O., Chiu F.-C.;  
 RT "Cloning and developmental expression of human 66 kd neurofilament  
 RT protein.";  
 RL Brain Res. Mol. Brain Res. 29:177-184(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: CLASS-IV NEURONAL INTERMEDIATE FILAMENT THAT IS ABLE TO  
 CC SELF-ASSEMBLE. IT IS INVOLVED IN THE MORPHOGENESIS OF NEURONS. IT  
 CC MAY FORM AN INDEPENDENT STRUCTURAL NETWORK WITHOUT THE INVOLVEMENT  
 CC OF OTHER NEUROFILAMENTS OR IT MAY COOPERATE WITH NF-L TO FORM THE  
 CC FILAMENTOUS BACKBONE TO WHICH NF-M AND NF-H ATTACH TO FORM THE  
 CC CROSS-BRIDGES.  
 CC -!- TISSUE SPECIFICITY: FOUND PREDOMINANTLY IN ADULT CNS.  
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN BRAIN AS EARLY AS THE 16TH OF  
 CC GESTATION, AND INCREASED RAPIDLY AND REACHED A STEADY STATE LEVEL  
 CC BY THE 18TH WEEK OF GESTATION.  
 CC -!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; S78296; AAB34482.1; -;  
 DR EMBL; BC006359; AAH06359.1; -;  
 DR MIM; 605338; -;  
 DR InterPro: IPR001664; IF.  
 DR Pfam: PF00038; filament; 1.  
 DR PROSITE; PS00226; IF; 1.  
 KW Intermediate filament; Coiled coil; Neurone.  
 FT DOMAIN 1 87  
 FT DOMAIN 88 408  
 FT DOMAIN 409 499  
 FT DOMAIN 499 499  
 FT DOMAIN 88 129  
 FT DOMAIN 130 142  
 FT DOMAIN 143 238  
 FT DOMAIN 239 262  
 FT DOMAIN 263 408  
 FT DOMAIN 449 454  
 FT CONFLICT 37 41  
 FT CONFLICT 67 67  
 FT CONFLICT 92 92  
 FT CONFLICT 128 132  
 FT CONFLICT 141 141  
 FT CONFLICT 147 152  
 FT CONFLICT 191 198  
 FT CONFLICT 244 244  
 FT CONFLICT 263 263  
 FT CONFLICT 301 301  
 FT CONFLICT 310 311  
 FT CONFLICT 318 318  
 SQ SEQUENCE 499 AA; 55390 MW; 4C972764E9E68D3E CRC64;  
 Query Match 81.8%; Score 27; DB 1; Length 499;  
 Best Local Similarity 71.4%; Pred. No. 41;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YRSQSIS 7  
 Db |||||  
 38 FRSQSL 44  
 RESULT 8  
 AINX\_MOUSE  
 ID AINX\_MOUSE STANDARD; PRT; 504 AA.  
 AC P46660; O61958;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Alpha-interneixin (Alpha-Inx) (66 kDa neurofilament protein)  
 DE (Neurofilament-66) (NF-66).  
 GN INA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B6/CBA; TISSUE=Spleen;  
 RX MEDLINE=95047490; PubMed=7959004;  
 RA Chien C.-L., Liem R.K.H.;  
 RT "Characterization of the mouse gene encoding the neuronal  
 RT intermediate filament protein alpha-interneixin.";  
 RL Gene 149:289-292(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=96322433; PubMed=8734438;  
 RA Chan S.-O., Chiu F.-C.;  
 RT "The 66-kDa neurofilament protein (NF-66): sequence analysis and  
 RT evolution.";  
 RL Neurochem. Res. 21:449-455(1996).



OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98204792; PubMed=9535817;  
 RA Tanaka N., Ohuchi N., Mukai Y., Ozaka Y., Ohtani Y., Tabuchi M.,  
 RA Bhyuiyan M.S., Fukui H., Harashima S., Takegawa K.;  
 RT "Isolation and characterization of an invertase and its repressor  
 genes from Schizosaccharomyces pombe.";  
 RL Biochem. Biophys. Res. Commun. 245:246-253(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RA Lyne M., Rajandream M.A., Barrell B.G., Voicckaert G.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 88-581 FROM N.A.  
 RC STRAIN=PR745;  
 RX MEDLINE=98162722; PubMed=9501991;  
 RA Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;  
 RT "Identification of open reading frames in Schizosaccharomyces pombe  
 cDNAs.";  
 RL DNA Res. 4:363-369(1997).  
 RN [4]  
 RP CARBOHYDRATES.  
 RX MEDLINE=90253381; PubMed=2187435;  
 RA Moreno S., Sanchez Y., Rodriguez L.;  
 RT "Purification and characterization of the invertase from  
 Schizosaccharomyces pombe.";  
 RL Biochem. J. 267:697-702(1990).  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-  
 fructofuranoside residues in beta-D-fructofuranosides.  
 CC -!- PTM: THE CARBOHYDRATE CONTENT OF THIS PROTEIN IS 67%. THIS IS  
 COMPOSED OF EQUIPOLAR AMOUNTS OF MANNOSE AND GALACTOSE. THERE IS  
 ALSO A SMALL AMOUNT OF GLUCOSAMINE PRESENT.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.  
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 CC -----  
 DR EMBL; AB011433; BAA25684.1; -;  
 DR EMBL; AL049644; CAB41057.1; -;  
 DR EMBL; D89242; BAA13903.1; -;  
 DR InterPro; IPR001362; Glyco\_hydro\_32.  
 DR Pfam; PF00251; Glyco\_hydro\_32; 1.  
 DR PROSITE; PS00609; GLYCOSYL\_HYDROL\_F32; 1.  
 KW Hydrolase; Glycosidase; Glycoprotein; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 581  
 FT ACT\_SITE 97 97  
 FT BY\_SIMILARITY  
 FT CARBOHYD 37 37 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 399 399 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 409 409 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 425 425 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 452 452 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 519 519 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CARBOHYD 519 519 N-LINKED (GLCNAC. .) (PROBABLE).

FT CARBOHYD 569 569 N-LINKED (GLCNAC. .) (PROBABLE).  
 FT CONFLICT 186 189 MISSING (IN REF. 3).  
 FT CONFLICT 190 190 H -> Y (IN REF. 3).  
 FT CONFLICT 195 195 A -> P (IN REF. 3).  
 FT CONFLICT 198 198 Q -> L (IN REF. 3).  
 FT CONFLICT 205 205 D -> N (IN REF. 3).  
 FT CONFLICT 243 243 I -> M (IN REF. 3).  
 FT CONFLICT 246 246 M -> L (IN REF. 3).  
 FT CONFLICT 256 256 S -> P (IN REF. 3).  
 SQ SEQUENCE 581 AA; 64407 MW; 70206A6CD1F27EC4 CRC64;  
 Query Match 81.8%; Score 27; DB 1; Length 581;  
 Best Local Similarity 85.7%; Pred. No. 49;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YRSQIS 7  
 DB 474 YRLQIS 480  
 RESULT 11  
 CADN\_DROME  
 ID CADN\_DROME STANDARD; PRG; 3097 AA.  
 AC O15943; Q9VJB7;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Neural-cadherin precursor (Cadherin-N protein) (DN-cadherin).  
 GN CADN OR CG7100.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephyroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Head, and Embryo;  
 RX MEDLINE=97388431; PubMed=9247265;  
 RA Iwai Y., Utsui T., Hirano S., Steward R., Takeichi M., Uemura T.;  
 RT "Axon patterning requires DN-cadherin, a novel neuronal adhesion  
 receptor, in the Drosophila embryonic CNS.";  
 RL Neuron 19:77-89(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
RN [3]  
RP INTERACTION WITH ARM  
RX MEDLINE=98298928; PubMed=9635189;  
RA Loureiro J., Peiffer M.;  
RT "Roles of Armadillo, a *Drosophila* catenin, during central nervous  
RT system development.";  
RL Curr. Biol. 8:622-632(1998).  
CC -1- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.  
CC THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC  
CC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE  
CC SORTING OF HETEROGENEOUS CELL TYPES. MAY ASSOCIATE WITH ARM NEURAL  
CC ISOFORM AND PARTICIPATE IN THE TRANSMISSION OF DEVELOPMENTAL  
CC INFORMATION.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, THE PROTEIN FIRST APPEARS IN  
CC THE MESODERM AT STAGE 9 AND IS PRESENT IN THE MYOBLASTS AND MUSCLE  
CC FIBERS BY STAGE 12 AND STAGE 14, RESPECTIVELY. AT STAGE 12 THE  
CC PROTEIN IS ALSO LOCATED IN THE AXONS OF THE ENTIRE CNS, BUT NOT IN  
CC THE GLIAL CELLS. IN THIRD INSTAR LARVAE PROTEIN IS EXPRESSED IN  
CC THE CNS NEUROFIL, PHOTORECEPTOR AXONS AND PRECURSORS OF ADULT  
CC MUSCLES.  
CC -1- SIMILARITY: CONTAINS 16 CADHERIN DOMAINS.  
CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.  
CC -----  
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CC -----  
CC EMBL; AB002397; BAA22151.1; -;  
CC EMBL; AE003656; AAF53635.1; -;  
CC HSP; P00740; I1YA  
CC Flybase; FBgn0015609; CadN.  
CC InterPro; IPR002126; Cadherin.  
CC InterPro; IPR000233; Cadherin\_C\_term.  
CC InterPro; IPR000561; EGF-like.  
CC InterPro; IPR000742; EGF\_2  
CC InterPro; IPR001881; EGF\_Ca.  
CC InterPro; IPR001791; Laminin\_G.  
CC Pfam; PF00028; cadherin; 14.  
CC Pfam; PF01049; Cadherin\_C\_term; 1.  
CC Pfam; PF00008; EGF; 3.  
CC Pfam; PF00054; laminin\_G; 2.  
CC PRINTS; PR00205; CADHERIN.  
CC SMART; SM00112; CA; 16.  
CC SMART; SM00179; EGF\_CA; 1.  
CC SMART; SM00001; EGF\_like; 3.  
CC SMART; SM00282; LamG; 2.  
CC PROSITE; PS00232; CADHERIN\_1; 9.  
CC PROSITE; PS00468; CADHERIN\_2; 16.  
CC PROSITE; PS00022; EGF\_1; 3.  
CC PROSITE; PS01186; EGF\_2; 3.  
CC PROSITE; PS00025; LAM\_G\_DOMAIN; 2.  
CC Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;  
KW Signal; EGF-like domain.  
FT SIGNAL 1 36 POTENTIAL.  
FT PROPEP 37 7

FT CHAIN ? 3097 ?  
FT DOMAIN 1454 ?  
FT TRANSMEM 1455  
FT DOMAIN 1476 3097  
FT DOMAIN 181 305  
FT DOMAIN 430 543  
FT DOMAIN 554 651  
FT DOMAIN 660 756  
FT DOMAIN 766 858  
FT DOMAIN 867 968  
FT DOMAIN 978 1078  
FT DOMAIN 1087 1183  
FT DOMAIN 1193 1299  
FT DOMAIN 1307 1414  
FT DOMAIN 1423 1514  
FT DOMAIN 1523 1630  
FT DOMAIN 1639 1742  
FT DOMAIN 1749 1861  
FT DOMAIN 1870 1966  
FT DOMAIN 1974 2085  
FT DOMAIN 2346 2377  
FT DOMAIN 2379 2585  
FT DOMAIN 2592 2627  
FT DOMAIN 2631 2822  
FT DOMAIN 2869 2902  
FT DISULFID 2346 2357  
FT DISULFID 2351 2366  
FT DISULFID 2368 2377  
FT DISULFID 2592 2607  
FT DISULFID 2601 2616  
FT DISULFID 2618 2627  
FT DISULFID 2869 2880  
FT DISULFID 2874 2891  
FT DISULFID 2893 2902  
FT CARBOHYD 97 97  
FT CARBOHYD 150 150  
FT CARBOHYD 325 325  
FT CARBOHYD 426 426  
FT CARBOHYD 930 930  
FT CARBOHYD 1266 1266  
FT VARIANT 1425 1425  
FT CONFLICT 1342 1342  
FT CONFLICT 2786 2786  
FT CONFLICT 3097 AA; 347201 MW; 082242F28D9B5CC3 CRC64;  
SQ SEQUENCE 3097 AA; 347201 MW; 082242F28D9B5CC3 CRC64;  
Query Match 81.8%; Score 27; DB 1; Length 3097;  
Best Local Similarity 71.4%; Pred. No. 3.1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YRSOSIS 7  
DB 2204 YRTQSMS 2210  
||:|:|:  
RESULT 12  
GRPE\_BACSU STANDARD; PRT; 186 AA.  
ID GRPE\_BACSU  
AC P15874;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE GrpE protein (HSP-70 cofactor).  
GN GRPE.  
OS *Bacillus subtilis*.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC *Bacillus/Staphylococcus* group; *Bacillus*.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168 / MB11;  
RX MEDLINE=90206795; PubMed=2108432;



RA Wetzstein M., Schumann W.;  
RT "Nucleotide sequence of a Bacillus subtilis gene homologous to the  
RL grpE gene of E. coli located immediately upstream of the dnaK gene."; Nucleic Acids Res. 18:1289-1289(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168 / MB11;  
RX MEDLINE=92250426; PubMed=1339421;  
RA Wetzstein M., Voelker U., Dedio J., Loebau S., Zuber U.,  
RA Schiesswohl M., Herget C., Hecker M., Schumann W.;  
RT "Cloning, sequencing, and molecular analysis of the dnaK locus from  
RL Bacillus subtilis."; J. Bacteriol. 174:3300-3310(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168 / JH642;  
RA Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,  
RA Sato T., Takeuchi M.;  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 1-10.  
RC STRAIN=ISS8;  
RX MEDLINE=94282319; PubMed=8012595;  
RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,  
RA Schmid R., Mach H., Hecker M.;  
RT "Analysis of the induction of general stress proteins of Bacillus  
RL subtilis."; Microbiology 140:741-752(1994).  
CC -!- FUNCTION: STIMULATES, JOINTLY WITH DNAJ, THE ATPASE ACTIVITY OF  
CC DNAK. HELPS TO RELEASE ADP FROM DNAK THUS ALLOWING DNAK TO RECYCLE  
CC MORE EFFICIENTLY (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE GRPE FAMILY.  
CC -----  
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CC -----  
CC EMBL; X51477; CAA35841.1; -;  
DR EMBL; M84964; AAA22527.1; -;  
DR EMBL; D84432; BAA12463.1; -;  
DR EMBL; Z99117; CAB14490.1; -;  
DR PIR; S08418; S08418.  
DR PIR; S27504; S27504.  
DR HSP; P09372; 1DKG.  
DR Subtilist; BG10663; grpe.  
DR InterPro; IPR000740; GrpE.  
DR Pfam; PF01025; GrpE; 1.  
DR PRINTS; PR00773; GRPEPROTEIN.  
DR PROSITE; PS01071; GRPE; 1.  
KW Chaperone; Heat shock; Complete proteome.  
FT INIT\_MET 0 0  
FT VARIANT 1 1 S -> H (IN STRAIN IS58).  
FT VARIANT 4 4 K -> T (IN STRAIN IS58).  
SQ SEQUENCE 186 AA; 21552 MW; A06216843F3C5FD7 CRC64;

Query Match 78.8%; Score 26; DB 1; Length 186;  
Best Local Similarity 83.3%; Pred. No. 25;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSI 6  
Db 79 YRSQNI 84

RESULT 13  
VE2\_HPV12  
ID VE2\_HPV12 STANDARD; PRT; 494 AA.  
AC P36782;

DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Regulatory protein E2.  
GN E2.  
OS Human papillomavirus type 12.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10604;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94265501; PubMed=8205838;  
RA Delius H., Hofmann B.;  
RT "Primer-directed sequencing of human papillomavirus types."; Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
CC -!- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.  
CC IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACNNNNNGT-3') PRESENT  
CC IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER  
CC ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION  
CC WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS  
CC BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION  
CC INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA  
CC REPLICATION.  
CC -!- SUBUNIT: BINDS DNA AS A DIMER.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; X74466; CAA52499.1; -;  
DR PIR; S36541; S36541.  
DR HSP; P17383; 1DHM.  
DR InterPro; IPR001866; E2\_N.  
DR InterPro; IPR000427; Early2\_C.  
DR Pfam; PF00511; E2\_C; 1.  
DR Pfam; PF00508; E2\_N; 1.  
DR ProDom; PD000672; Early2\_C; 1.  
DR ProDom; PD000678; E2\_N; 1.  
KW Early protein; Transcription regulation; Activator; DNA-binding;  
KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.  
SQ SEQUENCE 494 AA; 56039 MW; 3C20AAF3560C10EE CRC64;

Query Match 78.8%; Score 26; DB 1; Length 494;  
Best Local Similarity 85.7%; Pred. No. 72;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSI 7  
Db 266 YRSQNS 272

RESULT 14  
CBPY\_CANAL STANDARD; PRT; 542 AA.  
AC P30574;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Carboxypeptidase Y precursor (EC 3.4.16.5) (Carboxypeptidase YSCY).  
GN CPY1.  
OS Candida albicans (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5476;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93051356; PubMed=1427093;

RA Mukhtar M., Logan D.A., Kaufer N.F.;  
 RT "the carboxypeptidase Y-encoding gene from Candida albicans and its  
 RL transcription during yeast-to-hyphae conversion.";  
 CC Gene 121:173-177(1992).  
 CC -1- FUNCTION: INVOLVED IN DEGRADATION OF SMALL PEPTIDES.  
 CC -1- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a  
 CC broad specificity.  
 CC -1- SUBCELLULAR LOCATION: LYSOSOME-LIKE VACUOLES.  
 CC -1- INDUCTION: TRANSIENTLY DOWN-REGULATED DURING THE EARLY EVENTS OF  
 CC YEAST TO HYPAE CONVERSION.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10; ALSO KNOWN AS THE  
 CC SERINE CARBOXYPEPTIDASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; M95182; AAA34326.2; -;  
 DR PIR; JC1380; JC1380.  
 DR HSSP; P00729; 1CPY.  
 DR MEROPS; S10.001; -;  
 DR InterPro; IPR000379; Est\_lip\_thioest\_actsite.  
 DR Pfam; PF00450; serine\_carbpept; 1.  
 DR PRINTS; PR00724; CRBOXPTASEC.  
 DR PROSITE; PS00131; CARBOXYPEPT\_SER\_SER; 1.  
 DR PROSITE; PS00560; CARBOXYPEPT\_SER\_HIS; 1.  
 DR Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.  
 FT SIGNAL 1 21  
 FT PROPEP 1 21  
 FT CHAIN 128 542  
 FT ACT\_SITE 269 269  
 FT ACT\_SITE 461 461  
 FT ACT\_SITE 518 518  
 FT BINDING 464 464  
 FT BINDING 519 519  
 FT DISULFID 182 421  
 FT DISULFID 316 330  
 FT DISULFID 340 363  
 FT DISULFID 347 356  
 FT DISULFID 385 391  
 FT CARBOHYD 213 213  
 FT CARBOHYD 291 291  
 FT SEQUENCE 542 AA; 61044 MW; 7FA6B9F82F9D44AF CRC64;

Query Match 78.8%; Score 26; DB 1; Length 542;  
 Best Local Similarity 71.4%; Pred. No. 80;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
 | | | | |  
 Db 229 YSSQSVS 235

RESULT 15  
 NRK1\_YEAST  
 ID NRK1\_YEAST STANDARD; PRT; 1080 AA.  
 AC P38692;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Serine/threonine-protein kinase NRK1 (EC 2.7.1.37) (N-rich kinase 1).  
 GN NRK1 OR KIC1 OR YHR102W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=DC-5;  
 RA Fukami Y.;  
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RX MEDLINE=94378003; PubMed=8091229;  
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,  
 RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,  
 RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,  
 RA Latrelle P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,  
 RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,  
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,  
 RA Vaudin M.;  
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome  
 RT VIII";  
 RL Science 265:2077-2082(1994).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -----  
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 CC -----  
 CC EMBL; D29980; BAA06250.1; -;  
 DR EMBL; U00059; AAB88860.1; -;  
 DR PIR; S48944; S48944.  
 DR HSSP; P24941; 1AQ1.  
 DR SGD; S0001144; KIC1.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding.  
 FT DOMAIN 23 276  
 FT NP\_BIND 29 37  
 FT BINDING 52 52  
 FT ACT\_SITE 144 144  
 FT SEQUENCE 1080 AA; 117061 MW; 9989EAF315EE0B94 CRC64;

Query Match 78.8%; Score 26; DB 1; Length 1080;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RSQIS 7  
 | | | | |  
 Db 900 RSQIS 905

Search completed: August 19, 2002, 06:59:14  
 Job time: 1379 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:58:19 ; Search time 140.4 Seconds  
(without alignments)  
8.625 Million cell updates/sec

Title: US-09-339-922A-112

Perfect score: 33

Sequence: 1 YRSQIS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	30	90.9	362	2	Q9S162	Q9S162 erysipelo
2	30	90.9	362	2	Q9S161	Q9S161 erysipelo
3	30	90.9	362	2	Q9S160	Q9S160 erysipelo
4	30	90.9	606	2	O66380	O66380 erysipelo
5	30	90.9	626	2	Q9WXB8	Q9WXB8 erysipelo
6	30	90.9	629	5	Q9NA88	Q9NA88 caenorhabdi
7	29	87.9	406	16	Q97L94	Q97L94 clostridium
8	29	87.9	409	5	Q23046	Q23046 caenorhabdi
9	29	87.9	944	16	Q98PL2	Q98PL2 mycoplasma
10	28	84.8	191	16	Q92BN7	Q92BN7 listeria in
11	28	84.8	206	10	Q9M282	Q9M282 arabidopsis
12	28	84.8	250	16	Q9HZU3	Q9HZU3 pseudomonas
13	28	84.8	316	5	Q9V3Y4	Q9V3Y4 drosophila
14	28	84.8	414	13	Q90299	Q90299 xenopus lae
15	28	84.8	501	11	Q9D0C4	Q9D0C4 mus musculus
16	28	84.8	2028	8	Q32064	Q32064 chlamydomon

17	27	81.8	223	10	Q9LIJ9	Q9LIJ9 arabidopsis
18	27	81.8	367	5	Q22069	Q22069 caenorhabdi
19	27	81.8	384	2	O68157	O68157 treponema h
20	27	81.8	386	2	O30572	O30572 treponema h
21	27	81.8	389	2	O68156	O68156 treponema h
22	27	81.8	423	16	Q97H59	Q97H59 clostridium
23	27	81.8	493	10	O64609	O64609 arabidopsis
24	27	81.8	499	4	Q9BRC5	Q9BRC5 homo sapien
25	27	81.8	521	5	Q9VZX9	Q9VZX9 drosophila
26	27	81.8	543	10	Q9AY90	Q9AY90 oryza sativ
27	27	81.8	608	10	Q9FG35	Q9FG35 arabidopsis
28	27	81.8	644	16	Q92KK6	Q92KK6 rhizobium m
29	27	81.8	806	16	O34433	O34433 bacillus su
30	27	81.8	946	10	Q9LP09	Q9LP09 arabidopsis
31	27	81.8	1206	10	Q9FW39	Q9FW39 oryza sativ
32	27	81.8	1743	5	Q966V0	Q966V0 drosophila
33	27	81.8	2785	11	Q99MV3	Q99MV3 mus musculus
34	26	78.8	190	2	Q9LAE8	Q9LAE8 rhizobium l
35	26	78.8	199	4	Q96131	Q96131 homo sapien
36	26	78.8	207	10	Q9FNH5	Q9FNH5 arabidopsis
37	26	78.8	209	10	Q9SRN0	Q9SRN0 arabidopsis
38	26	78.8	217	4	Q9ULQ9	Q9ULQ9 homo sapien
39	26	78.8	237	11	Q9R0G3	Q9R0G3 marmota mar
40	26	78.8	255	16	O25494	O25494 helicobacte
41	26	78.8	255	16	Q9ZL30	Q9ZL30 helicobacte
42	26	78.8	290	10	Q943V4	Q943V4 oryza sativ
43	26	78.8	306	12	Q9DHW1	Q9DHW1 watermelon
44	26	78.8	306	12	Q9QIK9	Q9QIK9 watermelon
45	26	78.8	306	12	Q9QLR2	Q9QLR2 watermelon

#### ALIGNMENTS

RESULT 1

Q9S162 ID Q9S162 PRELIMINARY; PRT; 362 AA.  
AC Q9S162;  
DT 01-MAY-2000 (TREMREL. 13, Created)  
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE SPAA PROTEIN (FRAGMENT).  
GN SPAA.  
OS Erysipelothrix rhusiopathiae.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
OC Erysipelothrix group; Erysipelothrix.  
OX NCBI\_TaxID=1648;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KOGANEI;  
RX MEDLINE=99386823; PubMed=10456877;  
RA Imada Y., Goji N., Ishikawa H., Kishima M., Sekizaki T.;  
RT "Truncated surface protective antigen (SpA) of Erysipelothrix  
RT rhusiopathiae serotype la elicits protection against challenge with  
RT serotypes la and 2b in pigs."  
RL Infect. Immun. 67:4376-4382(1999).  
DR EMBL; AB024082; BAA84453.1; -  
FT NON\_TER 1  
FT NON\_TER 362  
SQ SEQUENCE 362 AA; 42371 MW; 9F406ADA1619C5B7 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 362;  
Best Local Similarity 85.7%; Pred. No. 33;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7

Db 298 YRAQIS 304

RESULT 2

Q9S161

ID Q9S161 PRELIMINARY; PRT; 362 AA.  
 AC Q9S161;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE SPAA PROTEIN (FRAGMENT).  
 GN SPAA.  
 OS Erysipelothrix rhusiopathiae.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 OC Erysipelothrix group; Erysipelothrix.  
 OX NCBI\_TaxID=1648;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC19414;  
 RX MEDLINE=99386823; PubMed=10456877;  
 RA Imada Y., Goji N., Ishikawa H., Kishima M., Sekizaki T.;  
 RT "Truncated surface protective antigen (SpaA) of Erysipelothrix  
 rhusiopathiae serotype Ia elicits protection against challenge with  
 serotypes Ia and 2b in pigs."  
 RL Infect. Immun. 67:4376-4382(1999).  
 DR EMBL; AB024083; BAA84454.1; -.  
 FT NON\_TER 1 362  
 FT NON\_TER 362 362  
 SQ SEQUENCE 362 AA; 42259 MW; F355931EEA3C206A CRC64;

Query Match 90.9%; Score 30; DB 2; Length 362;  
 Best Local Similarity 85.7%; Pred. No. 33;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
 ||:||||  
 DB 298 YRAQIS 304

RESULT 3  
 Q9S160  
 ID Q9S160 PRELIMINARY; PRT; 362 AA.  
 AC Q9S160;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE SPAA PROTEIN (FRAGMENT).  
 GN SPAA.  
 OS Erysipelothrix rhusiopathiae.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 OC Erysipelothrix group; Erysipelothrix.  
 OX NCBI\_TaxID=1648;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SE-9;  
 RX MEDLINE=99386823; PubMed=10456877;  
 RA Imada Y., Goji N., Ishikawa H., Kishima M., Sekizaki T.;  
 RT "Truncated surface protective antigen (SpaA) of Erysipelothrix  
 rhusiopathiae serotype Ia elicits protection against challenge with  
 serotypes Ia and 2b in pigs."  
 RL Infect. Immun. 67:4376-4382(1999).  
 DR EMBL; AB024084; BAA84455.1; -.  
 FT NON\_TER 1 362  
 FT NON\_TER 362 362  
 SQ SEQUENCE 362 AA; 42394 MW; 67C3ADA494FEE753 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 362;  
 Best Local Similarity 85.7%; Pred. No. 33;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
 ||:||||  
 DB 298 YRAQIS 304

RESULT 4

06380  
 ID O6380 PRELIMINARY; PRT; 606 AA.  
 AC O6380;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE SPAA.  
 GN SPAA.  
 OS Erysipelothrix rhusiopathiae.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 OC Erysipelothrix group; Erysipelothrix.  
 OX NCBI\_TaxID=1648;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TAMA-96;  
 RA Makino S., Yamamoto K., Murakami S., Shirahata T., Uemura K.,  
 RA Sawada T., Wakamoto H., Morita Y.;  
 RT "Properties of Repeat Domain Found in A Novel Protective Antigen,  
 SpAa, of Erysipelothrix rhusiopathiae."  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB012763; BAA28613.1; -.  
 DR InterPro; IPR002479; CW\_binding.  
 DR InterPro; IPR001899; Gram\_pos\_anchor.  
 DR Pfam; PF01473; CW\_binding\_1; 7.  
 DR PROSITE; PS00343; GRAM\_POS\_ANCHORING; UNKNOWN\_1.  
 SQ SEQUENCE 606 AA; 69960 MW; 4E9D0A9EB536D0B3 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 606;  
 Best Local Similarity 85.7%; Pred. No. 57;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
 ||:||||  
 DB 381 YRAQIS 387

RESULT 5  
 Q9WXB8  
 ID Q9WXB8 PRELIMINARY; PRT; 626 AA.  
 AC Q9WXB8;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE PROTECTIVE ANTIGEN SPAA.1.  
 GN SPAA.  
 OS Erysipelothrix rhusiopathiae.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 OC Erysipelothrix group; Erysipelothrix.  
 OX NCBI\_TaxID=1648;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FUJISAWA;  
 RX MEDLINE=99184982; PubMed=10084998;  
 RA Shimoji Y., Mori Y., Fischetti V.A.;  
 RT "Immunological characterization of a protective antigen of  
 Erysipelothrix rhusiopathiae: Identification of the region responsible  
 for protective immunity."  
 RL Infect. Immun. 67:1646-1651(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FUJISAWA;  
 RX MEDLINE=99386823; PubMed=10456877;  
 RA Imada Y., Goji N., Ishikawa H., Kishima M., Sekizaki T.;  
 RT "Truncated surface protective antigen (SpaA) of Erysipelothrix  
 rhusiopathiae serotype Ia elicits protection against challenge with  
 serotypes Ia and 2b in pigs."  
 RL Infect. Immun. 67:4376-4382(1999).  
 DR EMBL; AB017447; BAA76540.1; -.  
 DR EMBL; AB019124; BAA84452.1; -.  
 DR InterPro; IPR002479; CW\_binding.  
 DR InterPro; IPR001899; Gram\_pos\_anchor.  
 DR Pfam; PF01473; CW\_binding\_1; 8.

DR PROSITE: PS00343; GRAM\_POS\_ANCHORING; UNKNOWN\_1.  
SQ SEQUENCE 626 AA; 72276 MW; FB50BDB8CC1D9066 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 626;  
Best Local Similarity 85.7%; Pred. No. 59;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7  
||:|||||  
Db 381 YRAQIS 387

## RESULT 6

Q9NA88 PRELIMINARY; PRT; 629 AA.  
AC Q9NA88;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE Y57A10A.4 PROTEIN.  
GN Y57A10A.4.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Smye R.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; AL117195; CAB55009.1; -.  
SQ SEQUENCE 629 AA; 71450 MW; 7A068C2062048121 CRC64;

Query Match 90.9%; Score 30; DB 5; Length 629;  
Best Local Similarity 85.7%; Pred. No. 60;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7  
||:|||||  
Db 466 YRQIS 472

## RESULT 7

Q97L94 PRELIMINARY; PRT; 406 AA.  
AC Q97L94;  
DT 01-OCT-2001 (TREMBLrel. 18, Created)  
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE PREDICTED MEMBRANE PROTEIN.  
GN CAC0668.  
OS Clostridium acetobutylicum.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1488;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
RX MEDLINE=21359325; PubMed=11466286;  
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
RA Gibson R.L., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,  
RA Tatunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
RA Bennett G.N., Koonin E.V., Smith D.R.;  
RT "Genome sequence and comparative analysis of the solvent-producing  
bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).  
DR EMBL; AE007582; AAK78645.1; -.  
KW Complete proteome.  
SQ SEQUENCE 406 AA; 47239 MW; D020D1BAEFB707C8 CRC64;

Query Match 87.9%; Score 29; DB 16; Length 406;  
Best Local Similarity 85.7%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YRSQIS 7  
|||||||  
Db 193 YRSQIS 199

## RESULT 8

Q23046 PRELIMINARY; PRT; 409 AA.  
AC Q23046;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE T25F10.3 PROTEIN.  
GN T25F10.3.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,  
RA Smaildon N., Smith A., Sonnhammer E., Staden R., Sulston J.,  
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
elegans.";  
RL Nature 368:32-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RX Pauley, A., Gattung S.;  
RT "The sequence of C. elegans cosmid T25F10.";  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA Waterston R.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U64856; AAB04985.1; -.  
DR InterPro; IPR000561; EGF-like.  
DR SMART; SM00181; EGF; 2.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_3.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
SQ SEQUENCE 409 AA; 45218 MW; F4F0BC370F09BED7 CRC64;

Query Match 87.9%; Score 29; DB 5; Length 409;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQSI 6  
|||||||  
Db 133 YRSQSI 138

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RESULT 9
Q98PL2
ID Q98PL2 PRELIMINARY; PRT; 944 AA.
AC Q98PL2;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE EXCNUCLEASE ABC SUBUNIT A.
GN MYPU_7100.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Molllicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chabaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis."
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL445565; CAC13883.1; -.
DR MypuList; MYPU_7100; -.
DR InterPro; IPR003593; AAA.
DR Pfam; PF00005; ABC_tran; 2.
DR SMART; SM00382; AAA; 2.
KW Complete proteome.
SQ SEQUENCE 944 AA; 105297 MW; 5EE52AC2B5F9E507 CRC64;

Query Match 87.9%; Score 29; DB 16; Length 944;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7
DB 784 YRSKIS 790

RESULT 10
Q92BN7
ID Q92BN7 PRELIMINARY; PRT; 191 AA.
AC Q92BN7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HEAT SHOCK PROTEIN GRPE.
GN GRPE OR LIN1511.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / SEROVAR 6A;
RX PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species."
RL Science 294:849-852(2001).
DR EMBL; AL596168; CAC96742.1; -.

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DR ListList; LIN01511; -.
KW Complete proteome.
SQ SEQUENCE 191 AA; 21952 MW; 853F11392E126981 CRC64;

Query Match 84.8%; Score 28; DB 16; Length 191;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7
DB 84 YRSQSLA 90

RESULT 11
Q9M282
ID Q9M282 PRELIMINARY; PRT; 206 AA.
AC Q9M282;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 22.7 KDA PROTEIN.
GN T22K7_110.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RW EMBL; AL138641; CAB86921.1; -.
KW Hypothetical protein.
SQ SEQUENCE 206 AA; 22651 MW; B5651312ABDE614B CRC64;

Query Match 84.8%; Score 28; DB 10; Length 206;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7
DB 107 YRSKVS 113

RESULT 12
Q9HZU3
ID Q9HZU3 PRELIMINARY; PRT; 250 AA.
AC Q9HZU3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE PRECORRN-2 METHYLTRANSFERASE COBI.
GN COBI OR PA2904.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

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RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an  
 opportunistic pathogen.";  
 RL Nature 406:959-964 (2000).  
 DR EMBL; AF004716; AAG06292.1; -;  
 DR InterPro: IPR000878; Cortin\_porph\_mthyltrnf.  
 DR Pfam: PF00590; TP\_methylase\_1  
 DR PROSITE; PS00215; MITOCH\_CARRIER; UNKNOWN\_1.  
 KW Transferase; Methyltransferase; Complete proteome.  
 SQ SEQUENCE 250 AA; 27274 MW; 3AC4B437C77F477E CRC64;

Query Match 84.8%; Score 28; DB 16; Length 250;  
 Best Local Similarity 71.4%; Pred. No. 70;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7  
 :||:|  
 Db 154 YRNQSL 160

## RESULT 13

Q9V3V4  
 ID Q9V3V4 PRELIMINARY; PRT; 316 AA.  
 AC Q9V3V4;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE MTCH PROTEIN (LD43650P).  
 GN MTCH OR CG6851.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; *Drosophila*.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yeaman M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brattier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,  
 RA Fosler C., Gabrielista C.C., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobbart B., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Jang J.S., Hahn Y., Park C., Chung J.H.;  
 RT "Identification of an evolutionary conserved mitochondrial carrier  
 family from various organisms.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Y, CN BW SP;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003467; AAF47342.1; -;  
 DR EMBL; AF176011; AAD52649.1; -;  
 DR EMBL; AY051973; AAK93397.1; -;  
 DR FlyBase; FBgn0027786; Mtch.  
 DR InterPro: IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_carr; 1.  
 SQ SEQUENCE 316 AA; 35011 MW; 4545D305A57A9991 CRC64;

Query Match 84.8%; Score 28; DB 5; Length 316;  
 Best Local Similarity 85.7%; Pred. No. 89;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7  
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 Db 292 WRSQIS 298

## RESULT 14

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 ID Q90Z99 PRELIMINARY; PRT; 414 AA.  
 AC Q90Z99;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PDCD9.  
 GN PDCD9.  
 OS *Xenopus laevis* (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; *Xenopus*.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carrodegas J.A., Bogenhagen D.F.;  
 RT "The *Xenopus* homolog of chicken pro-apoptotic protein p52 and human  
 PDCD9 is a mitochondrial protein.";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF317657; AAK56969.1; -;  
 SQ SEQUENCE 414 AA; 47229 MW; 45BB1A4C9EDFCA86 CRC64;

Query Match 84.8%; Score 28; DB 13; Length 414;  
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YRSQIS 7  
 :|||:|  
 Db 150 WRSQIS 156

RESULT 15  
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AC O9DOC4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 2610027018RIK PROTEIN (RIKEN CDNA 2610027018 GENE).
GN 2610027018RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK011576; BAB2710.1; -.
DR EMBL; BC012521; AAH12521.1; -.
DR MGD; MGI:1923607; 2610027018Rik.
DR InterPro; IPR003402; Met_10.
DR Pfam; PF02475; Met_10; 1.
SQ SEQUENCE 501 AA; 56794 MW; 55816182B08766C0 CRC64;

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Query Match      84.8%; Score 28; DB 11; Length 501;
Best Local Similarity 71.4%; Pred.No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YRSQSIS 7
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Db 467 YRNQSL 473

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Job time: 1412 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 06:39:14 ; Search time 180.34 Seconds  
(without alignments)  
4.311 Million cell updates/sec

Title: US-09-339-922A-112

Perfect score: 33

Sequence: 1 YRSQSIS 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	7	22 AAB61404	Enhanced 6H6LH lig
2	33	100.0	11	19 AAW76012	LM609 grafted anti
3	33	100.0	11	22 AAB61370	LM609 VL CDR2 pept
4	33	100.0	107	19 AAW76006	LM609 grafted anti
5	33	100.0	107	19 AAW76002	Vitaxin antibody 1
6	33	100.0	107	19 AAW76004	LM609 antibody lig
7	33	100.0	107	22 AAG63588	A light chain vari
8	33	100.0	107	22 AAG63590	A light chain vari
9	33	100.0	107	22 AAB61360	Vitaxin light chai
10	33	100.0	107	22 AAB61362	Antibody LM609 lig
11	33	100.0	107	22 AAB61364	Light chain variab

12	30	90.9	402	21	AAB14800	Erysipelothrix rhu
13	30	90.9	606	20	AAV43219	E. rhusiopathiae s
14	30	90.9	626	21	AAV95782	Erysipelothrix rhu
15	28	84.8	316	22	ABB62737	Drosophila melanog
16	28	84.8	368	10	AAV90471	Human cytomegalovi
17	27	81.8	11	19	AAW76032	LM609 grafted anti
18	27	81.8	11	22	AAB61390	Mutant VL CDR2 pep
19	27	81.8	44	22	AAW87562	Human immune/haema
20	27	81.8	64	22	AAW95618	Human reproductive
21	27	81.8	88	21	AAV56653	Partial peptide fr
22	27	81.8	102	22	AAW77337	Human bone marrow
23	27	81.8	105	20	AAW87456	JK gene product.
24	27	81.8	105	20	AAW87458	Humanised anti-alp
25	27	81.8	107	13	AAW25729	Humanised VL regio
26	27	81.8	107	14	AAW38601	HYH light chain.
27	27	81.8	107	19	AAW58482	Murine HyH antibod
28	27	81.8	107	20	AAW84098	Humanised anti-alp
29	27	81.8	107	21	AAV71238	Humanised antibody
30	27	81.8	107	21	AAV71240	Humanised antibody
31	27	81.8	107	21	AAV71472	Mouse monoclonal a
32	27	81.8	107	22	AAW69677	Murine CMV5 antio
33	27	81.8	107	22	AAW69678	Humanised CMV5 ant
34	27	81.8	107	22	AAW69690	Human Wol antibody
35	27	81.8	108	17	AAW04333	Light chain of mon
36	27	81.8	108	20	AAW84094	Murine vitronectin
37	27	81.8	109	15	AAW52033	Light chain variab
38	27	81.8	109	20	AAW06380	Murine monoclonal
39	27	81.8	112	20	AAW84100	Vitronectin alpha-
40	27	81.8	114	22	AAW98665	Murine protein #2.
41	27	81.8	127	15	AAW54093	Sequence of mouse
42	27	81.8	127	22	AAW69687	Murine CMV5 antio
43	27	81.8	128	21	AAV56718	Amino acid sequenc
44	27	81.8	259	21	AAW09775	TMV 30K movement p
45	27	81.8	274	21	AAG24104	Arabidopsis thalia

#### ALIGNMENTS

RESULT 1  
AAB61404  
ID AAB61404 standard; peptide; 7 AA.  
XX AAB61404;  
AC  
DT 03-APR-2001 (first entry)  
XX  
DE Enhanced 6H6LH light chain CDR2.  
XX  
KW LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis.  
XX  
OS Unidentified.  
XX  
PN WO200078815-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 23-JUN-2000; 2000WO-US17454.  
XX  
PR 24-JUN-1999; 99US-0339922.  
XX  
(MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;  
XX WPI; 2001-050110/06.  
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
XX osteoporosis -

PS Claim 4; Page 46; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta<sub>3</sub> integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 33; DB 22; Length 7;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQIS 7

Db 1 yrsqsis 7

RESULT 2

AAW76012

ID AAW76012 standard; Protein; 11 AA.

XX AC AAW76012;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-L region CDR2 protein fragment #1.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

XX KW macular degeneration; osteoporosis; primer; V-L region; CDR;

XX KW complementarity determining region.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX DR WPI; 1998-437472/37.

XX DR N-PSDB; AAV49849.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta<sub>3</sub>

XX PT integrin - and related grafted antibodies based on murine monoclonal

XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose

XX PT angiogenesis or restenosis

XX PS Disclosure; Page 40; 129pp; English.

XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody

XX CC LM609 heavy and light chain variable region. LM609 and the antibody

XX CC vitaxin bind selectively to integrin alphavbeta<sub>3</sub> and can be used to

XX CC inhibit binding of alphavbeta<sub>3</sub> to a ligand and thus block

XX CC integrin-mediated signal transduction. This is useful in the treatment,

XX CC prevention and diagnosis of alphavbeta<sub>3</sub>-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 33; DB 19; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQIS 7

Db 5 yrsqsis 11

RESULT 3

AA61370

ID AAB61370 standard; peptide; 11 AA.

XX AC AAB61370;

XX DT 03-APR-2001 (first entry)

XX DE LM609 VL CDR2 peptide.

XX KW LM609; grafted antibody; alphavbeta<sub>3</sub> integrin; angiogenesis;

XX KW inflammatory; cancer; retina; restenosis; osteoporosis.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX DR WPI; 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity

XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

XX PT osteoporosis -

XX PS Disclosure; Page 39; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies

XX CC exhibiting selective binding affinity to alphavbeta<sub>3</sub> integrin or

XX CC their functional fragments. The antibodies or their functional

XX CC fragments can be used in the diagnosis and treatment of

XX CC alphavbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory

XX CC diseases (such as psoriasis and chronic articular rheumatism),

XX CC disorders associated with inappropriate or inopportune invasion of

XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and

XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

XX CC diseases (such as macular degeneration), restenosis and

XX CC osteoporosis.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 33; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 YRSQSTS 7
Db 5 YRSQSTS 11

RESULT 4
AAW76006
ID AAW76006 standard; Protein; 107 AA.
XX AC
XX AC AAW76006;
XX DT 02-NOV-1998 (first entry)
XX DE LM609 grafted antibody light chain variable region protein fragment.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis.
XX OS Mus sp.
XX PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX N-PSDB; AAV49843.
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX Claim 19; Fig 7; 129pp; English.
XX This sequence represents a LM609 grafted antibody variable light chain
XX region. LM609 and the antibody vitaxin bind selectively to integrin
XX alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
XX and thus block integrin-mediated signal transduction. This is useful in
XX the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX etc.). The antibodies contain non-murine framework regions so are
XX suitable for use in humans. Enhanced types of LM609 have affinity more
XX than 90 times greater than that of parent the parent antibody.
XX Sequence 107 AA;

Query Match 100.0%; Score 33; DB 19; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQSTS 7
Db 50 YRSQSTS 56

RESULT 6
AAW76004
ID AAW76004 standard; Protein; 107 AA.
XX AC
XX AC AAW76004;
XX DT 02-NOV-1998 (first entry)
XX XX

RESULT 5
AAW76002
ID AAW76002 standard; Protein; 107 AA.
XX AC
XX AC AAW76002;
XX DT 02-NOV-1998 (first entry)
XX DE Vitaxin antibody light chain variable region protein fragment.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis.
XX OS Mus sp.
XX PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX WPI; 1998-437472/37.
XX N-PSDB; AAV49821.
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX integrin - and related grafted antibodies based on murine monoclonal
XX LM609, also related nucleic acid, used to treat, prevent or diagnose
XX angiogenesis or restenosis
XX Claim 1; Fig 1b; 129pp; English.
XX This sequence represents the vitaxin antibody variable light chain
XX region. Vitaxin and the antibody LM609 bind selectively to integrin
XX alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
XX ligand and thus block integrin-mediated signal transduction. This is
XX useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
XX disease, specifically angiogenesis and restenosis (but also e.g.
XX (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
XX cancer, psoriasis, rheumatoid arthritis, macular degeneration,
XX osteoporosis etc.). The antibodies contain non-murine framework regions
XX so are suitable for use in humans. Enhanced types of LM609 have affinity
XX more than 90 times greater than that of parent the parent antibody.
XX Sequence 107 AA;

Query Match 100.0%; Score 33; DB 19; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQSTS 7
Db 50 YRSQSTS 56

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XX PN US2001011125-A1.  
 XX PD 02-AUG-2001.  
 XX PF 30-JAN-1997; 97US-0790540.  
 XX PR 30-JAN-1997; 97US-0790540.  
 XX PA (HUSE/) HUSE W D.  
 XX PI Huse WD;  
 XX DR WPI: 2001-496171/54.  
 XX DR N-PSDB; AAH74626.  
 XX  
 PT New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer -  
 XX  
 PS Disclosure; Fig 2B; 25pp; English.  
 XX  
 CC The present sequence represents the light chain variable region of the  
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically  
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.  
 CC The specification describes a LM609 grafted antibody which has the  
 CC complementarity determining regions (CDRs) substituted into a non-murine  
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain  
 CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis  
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
 CC disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 CC an alphavbeta3-mediated disease.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 100.0%; Score 33; DB 22; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YRSQSIS 7  
 Db 50 yrsqsis 56  
 RESULT 9  
 AAB61360  
 ID AAB61360 standard; protein; 107 AA.  
 XX AC AAB61360;  
 XX DT 03-APR-2001 (first entry)  
 XX DE Vitaxin light chain variable region protein.  
 XX KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 XX KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 XX OS Unidentified.  
 XX PN WO200078815-A1.  
 XX PD 28-DEC-2000.  
 XX PF 23-JUN-2000; 2000WO-US17454.  
 XX PR 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.  
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX PI Huse WD, Wu H;  
 XX DR WPI: 2001-050110/06.  
 XX  
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Fig 1; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 100.0%; Score 33; DB 22; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YRSQSIS 7  
 Db 50 yrsqsis 56  
 RESULT 10  
 AAB61362  
 ID AAB61362 standard; protein; 107 AA.  
 XX AC AAB61362;  
 XX DT 03-APR-2001 (first entry)  
 XX DE Antibody LM609 light chain variable region protein.  
 XX KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 XX KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 XX OS Unidentified.  
 XX PN WO200078815-A1.  
 XX PD 28-DEC-2000.  
 XX PF 23-JUN-2000; 2000WO-US17454.  
 XX PR 24-JUN-1999; 99US-0339922.  
 XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX PI Huse WD, Wu H;  
 XX DR WPI: 2001-050110/06.  
 XX  
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -

XX Disclosure; Fig 2; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 100.0%; Score 33; DB 22; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YRSQSIS 7  
 Db 50 yrsqsis 56  
 |||||  
 RESULT 11  
 AAB61364  
 ID AAB61364 standard; protein; 107 AA.  
 XX  
 AC AAB61364;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Light chain variable region of LM609.  
 XX  
 KW LM609; grafted antibody; alphaVbeta<sub>3</sub> integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 DR WPI; 2001-050110/06.  
 XX  
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta<sub>3</sub> integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Fig 7; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 100.0%; Score 33; DB 22; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YRSQSIS 7  
 Db 50 yrsqsis 56  
 |||||  
 RESULT 12  
 AAB14800  
 ID AAB14800 standard; Protein; 402 AA.  
 XX  
 AC AAB14800;  
 XX  
 DT 11-DEC-2000 (first entry)  
 XX  
 DE Erysielothrix rhusiopathiae protective polypeptide antigen fragment.  
 XX  
 KW Protective polypeptide antigen; PPA; Fujisawa strain; swine erysipelas;  
 KW recombinant production; Immunogenic; subunit vaccine;  
 KW transmucous administration.  
 OS  
 XX Erysielothrix rhusiopathiae.  
 XX  
 PN JP3072345-B1.  
 XX  
 PD 31-JUL-2000.  
 XX  
 PF 31-MAR-1999; 99JP-0094004.  
 XX  
 PR 31-MAR-1999; 99JP-0094004.  
 XX  
 PA (NORQ) NORINSANSO KACHIKU EISEI SHIKENJOCHO.  
 PA (HGET) HIGETA SHOYU KK.  
 PA (FUJI-) FUJITA GAKUEN.  
 XX  
 DR WPI; 2000-551432/51.  
 DR N-PSDB; AAA72313, AAA72317, AAA72318.  
 XX  
 PT Novel recombinant protective polypeptide antigen useful as a vaccine  
 PT for protecting livestock against Erysielothrix rhusiopathiae  
 PT infection -  
 XX  
 PS Claim 1; Page 14-15; 23pp; Japanese.  
 XX  
 CC This sequence represents a 46.5 kD immunogenic fragment of the  
 CC protective polypeptide antigen (PPA) of the bacterium Erysielothrix  
 CC rhusiopathiae. This bacterium infects livestock, particularly pigs  
 CC (swine erysipelas), and is also able to cause disease in humans. The  
 CC recombinantly produced PPA fragment may be used as a subunit vaccine for  
 CC stimulating an immune response in animals against Erysielothrix  
 CC rhusiopathiae. As the vaccine can be produced recombinantly, it can be  
 CC produced on a large scale. The vaccine is suitable for transmucous  
 CC administration.  
 XX  
 SQ Sequence 402 AA;  
 Query Match 90.9%; Score 30; DB 21; Length 402;  
 Best Local Similarity 85.7%; Pred. No. 80;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YRSQSIS 7  
 Db 352 yrsqsis 358  
 |||||

```

RESULT 13
AA43219
ID AAY43219 standard; Protein; 606 AA.
XX
AC
AAY43219;
DT
13-JAN-2000 (first entry)
XX
DE E. rhusiopathiae surface layer protein sequence.
XX
KW Surface layer protein; Immunological detection; antigen; pig erysipelas;
genetic detection.
XX
OS Erysipelothrix rhusiopathiae.
XX
PN JP11262391-A.
XX
PD 28-SEP-1999.
XX
PF 17-MAR-1998; 98JP-0067258.
XX
PR 17-MAR-1998; 98JP-0067258.
XX
PA (CHCC ) CHISSO CORP.
XX
WPI; 1999-603802/52.
DR N-PSDB; AA231581.
XX
PT New surface layer protein of Erysipelothrix rhusiopathiae - useful for
detecting antibody against E. rhusiopathiae
XX
PS Claim 1; Page 8-11; 14pp; Japanese.
XX
CC This sequence is the Erysipelothrix rhusiopathiae surface layer
protein of the invention. The surface layer protein can be used as an
antigen in a method for the immunological detection of E. rhusiopathiae.
CC It can also be used as an antigen: (1) in a method for the immunological
detection of an antibody against E. rhusiopathiae; and (2) in a method
for the immunological detection of pig erysipelas. The DNA sequence can
be used in a method for the genetic detection of E. rhusiopathiae or pig
erysipelas. The methods are simple and rapid.
XX
SQ Sequence 606 AA;

Query Match 90.9%; Score 30; DB 20; Length 606;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRSQSIS 7
Db 381 yraqsis 387

RESULT 14
AA43219
ID AAY95782 standard; Protein; 626 AA.
XX
AC
AAY95782;
DT
07-NOV-2000 (first entry)
XX
DE Erysipelothrix rhusiopathiae erysipelas protective antigen.
XX
KW Erysipelothrix protective antigen; Epa; SpaA.1; vaccine; infection;
immuno-protective epitope.
XX
OS Erysipelothrix rhusiopathiae.
XX
FH Location/Qualifiers
FT Peptide 1..29
FT Protein 30..626

```

```

FT Region /label= Mature_protein
FT 50...55 /note= "LPXTGX motif"
FT Peptide 448..467
FT /label= Repeat_R1
FT Peptide 468..487
FT /label= Repeat_R2
FT Peptide 488..507
FT /label= Repeat_R3
FT Peptide 508..527
FT /label= Repeat_R4
FT Peptide 528..547
FT /label= Repeat_R5
FT Peptide 548..567
FT /label= Repeat_R6
FT Peptide 568..587
FT /label= Repeat_R7
FT Peptide 588..607
FT /label= Repeat_R8
FT Peptide 608..626
FT /label= Repeat_R9
XX WO200047744-A1.
PN
XX 17-AUG-2000.
PD
XX
XX 10-FEB-2000; 2000WO-US03789.
XX
XX 10-FEB-1999; 99US-0119389.
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Fischetti VA, Shimoji Y;
PI
XX WPI; 2000-524541/47.
XX N-PSDB; AAA50205.
DR
XX
XX Vaccines for protecting turkeys and pigs against Erysipelothrix
PT rhusiopathiae infections comprising a polypeptide sequence from the
PT N-terminal region of an erysipelas protective antigen -
XX
PS Claim 2; Fig 2; 61pp; English.
XX
CC The present sequence is that of the erysipelas protective antigen
CC (Epa or SpaA.1) of Erysipelothrix rhusiopathiae strain Fujisawa, as
CC deduced from an isolate Epa gene (see AAA50205). E. rhusiopathiae is
CC the causative agent of erysipelas in animals and erysipeloid in
CC humans. Epa shows structural and sequence similarities to
CC pneumococcal surface protein A (PspA) and other choline binding
CC proteins of Streptococcus pneumoniae. Its C-terminal region
CC consists of a series of conserved 20-amino acid repeats (R1-R9).
CC The N-terminal portion of the Epa protein, especially a polypeptide
CC comprising residues 12-195 of the present sequence, was identified
CC as a vaccine antigen, protecting mice and pigs from a lethal
CC challenge with E. rhusiopathiae. Vaccines containing immunogenic
CC polypeptides of E. rhusiopathiae, where the immunogenic polypeptide
CC comprises an immuno-protective epitope from the N-terminal region
CC of Epa, especially residues 30-447, 30-195 or 30-100 of the present
CC sequence, are claimed. A claimed method for protecting an animal,
CC especially a turkey or pig, from infection by E. rhusiopathiae
CC involves administering the vaccine, or an expression vector
CC comprising a nucleic acid encoding the N-terminal portion or
CC full-length Epa. A claimed method for detecting the presence of
CC protective antibodies to E. rhusiopathiae involves detecting
CC binding of antibodies in a biological sample with a polypeptide
CC comprising an immunoprotective epitope of Epa.
XX
SQ Sequence 626 AA;

```

```

Query Match 90.9%; Score 30; DB 21; Length 626;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 YRSQSIG 7  
 II:IIII  
 Db 381 yrsqsis 387

## RESULT 15

ABB62737  
 ID ABB62737 standard; Protein; 316 AA.

XX AC ABB62737;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 15003.

XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.

XX PR 23-MAR-2000; 2000US-191637P.

XX PR 11-JUL-2000; 2000US-0614150.

XX PA (PEKE ) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR N-PSDB; ABL06840.

PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

PS Disclosure; SEQ ID NO 15003; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 316 AA;

Query Match 84.8%; Score 28; DB 22; Length 316;

Best Local Similarity 85.7%; Pred. No. 1.8e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRSQSIG 7

II:IIII

Db 292 wrsqsis 298

Search completed: August 19, 2002, 06:39:15

Job time: 1476 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 06:34:43 ; Search time 61.75 Seconds  
(without alignments)  
2.769 Million cell updates/sec

Title: US-09-339-922A-112

Perfect score: 33

Sequence: 1 YRSQIS 7

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents,AA:\*

- 1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/prodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	81.8	33	4	US-08-525-539A-12
2	27	81.8	96	2	US-08-737-560A-9
3	27	81.8	100	1	US-08-436-463-19
4	27	81.8	103	1	US-08-436-463-21
5	27	81.8	107	1	US-07-634-278-62
6	27	81.8	107	1	US-07-634-278-63
7	27	81.8	107	1	US-07-634-278-87
8	27	81.8	107	1	US-08-477-728-62
9	27	81.8	107	1	US-08-477-728-63
10	27	81.8	107	1	US-08-477-728-87
11	27	81.8	107	1	US-08-474-040-62
12	27	81.8	107	1	US-08-474-040-63
13	27	81.8	107	1	US-08-474-040-87
14	27	81.8	107	1	US-08-487-200-62
15	27	81.8	107	1	US-08-487-200-63
16	27	81.8	107	1	US-08-487-200-87
17	27	81.8	107	1	US-08-436-463-20
18	27	81.8	107	1	US-08-107-669D-1
19	27	81.8	107	1	US-08-472-788A-1
20	27	81.8	107	2	US-08-477-531B-1
21	27	81.8	107	2	US-08-082-842A-1
22	27	81.8	107	4	US-08-484-537-62
23	27	81.8	107	4	US-08-484-537-63
24	27	81.8	107	4	US-08-484-537-87
25	27	81.8	108	2	US-08-737-560A-11
26	27	81.8	109	1	US-07-942-245-4
27	27	81.8	127	1	US-07-634-278-83

28	27	81.8	127	1	US-08-477-728-83	Sequence 83, Appl
29	27	81.8	127	1	US-08-474-040-83	Sequence 83, Appl
30	27	81.8	127	1	US-08-487-200-83	Sequence 83, Appl
31	27	81.8	127	1	US-08-436-463-4	Sequence 4, Appl
32	27	81.8	127	1	US-08-436-463-18	Sequence 18, Appl
33	27	81.8	127	4	US-08-484-537-83	Sequence 83, Appl
34	27	81.8	581	4	US-09-331-581-2	Sequence 2, Appl
35	26	78.8	909	4	US-09-425-383-2	Sequence 2, Appl
36	26	78.8	1784	4	US-09-040-738-2	Sequence 2, Appl
37	26	78.8	1784	4	US-08-652-426A-2	Sequence 2, Appl
38	25	75.8	325	4	US-09-041-886-33	Sequence 33, Appl
39	25	75.8	330	2	US-08-815-176-1	Sequence 1, Appl
40	25	75.8	409	1	US-08-403-545-2	Sequence 2, Appl
41	25	75.8	409	4	US-08-404-381-2	Sequence 2, Appl
42	25	75.8	1004	4	US-08-916-352-2	Sequence 2, Appl
43	25	75.8	1052	2	US-08-852-806-2	Sequence 2, Appl
44	25	75.8	1052	3	US-09-163-669-2	Sequence 2, Appl
45	25	75.8	1137	1	US-08-369-043-2	Sequence 2, Appl

#### ALIGNMENTS

##### RESULT 1

US-08-525-539A-12  
; Sequence 12, Application US/08525539A  
; Patent No. 6309636  
; GENERAL INFORMATION:  
; APPLICANT: DO COUTO, FERNANDO J.R.  
; APPLICANT: CERIANI, ROBERTO L.  
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/525,539A  
; FILING DATE: 14-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DYLAN, TYLER  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 27633-20001.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-525-539A-12

Query Match 81.8%; Score 27; DB 4; Length 33;  
Best Local Similarity 85.7%; Pred. No. 7.2;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YRSQIS 7

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Db      1 111111
1 YASQSIS 7

RESULT 2
US-08-737-560A-9
; Sequence 9, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuul
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuul
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; CITY: Kwanak-gu
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: VK23.32'CL
US-08-737-560A-9

Query Match      81.8%; Score 27; DB 2; Length 96;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YRSQSIS 7
Db      50 YASQSIS 56

RESULT 3
US-08-436-463-19
; Sequence 19, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-436-463-19

Query Match      81.8%; Score 27; DB 1; Length 100;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YRSQSIS 7
Db      50 YASQSIS 56

RESULT 4
US-08-436-463-21
; Sequence 21, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,463  
FILING DATE: 26-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 341255/1992  
FILING DATE: 28-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: KIMACHI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 103 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-463-21

Query Match 81.8%; Score 27; DB 1; Length 103;  
Best Local Similarity 85.7%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
Db 48 YASQIS 54  
| | | | |

RESULT 5  
US-07-634-278-62  
Sequence 62, Application US/07634278  
Patent No. 5530101  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:

ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-634-278-62

Query Match 81.8%; Score 27; DB 1; Length 107;  
Best Local Similarity 85.7%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
Db 50 YASQIS 56  
| | | | |

RESULT 6  
US-07-634-278-63  
Sequence 63, Application US/07634278  
Patent No. 5530101  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:

; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-634-278-63

Query Match 81.8%; Score 27; DB 1; Length 107;  
Best Local Similarity 85.7%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
| | | | |  
Db 50 YASQIS 56

RESULT 7  
; Sequence 87, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO. Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIORITY INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-634-278-87

Query Match 81.8%; Score 27; DB 1; Length 107;

Best Local Similarity 85.7%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
| | | | |  
Db 50 YASQIS 56

RESULT 8  
US-08-477-728-62  
; Sequence 62, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIORITY INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-477-728-62

Query Match 81.8%; Score 27; DB 1; Length 107;  
Best Local Similarity 85.7%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
| | | | |  
Db 50 YASQIS 56

RESULT 9

US-08-477-728-63  
 ; Sequence 63, Application US/08477728  
 ; Patent No. 5585089  
 ; GENERAL INFORMATION:  
 ; APPLICANT: QUEEN, Cary L.  
 ; APPLICANT: SCHNEIDER, William P.  
 ; APPLICANT: SELICK, Harold E.  
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 ; NUMBER OF SEQUENCES: 113  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/477,728  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/634,278  
 ; FILING DATE: 19-DEC-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/590,274  
 ; FILING DATE: 28-SEP-1990  
 ; APPLICATION NUMBER: US 07/310,252  
 ; FILING DATE: 13-FEB-1989  
 ; APPLICATION NUMBER: US 07/290,975  
 ; FILING DATE: 28-DEC-1988  
 ; APPLICATION DATA:  
 ; NAME: Smith, William M  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE/DOCKET NUMBER: 11823-002600  
 ; TELEPHONE: (415) 326-2400  
 ; TELEFAX: (415) 326-2422  
 ; INFORMATION FOR SEQ ID NO: 63:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 107 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-477-728-63

Query Match 81.8%; Score 27; DB 1; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 25;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
 Db 50 YASQIS 56

RESULT 10  
 US-08-477-728-87  
 ; Sequence 87, Application US/08477728  
 ; Patent No. 5585089  
 ; GENERAL INFORMATION:  
 ; APPLICANT: QUEEN, Cary L.  
 ; APPLICANT: SCHNEIDER, William P.  
 ; APPLICANT: SELICK, Harold E.  
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 ; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/477,728  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/634,278  
 ; FILING DATE: 19-DEC-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/590,274  
 ; FILING DATE: 28-SEP-1990  
 ; APPLICATION NUMBER: US 07/310,252  
 ; FILING DATE: 13-FEB-1989  
 ; APPLICATION NUMBER: US 07/290,975  
 ; FILING DATE: 28-DEC-1988  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE/DOCKET NUMBER: 11823-002600  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 326-2400  
 ; TELEFAX: (415) 326-2422  
 ; INFORMATION FOR SEQ ID NO: 87:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 107 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-477-728-87

Query Match 81.8%; Score 27; DB 1; Length 107;  
 Best Local Similarity 85.7%; Pred. No. 25;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
 Db 50 YASQIS 56

RESULT 11  
 US-08-474-040-62  
 ; Sequence 62, Application US/08474040  
 ; Patent No. 5693761  
 ; GENERAL INFORMATION:  
 ; APPLICANT: QUEEN, Cary L.  
 ; APPLICANT: CO, Man Sung  
 ; APPLICANT: SCHNEIDER, William P.  
 ; APPLICANT: LANDOLFI, Nicholas F.  
 ; APPLICANT: COELINGH, Kathleen L.  
 ; APPLICANT: SELICK, Harold E.  
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 ; NUMBER OF SEQUENCES: 113  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew  
 ; STREET: 379 Lytton Avenue  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: US

; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-474-040-62

Query Match 81.8%; Score 27; DB 1; Length 107;  
Best Local Similarity 85.7%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
| | | | |  
Db 50 YASQIS 56

RESULT 12  
US-08-474-040-63  
; Sequence 63, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO. Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-474-040-63

Query Match 81.8%; Score 27; DB 1; Length 107;  
Best Local Similarity 85.7%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQIS 7  
| | | | |  
Db 50 YASQIS 56

RESULT 13  
US-08-474-040-87  
; Sequence 87, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO. Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274

; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-474-040-87

Query Match 81.8%; Score 27; DB 1; Length 107;  
Best Local Similarity 85.7%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YRSQSIS 7  
| | | | |  
Db 50 YASQSIS 56

RESULT 14  
US-08-487-200-62  
; Sequence 62, Application US/08487200  
; Patent No. 5693762  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
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; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
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; APPLICATION NUMBER: US/08/487,200  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
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; FILING DATE: 28-SEP-1990  
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; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002610  
; TELECOMMUNICATION INFORMATION:

; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002610  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
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; STRANDEDNESS: single  
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; MOLECULE TYPE: peptide  
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Db 50 YASQSIS 56

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; Sequence 63, Application US/08487200  
; Patent No. 5693762  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
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; FILING DATE: 28-SEP-1990  
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; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002610  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
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; LENGTH: 107 amino acids  
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; TOPOLOGY: linear  
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US-08-487-200-63

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Job time: 1204 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 08:06:25 ; Search time 2408.76 seconds  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
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Listing first 45 summaries

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33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	30	100.0	351	6	AX060780	Sequence
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5	28.4	94.7	132	6	BD004458	Therapeut
6	28.4	94.7	132	6	BD004519	Therapeut
7	28.4	94.7	132	6	BD008352	Inhibitin
8	28.4	94.7	132	6	E23322	Antibody ag
9	28.4	94.7	132	6	E27091	Remedy for
10	28.4	94.7	282	10	MMHIGVL	X58652 Mouse reari
11	28.4	94.7	411	6	BD004423	Ameliorat
12	28.4	94.7	411	6	BD004479	Therapeut
13	28.4	94.7	411	6	BD004540	Therapeut
14	28.4	94.7	411	6	BD008373	Inhibitin
15	28.4	94.7	411	6	E23343	Antibody ag
16	28.4	94.7	411	6	E27112	Remedy for
17	27	90.0	330	9	AF103085	AF103085 Homo sapi
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22	26.8	89.3	114	10	MMIGM9	V00824 Mouse mRNA
23	26.8	89.3	226	10	MMU04232	U04232 Mus musculu
24	26.8	89.3	237	10	AF023238	Mus muscu
25	26.8	89.3	249	10	AF023235	Mus muscu
26	26.8	89.3	251	10	AF290966	Mus muscu
27	26.8	89.3	258	10	MM718312	X67410 Mouse VH718
28	26.8	89.3	261	10	MM718310	X67408 Mouse VH718
29	26.8	89.3	261	10	MM718314	X67412 Mouse VH718
30	26.8	89.3	261	10	MM71839	X67407 Mouse VH718
31	26.8	89.3	262	10	AF318409	Mus muscu
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33	26.8	89.3	263	10	AF318463	Mus muscu
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36	26.8	89.3	269	10	AF318408	Mus muscu
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41	26.8	89.3	272	10	AF318419	Mus muscu
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43	26.8	89.3	273	10	AF318456	Mus muscu
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AX060812	DEFINITION	Sequence 33 from Patent WO0078815.				
AX060812	ACCESSION	AX060812				
AX060812	VERSION	AX060812.1	GI:12406190			
AX060812	KEYWORDS	house mouse.				
AX060812	SOURCE	Mus musculus				
AX060812	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AX060812	REFERENCE	1 (bases 1 to 30)				
AX060812	AUTHORS	Huse,W.D. and Wu,H.				
AX060812	TITLE	Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use				
AX060812	JOURNAL	Patent: WO 0078815-A 33 28-DEC-2000;				
AX060812	FEATURES	Applied Molecular Evolution (US)				
AX060812	source	Location/Qualifiers				
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 ACCESSION AX060789  
 VERSION AX060789.1 GI:12406169  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM  
 Huse,W.D. and Wu,H.  
 TITLE Anti-g(a) v2\_g(b)3? recombinant human antibodies, nucleic acids  
 JOURNAL Patent: WO 0078815-A 10 28-DEC-2000;  
 Applied Molecular Evolution (US)  
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RESULT 3  
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 LOCUS  
 DEFINITION Sequence 1 from Patent WO0078815.  
 ACCESSION AX060780  
 VERSION AX060780.1 GI:12406160  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM  
 Huse,W.D. and Wu,H.  
 TITLE Anti-g(a) v2\_g(b)3? recombinant human antibodies, nucleic acids  
 JOURNAL Patent: WO 0078815-A 1 28-DEC-2000;  
 Applied Molecular Evolution (US)  
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 LOCUS  
 DEFINITION Ameliorative agent for low vasopressin concentration.  
 ACCESSION BD004402  
 VERSION BD004402.1 GI:18632363  
 KEYWORDS JP 03074312-T/25.  
 SOURCE synthetic construct.  
 ORGANISM  
 Ogata,E., Onuma,E., Tsunenari,T., Saito,H. and Azuma,Y.  
 TITLE Ameliorative agent for low vasopressin concentration  
 JOURNAL Patent: JP 03074312-T 25 12-JAN-2001;  
 CHUGAI PHARM CO LTD,ETSURO OGATA,ETSURO ONUMA,TOSHIKI TSUNENARI,  
 HIDEKI SAITO,YUMIKO AZUMA  
 COMMENT OS Artificial Sequence  
 PN JP 03074312-T/25  
 PD 12-JAN-2001  
 PF 03-JUL-2000 JP 2000004413  
 PR 02-JUL-1999 JP 99P 189322  
 PI ETSURO OGATA,ETSURO ONUMA,TOSHIKI TSUNENARI,HIDEKI SAITO, PI  
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 Db 92 GGATTCACCTTCAGTAGCTATGACATGTCT 63

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 DEFINITION Therapeutic agent for diseases caused with PTH or PTHrP.  
 ACCESSION BD004458  
 VERSION BD004458.1 GI:18632419  
 KEYWORDS JP 03074341-T/25.  
 SOURCE synthetic construct.

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ORGANISM      synthetic construct
               artificial sequence.
REFERENCE      1 (bases 1 to 132)
AUTHORS        Ogata,E., Sato,K., Onuma,E., Tsunenari,T., Saito,H. and Azuma,Y.
TITLE          Therapeutic agent for diseases caused with PTH or PTHrP
JOURNAL        Patent: JP 03074341-T 25 12-JAN-2001;
               CHUGAI PHARM CO LTD,ETSURO OGATA,KO SATO,ETSURO ONUMA, OSHIYAKI
               TSUNENARI, HIDEKI SAITO,YUMIKO AZUMA
COMMENT        OS Artificial Sequence
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               PF 03-JUL-2000 JP 2000004414
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               PI ETSURO OGATA,KO SATO,ETSURO ONUMA,TOSHIYAKI TSUNENARI, PI
               HIDEKI SAITO,
               PI YUMIKO AZUMA
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DEFINITION    Therapeutic agent for treating drug-resistant hypercalcemia.
ACCESSION     BD004519
VERSION        BD004519.1 GI:18632480
KEYWORDS      JP 03074428-T/25.
SOURCE        synthetic construct.
ORGANISM      artificial sequence.
REFERENCE      1 (bases 1 to 132)
AUTHORS        Saito,H., Tsunenari,T. and Onuma,E.
TITLE          Therapeutic agent for treating drug-resistant hypercalcemia
JOURNAL        Patent: JP 03074428-T 25 19-JAN-2001;
               CHUGAI PHARM CO LTD,HIDEKI SAITO,TOSHIYAKI TSUNENARI,ETSURO ONUMA
COMMENT        OS Artificial Sequence
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ORGANISM      synthetic construct
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REFERENCE      1 (bases 1 to 132)
AUTHORS        Saito,H., Tsunenari,T. and Onuma,E.
TITLE          Therapeutic agent for treating drug-resistant hypercalcemia
JOURNAL        Patent: JP 03074428-T 25 19-JAN-2001;
               CHUGAI PHARM CO LTD,HIDEKI SAITO,TOSHIYAKI TSUNENARI,ETSURO ONUMA
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               PF 06-JUL-2000 JP 2000004523
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ORGANISM      synthetic construct
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REFERENCE      1 (bases 1 to 132)
AUTHORS        Saito,H., Tsunenari,T., Onuma,E. and Sato,K.
TITLE          Inhibiting agent for tissue degradation
JOURNAL        Patent: JP 03075669-T 25 27-FEB-2001;
               CHUGAI PHARMACEUTICAL CO LTD,HIDEKI SAITO,TOSHIYAKI TSUNENARI, TSURO
               ONUMA, KO SATO
COMMENT        OS Artificial Sequence
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               PD 27-FEB-2001
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DEFINITION    Inhibiting agent for tissue degradation.
ACCESSION     BD008352
VERSION        BD008352.1 GI:18636725
KEYWORDS      JP 03075669-T/25.
SOURCE        synthetic construct.
ORGANISM      artificial sequence.
REFERENCE      1 (bases 1 to 132)
AUTHORS        Saito,H., Tsunenari,T., Onuma,E. and Sato,K.
TITLE          Inhibiting agent for tissue degradation
JOURNAL        Patent: JP 03075669-T 25 27-FEB-2001;
               CHUGAI PHARMACEUTICAL CO LTD,HIDEKI SAITO,TOSHIYAKI TSUNENARI, TSURO
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DEFINITION    Antibody against human parathormone related peptide.
ACCESSION     E23322
VERSION        E23322.1 GI:13024346
KEYWORDS      JP 1999092500-A/25.
SOURCE        unidentified.
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 132)
AUTHORS        Isoa,S.Y.W.W. and Yabuta.
TITLE          Antibody against human parathormone related peptide
JOURNAL        Patent: JP 1999092500-A 25 06-APR-1999;
               CHUGAI PHARMACEUT CO LTD
COMMENT        OS Unidentified
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               PR
               PI ISAO SATO,YUJI WAKAHARA,NAOHIRO YABUTA
               PC C07K16/46,A61K39/395,C07H21/04,C07K16/18,C07K16/26,C12N1/21,
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PC (C12N5/10,C12R1:91),(C12P21/08,C12R1:91),C12N5/00,C12N15/00,  
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PC A61K37/02,(C12N5/00,C12R1:91)  
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Db 92 GGATTCACCTTCAGTAGCATGTCT 63  
RESULT 9  
E27091/c  
LOCUS E27091 132 bp DNA linear PAT 07-FEB-2001  
DEFINITION Remedy for cachexia.  
ACCESSION E27091  
VERSION E27091.1 GI:13025195  
KEYWORDS JP 1999080025-A/25.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 132)  
AUTHORS Iseo,S.T.T. and Ishii.  
TITLE Remedy for cachexia  
JOURNAL Patent: JP 1999080025-A 25 23-MAR-1999;  
CHUGAI PHARMACEUT CO LTD  
COMMENT OS Unidentified  
PN JP 1999080025-A/25  
PD 23-MAR-1999  
PF 13-MAY-1998 JP 1998130715  
PR ISAO SATO,TOSHIKI TSUNENARI,KIMIE ISHII  
PC A61K39/395,A61K39/395,A61K45/00,C12N15/09//C12P21/08, PC  
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PC C12N15/00  
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CC Topology: Linear;  
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RESULT 10

MMHIGVL 282 bp mRNA linear ROD 13-JAN-1994  
LOCUS Mouse rearranged immunoglobulin mRNA for heavy chain variable  
DEFINITION region, isolate PPC-1-5.  
ACCESSION X58652  
VERSION X58652.1 GI:51293  
KEYWORDS Ig heavy chain; Ig variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 282)  
AUTHORS Chen,Q.  
TITLE Direct Submission  
JOURNAL Submitted (26-MAR-1991) Q. Chen, Oregon Health Science University,  
Department of Microbiology and Immunology L-220, OHSU, Portland,  
OR 97201, usa  
REFERENCE 2 (bases 1 to 282)  
AUTHORS Chen,C., Stenzel-Poore,M.P. and Rittenberg,M.B.  
TITLE Natural auto- and polyreactive antibodies differing from  
antigen-induced antibodies in the H chain CDR3  
JOURNAL J. Immunol. 147 (7), 2359-2367 (1991)  
MEDLINE 92013033  
COMMENT See X58641-X58666 for related sequences.  
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RESULT 11  
BD004423 411 bp DNA linear PAT 31-JAN-2002  
LOCUS Ameliorative agent for low vasopressin concentration.  
DEFINITION  
ACCESSION BD004423  
VERSION BD004423.1 GI:18632384  
KEYWORDS JP 03074312-T/46.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 411)  
AUTHORS Ogata,E., Onuma,E., Tsunenari,T., Saito,H. and Azuma,Y.  
TITLE Ameliorative agent for low vasopressin concentration  
JOURNAL Patent: JP 03074312-T 46 12-JAN-2001;  
CHUGAI PHARM CO LTD,ETSURO OGATA,ETSURO ONUMA,TOSHIKI TSUNENARI,  
HIDEMI SAITO,YUNIKO AZUMA  
COMMENT OS Homo sapiens (human)  
PN JP 03074312-T/46  
PD 12-JAN-2001

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PF 03-JUL-2000 JP 2000004413
PR 02-JUL-1999 JP 99P 189322
PI ETSURO OGATA, ETSURO ONUMA, TOSHIAKI TSUNENARI, HIDEKI SAITO, PI
YUMIKO AZUMA
PC A61K45/00, A61K39/395
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Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30
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LOCUS 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Therapeutic agent for diseases caused with PTH or PTHrP.
ACCESSION BD004479
VERSION BD004479.1 GI:18632440
KEYWORDS JP 03074341-T/46.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 411)
Ogata, E., Sato, K., Onuma, E., Tsunenari, T., Saito, H. and Azuma, Y.
Therapeutic agent for diseases caused with PTH or PTHrP
Patent: JP 03074341-T 46 12-JAN-2001;
CHUGAI PHARM CO LTD, ETSURO OGATA, KO SATO, ETSURO ONUMA, OSHIAKI
TSUNENARI, HIDEKI SAITO, YUMIKO AZUMA
OS Homo sapiens (human)
PN JP 03074341-T/46
PD 12-JAN-2001
PF 03-JUL-2000 JP 2000004414
PR 02-JUL-1999 JP 99P 189793
PI ETSURO OGATA, KO SATO, ETSURO ONUMA, TOSHIAKI TSUNENARI, PI
HIDEKI SAITO,
YUMIKO AZUMA
PC A61K45/00, A61K39/395, A61P3/14, A61P29/00, A61P37/02 CC
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RESULT 13
BD004479
LOCUS 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Therapeutic agent for diseases caused with PTH or PTHrP.
ACCESSION BD004479
VERSION BD004479.1 GI:18632440
KEYWORDS JP 03074341-T/46.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 411)
Ogata, E., Sato, K., Onuma, E., Tsunenari, T., Saito, H. and Azuma, Y.
Therapeutic agent for diseases caused with PTH or PTHrP
Patent: JP 03074341-T 46 12-JAN-2001;
CHUGAI PHARM CO LTD, ETSURO OGATA, KO SATO, ETSURO ONUMA, OSHIAKI
TSUNENARI, HIDEKI SAITO, YUMIKO AZUMA
OS Homo sapiens (human)
PN JP 03074341-T/46
PD 12-JAN-2001
PF 03-JUL-2000 JP 2000004414
PR 02-JUL-1999 JP 99P 189793
PI ETSURO OGATA, KO SATO, ETSURO ONUMA, TOSHIAKI TSUNENARI, PI
HIDEKI SAITO,
YUMIKO AZUMA
PC A61K45/00, A61K39/395, A61P3/14, A61P29/00, A61P37/02 CC
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RESULT 14
BD008373
LOCUS 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Inhibiting agent for tissue degradation.
ACCESSION BD008373
VERSION BD008373.1 GI:18636746
KEYWORDS JP 03075669-T/46.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 411)
Saito, H., Tsunenari, T., Onuma, E. and Sato, K.
Inhibiting agent for tissue degradation
Patent: JP 03075669-T 46 27-FEB-2001;
CHUGAI PHARMACEUTICAL CO LTD, HIDEKI SAITO, TOSHIAKI TSUNENARI, TSURO
ONUMA, KO SATO
OS Homo sapiens (human)
PN JP 03075669-T/46
PD 27-FEB-2001
PF 30-AUG-2000 JP 2000005886
PR 28-FEB-2000 JP 00P 052414
PI HIDEKI SAITO, TOSHIAKI TSUNENARI, ETSURO ONUMA, KO SATO, PC
A61K45/00, A61K39/395, A61P7/02, A61P17/02, A61P21/04, A61P35/00 CC
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LOCUS 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Therapeutic agent for treating drug-resistant hypercalcemia.
ACCESSION BD004540
VERSION BD004540.1 GI:18632501
KEYWORDS JP 03074428-T/46.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 411)
Saito, H., Tsunenari, T. and Onuma, E.
Therapeutic agent for treating drug-resistant hypercalcemia
Patent: JP 03074428-T 46 19-JAN-2001;
CHUGAI PHARM CO LTD, HIDEKI SAITO, TOSHIAKI TSUNENARI, ETSURO ONUMA
OS Homo sapiens (human)
PN JP 03074428-T/46
PD 19-JAN-2001
PF 06-JUL-2000 JP 2000004523
PR 06-JUL-1999 JP 99P 192270
PI HIDEKI SAITO, TOSHIAKI TSUNENARI, ETSURO ONUMA
PC A61K45/00, A61K39/395, A61P3/14, A61P5/18
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Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 133 GGATTCACCTTCAGTAGCTATGGCATGTCT 162

RESULT 14
BD008373
LOCUS 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Inhibiting agent for tissue degradation.
ACCESSION BD008373
VERSION BD008373.1 GI:18636746
KEYWORDS JP 03075669-T/46.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 411)
Saito, H., Tsunenari, T., Onuma, E. and Sato, K.
Inhibiting agent for tissue degradation
Patent: JP 03075669-T 46 27-FEB-2001;
CHUGAI PHARMACEUTICAL CO LTD, HIDEKI SAITO, TOSHIAKI TSUNENARI, TSURO
ONUMA, KO SATO
OS Homo sapiens (human)
PN JP 03075669-T/46
PD 27-FEB-2001
PF 30-AUG-2000 JP 2000005886
PR 28-FEB-2000 JP 00P 052414
PI HIDEKI SAITO, TOSHIAKI TSUNENARI, ETSURO ONUMA, KO SATO, PC
A61K45/00, A61K39/395, A61P7/02, A61P17/02, A61P21/04, A61P35/00 CC
FH Key Location/Qualifiers
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Best Local Similarity 96.7%; Pred. NO. 0.027;  
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Db 133 GGATTCACCTTCAGTAGCATGCGATGCT 162

## RESULT 15

E23343 411 bp DNA linear PAT 07-FEB-2001  
LOCUS Antibody against human parathormone related peptide.

DEFINITION E23343

ACCESSION E23343

VERSION E23343.1 GI:13024367

KEYWORDS JP199092500-A/46.

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 411)

AUTHORS Isao, S.Y.W.W. and Yabuta.

TITLE Antibody against human parathormone related peptide

JOURNAL Patent: JP 199092500-A 46 06-APR-1999;

COMMENT CHUGAI PHARMACEUT CO LTD

OS Unidentified

PN JP 199092500-A/46

PD 06-APR-1999

PF 24-SEP-1997 JP 1997258739

PR

PI ISAO SATO, YUJI WAKAHARA, NAOHIRO YABUTA

PC C07K16/46, A61K39/395, C07H21/04, C07K16/18, C07K16/26, C12N1/21,

PC C12N5/10,

PC C12N15/02, C12N15/09, C12P21/08, A61K38/00, (C12N1/21, C12R1:19),

PC (C12N5/10, C12R1:91), (C12P21/08, C12R1:91), C12N5/00, C12N15/00,

PC C12N15/00,

PC A61K37/02, (C12N5/00, C12R1:91)

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CC Topology: Linear;

EH Key Location/Qualifiers

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Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 133 GGATTCACCTTCAGTAGCATGCGATGCT 162

Search completed: August 21, 2002, 10:48:56  
Job time: 9751 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 07:20:37 ; Search time 6260.2 Seconds  
(without alignments)  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em\_estin.\*  
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5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_htc.\*  
12: gb\_gss.\*  
13: em\_gss\_hum.\*  
14: em\_gss\_inv.\*  
15: em\_gss\_pln.\*  
16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	28.4	94.7	913	10 BF162056	BF162056 601768714
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5	26.8	89.3	469	9 A1645111	A1645111 ms87g10.y
6	26.8	89.3	823	9 AA170256	AA170256 ms87g10.r
7	26.8	89.3	877	10 BF144493	BF144493 601790133
8	26.8	89.3	1559	10 BF138708	BF138708 601781893
9	25.4	84.7	217	10 BG757190	BG757190 602710561
10	25.4	84.7	239	10 BG756793	BG756793 602710266
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15	25.4	84.7	452	10 BI017414	BI017414 PM3-ET027
16	25.4	84.7	456	10 BG503730	BG503730 602349705
17	25.4	84.7	678	10 BG340648	BG340648 602462226

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23	25.4	84.7	886	10 BF664039	BF664039 602145719
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36	25.2	84.0	837	10 BG966355	BG966355 602832843
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## ALIGNMENTS

RESULT 1  
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DEFINITION 601772386F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3991460 5', mRNA linear EST 30-OCT-2000  
ACCESSION BF163874  
VERSION BF163874.1 GI:11044152  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 662)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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High quality sequence stop: 658.  
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Library constructed by Life Technologies. Investigator

FEATURES  
source

BASE COUNT 155 a 166 c 183 g 157 t 1 others  
ORIGIN providing samples: Gilbert Smith, NIH

Query Match 94.7%; Score 28.4; DB 10; Length 662;  
Best Local Similarity 96.7%; Pred. No. 0.16;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2  
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DEFINITION mRNA sequence. EST 30-OCT-2000

ACCESSION BF161883  
VERSION 1 (bases 1 to 908)  
KEYWORDS NIH-MGC http://mgc.nci.nih.gov/  
SOURCE National Institutes of Health, Mammalian Gene Collection (MGC)  
ORGANISM Unpublished (1999)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 908)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabps-femail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: LAM9182 row: e column: 05  
High quality sequence stop: 662.  
Location/Qualifiers

FEATURES  
Source

1..908  
/organism="Mus musculus"  
/strain="CZECH II (feral)"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3982828"  
/clone\_lib="NCI\_CGAP\_Lu29"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
Stem cell origin.  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: Sali;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

BASE COUNT 214 a 228 c 253 g 213 t  
ORIGIN

Query Match 94.7%; Score 28.4; DB 10; Length 908;  
Best Local Similarity 96.7%; Pred. No. 0.18;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattacccttcagtagctatgacatgtct 30  
||||| ||||||| ||||||| ||||||| |||||||  
Db 195 GGATTCACCTTTCAGTAGCTATGACATGTCT 224

RESULT 3  
BF162056  
LOCUS 60176814F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3987986 5',  
DEFINITION mRNA sequence. EST 30-OCT-2000

ACCESSION BF162056  
VERSION 1 (bases 1 to 913)  
KEYWORDS NIH-MGC http://mgc.nci.nih.gov/  
SOURCE National Institutes of Health, Mammalian Gene Collection (MGC)  
ORGANISM Unpublished (1999)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 913)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabps-femail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: LAM9195 row: 1 column: 03  
High quality sequence stop: 581.  
Location/Qualifiers

1..913  
/organism="Mus musculus"  
/strain="CZECH II (feral)"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3987986"  
/clone\_lib="NCI\_CGAP\_Lu29"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
Stem cell origin.  
/lab\_host="DH10B"

/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: Sali;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

BASE COUNT 218 a 248 c 260 g 187 t  
ORIGIN

Query Match 94.7%; Score 28.4; DB 10; Length 913;  
Best Local Similarity 96.7%; Pred. No. 0.18;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattacccttcagtagctatgacatgtct 30  
||||| ||||||| ||||||| ||||||| |||||||  
Db 202 GGATTCACCTTTCAGTAGCTATGACATGTCT 231

RESULT 4  
BB869694  
LOCUS B869694 RIKEN full-length enriched adult male accessory axillary  
DEFINITION lymph node Mus musculus cDNA clone G630015C08 5', mRNA sequence.  
ACCESSION BB869694  
VERSION BB869694.1 GI:17115904  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 342)

AUTHORS Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,  
Hayatsu, N., Hiramoto, K., Hirao, T., Hirozane, T., Imotani, K., Ishii,  
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,  
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,  
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,  
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa,  
A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,  
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.,  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.  
2001)  
JOURNAL Unpublished (2001)



## COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh  
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. . 10 (10), 1617-1630 (2000)  
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,  
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura  
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and  
Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res. .  
10 (11), 1757-1771 (2000)  
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara  
,Y. and Hayashizaki,Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
e mouse tissues.

## FEATURES

source Location/Qualifiers

1..342  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="G630015C08"  
/clone\_lib="RIKEN full-length enriched, adult male  
accessory axillary lymph node"  
/sex="male"  
/tissue\_type="accessory axillary lymph node"  
/dev\_stage="adult"

BASE COUNT 73 a 83 c 98 g 88 t

## ORIGIN

Query Match 89.3%; Score 26.8; DB 9; Length 342;  
Best Local Similarity 93.3%; Pred. No. 0.58;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ggattcaaccttcagtagctatgcattgtct 30  
||||| ||||| ||||| ||||| |||||

Db 215 GGATTCACTTTTCAGTAGCTATGCATGTCT 244

## RESULT 5

AI645111

## LOCUS

DEFINITION ms87g10.y1 Soares mouse 3NDMS Mus musculus cDNA clone IMAGE:618594  
5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-III REGION  
(HUMAN); gb:U23089 Mus musculus CB17 SCID immunoglobulin heavy  
chain V region mRNA, (MOUSE);, mRNA sequence.

## ACCESSION

AI645111

## VERSION

AI645111.1 GI:4723586

## KEYWORDS

EST.

## SOURCE

house mouse.

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 469)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Stentoe,M., Pape,D., Harvey,N., Schurk,R., Ritter

,E., Kohn,S., Shint,T., Jackson,Y., Cardenas,M., McCann,R.,

Waterston,R. and Wilson,R.

## TITLE

JOURNAL

## COMMENT

The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LUNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
This read is a RESEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)  
MGI:379438

Seq primer: -40RP from Gibco.

## FEATURES

source

1..469  
Location/Qualifiers  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:618594"  
/clone\_lib="Soares mouse 3NDMS"  
/sex="male"  
/tissue\_type="Spleen"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"

/note="vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. RNA  
provided by Dr. Bertrand Jordan. Library went through  
three rounds of normalization, and was constructed by  
Bento Soares and M.Fatina Bonaldo."

BASE COUNT 113 a 112 c 121 g 123 t

## ORIGIN

Query Match 89.3%; Score 26.8; DB 9; Length 469;  
Best Local Similarity 93.3%; Pred. No. 0.65;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ggattcaaccttcagtagctatgcattgtct 30  
||||| ||||| ||||| ||||| |||||

Db 193 GGATTCACTTTTCAGTAGCTATGCCATGTCT 222

## RESULT 6

AA170256

## LOCUS

DEFINITION AA170256 823 bp mRNA linear EST 16-FEB-1997  
ms87g10.rl Soares mouse 3NDMS Mus musculus cDNA clone IMAGE:618594  
5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-III REGION  
(HUMAN); gb:U0821 Mouse mRNA fragment for immunoglobulin mu  
encoding the C00821 mouse (MOUSE);, mRNA sequence.

## ACCESSION

AA170256

## VERSION

AA170256.1 GI:1748794

## KEYWORDS

EST.

## SOURCE

house mouse.

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 823)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HHMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:379418

Putative full length read

vector to vector length is 867  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 492.

#### FEATURES

Location/Qualifiers

1..823  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_lib="IMAGE:618594"  
/clone\_lib="Soares mouse 3NbMS"  
/sex="male"  
/tissue\_type="Spleen"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCTGAAGTGGAGCGCGCTGTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. RNA  
provided by Dr. Bertrand Jordan. Library went through  
three rounds of normalization, and was constructed by  
Bento Soares and M.Fatima Bonaldo."

BASE COUNT 200 a 208 c 202 g 213 t  
ORIGIN

Query Match 89.3%; Score 26.8; DB 9; Length 823;  
Best Local Similarity 93.3%; Pred. No. 0.78;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcacccttcagctagctatgacatgtct 30  
||||||| ||||||| ||||||| |||||||

Db 193 GGATTCACCTTTCAGTAGCTATGCCATGTCT 222

#### RESULT

BF144493

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF144493 877 bp mRNA linear EST 24-OCT-2000  
601790133F1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4020753 5',  
mRNA sequence.

BF144493

BF144493.1 GI:10983533

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 877)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9275 row: a column: 10  
High quality sequence stop: 644.

#### FEATURES

source

Location/Qualifiers

1..877  
/organism="Mus musculus"  
/strain="CZECH II"  
/db\_xref="taxon:10090"  
/clone\_lib="IMAGE:4020753"  
/clone\_lib="NCI\_CGAP\_Lu30"  
/tissue\_type="tumor, metastatic to mammary"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; transgenic model WNT-1, expression driven by  
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo  
dT. Library constructed by Life Technologies.  
Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 198 a 233 c 254 g 192 t  
ORIGIN

Query Match 89.3%; Score 26.8; DB 10; Length 877;  
Best Local Similarity 93.3%; Pred. No. 0.8;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcacccttcagctagctatgacatgtct 30  
||||||| ||||||| ||||||| |||||||

Db 170 GGATTCACCTTTCAGTAGCTATGCCATGTCT 199

#### RESULT

BF138708

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF138708 1559 bp mRNA linear EST 24-OCT-2000  
601781893F1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4009847 5',  
mRNA sequence.  
BF138708  
BF138708.1 GI:10977748  
EST.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1559)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9246 row: j column: 24  
High quality sequence stop: 562.

#### FEATURES

source

Location/Qualifiers

1..1559  
/organism="Mus musculus"  
/strain="CZECH II"  
/db\_xref="taxon:10090"  
/clone\_lib="IMAGE:4009847"  
/clone\_lib="NCI\_CGAP\_Lu30"  
/tissue\_type="tumor, metastatic to mammary"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; transgenic model WNT-1, expression driven by  
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo  
dT. Library constructed by Life Technologies.  
Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 482 a 376 c 432 g 268 t  
ORIGIN

Query Match 89.3%; Score 26.8; DB 10; Length 1559;

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Best Local Similarity 93.3%; Pred. No. 0.96;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30
||||| ||||||||| ||||||||| |||
Db 184 GGATTTACCTTCAGTAGTATGACATGTCT 213

RESULT 9
BG757190 217 bp mRNA linear EST 15-MAY-2001
LOCUS 602710561F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850798 5',
DEFINITION mRNA sequence.
ACCESSION BG757190
VERSION BG757190.1 GI:14067843
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 217)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM1692 row: j column: 15
High quality sequence stop: 217.
FEATURES
source
1..217
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4850798"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 35 a 53 c 72 g 57 t
ORIGIN
Query Match 84.7%; Score 25.4; DB 10; Length 217;
Best Local Similarity 96.3%; Pred. No. 1.9;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatg 27
||||| ||||||||| ||||||||| |||
Db 175 GGATTCACCTTCAGTAGCTATGGCATG 201

RESULT 10
BG756793 239 bp mRNA linear EST 15-MAY-2001
LOCUS 602710266F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850632 5',
DEFINITION mRNA sequence.
ACCESSION BG756793
VERSION BG756793.1 GI:14067446
KEYWORDS EST.

```

```

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 239)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM1692 row: c column: 17
High quality sequence stop: 239.
FEATURES
source
1..239
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4850632"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 40 a 59 c 80 g 60 t
ORIGIN
Query Match 84.7%; Score 25.4; DB 10; Length 239;
Best Local Similarity 96.3%; Pred. No. 1.9;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatg 27
||||| ||||||||| ||||||||| |||
Db 197 GGATTCACCTTCAGTAGCTATGGCATG 223

RESULT 11
BF870873/c 253 bp mRNA linear EST 17-JAN-2001
LOCUS IL0-ET0152-301000-501-b05 ET0152 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF870873
ACCESSION BF870873
VERSION BF870873.1 GI:12261003
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 253)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL MEDLINE
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics

```

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 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL0&t2=IL0-ET0152-301000-501-b05&t3=2000-10-30&t4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 253.

## FEATURES

source

1. .253  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="ET0152"  
 /dev\_stage="Adult"  
 /note="Organ: lung\_tumor; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 62 a 81 c 64 g 46 t

BASE COUNT  
 ORIGIN

Query Match 84.7%; Score 25.4; DB 10; Length 253;  
 Best Local Similarity 96.3%; Pred. No. 2;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27  
 |||||  
 Db 60 GGATTCACCTTCAGTAGCTATGCGATG 34

## RESULT 12

BE827456  
 LOCUS BE827456 319 bp mRNA linear EST 22-SEP-2000  
 DEFINITION CM2-ET0016-310500-206-d09 ET0016 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BE827456  
 VERSION BE827456.1 GI:10259821  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 319)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags

JOURNAL

MEDLINE

COMMENT

20202663  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2-ET0016-310500-206-d09&t3=2000-05-31&t4=1>)  
 Seq primer: puc 18 forward

High quality sequence start: 7  
 High quality sequence stop: 319.  
 Location/Qualifiers  
 1. .319  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="ET0016"  
 /dev\_stage="Adult"

/note="Organ: lung\_tumor; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 71 a 74 c 98 g 76 t

BASE COUNT  
 ORIGIN

Query Match 84.7%; Score 25.4; DB 10; Length 319;  
 Best Local Similarity 96.3%; Pred. No. 2.1;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27  
 |||||  
 Db 113 GGATTCACCTTCAGTAGCTATGCGATG 139

## RESULT 13

H73816  
 LOCUS H73816 419 bp mRNA linear EST 31-OCT-1995  
 DEFINITION yslib01.r1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone  
 (IMAGE:214441 5' similar to gb:M62726 IG HEAVY CHAIN V-III REGION  
 (HUMAN));, mRNA sequence.

ACCESSION

VERSION

H73816.1 GI:1046750

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 419)  
 Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,  
 Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins  
 ,B., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore  
 ,M., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,  
 Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasakis,E.,  
 Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.  
 Generation and analysis of 280,000 human expressed sequence tags  
 Genome Res. 6 (9), 807-828 (1996)

97044478

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewartson.wustl.edu

Insert Size: 2006

High quality sequence stops: 261

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 2006 Std Error: 0.00

Seq primer: M13p1

High quality sequence stop: 261.

Location/Qualifiers

1. .419

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="IMAGE:214441"

/clone\_lib="Soares fetal liver spleen lNFLS"

/sex="male"

/dev\_stage="20 week-post conception fetus"

```

/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' - AACTGGAAGAATTAATAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      91 a   100 c   116 g   102 t
ORIGIN

Query Match      84.7%; Score 25.4; DB 10; Length 419;
Best Local Similarity 96.3%; Pred. No. 2.3;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 ggattcaccttcagtagctatgacatg 27
|||||
Db  62 GGATTCACCTTCAGTAGCTATGGCATG 88

RESULT 14
AW402311      436 bp      mRNA      linear      EST 16-FEB-2000
LOCUS
DEFINITION
IMAGE:3054175 5', mRNA sequence.
ACCESSION
AW402311
VERSION
AW402311.1 GI:6920997
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 436)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES
Location/Qualifiers
source
1..436
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3054175"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/notes="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      89 a   109 c   136 g   102 t
ORIGIN

Query Match      84.7%; Score 25.4; DB 9; Length 436;
Best Local Similarity 96.3%; Pred. No. 2.4;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' - AACTGGAAGAATTAATAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      91 a   100 c   116 g   102 t
ORIGIN

Query Match      84.7%; Score 25.4; DB 10; Length 419;
Best Local Similarity 96.3%; Pred. No. 2.3;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 ggattcaccttcagtagctatgacatg 27
|||||
Db  62 GGATTCACCTTCAGTAGCTATGGCATG 88

RESULT 15
BI017414      452 bp      mRNA      linear      EST 13-JUN-2001
LOCUS
DEFINITION
IMAGE:3054175 5', mRNA sequence.
ACCESSION
BI017414
VERSION
BI017414.1 GI:14421485
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 452)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordln,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-ET0272-
020401-007-d05&t3=2001-04-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 398.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="ET0272"
/dev_stage="Adult"
/notes="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      103 a   103 c   134 g   112 t
ORIGIN

Query Match      84.7%; Score 25.4; DB 10; Length 452;
Best Local Similarity 96.3%; Pred. No. 2.4;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 ggattcaccttcagtagctatgacatg 27
|||||
Db  203 GGATTCACCTTCAGTAGCTATGGCATG 229

Search completed: August 21, 2002, 09:55:34
Job time: 9297 sec

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Result No.	Score	Query Match	Length	DB	ID	Description
1	30	100.0	30	19	AAV49844	LM609 grafted anti
2	30	100.0	30	22	AAF28200	DNA encoding LM609
C 3	30	100.0	84	19	AAV49825	LM609 grafted anti
C 4	30	100.0	84	22	AAH74628	PCR primer for hea
C 5	30	100.0	84	22	AAF28180	Oligonucleotide #2
6	30	100.0	351	19	AAV49820	Vitaxin antibody h
7	30	100.0	351	22	AAH74623	DNA encoding heavy
8	30	100.0	351	22	AAF28175	Vitaxin heavy chai
C 9	28.4	94.7	132	19	AAF24268	Chimeric antibody

DR P-PSDB; AAW76007.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Disclosure; Page 40; 129pp; English.

XX

CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal

CC antibody LM609 heavy and light chain variable region. LM609 and the

CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used

CC to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX

SQ Sequence 30 BP; 7 A; 7 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 30; DB 19; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00042;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ggattcaccctcagtagctatgacatgtct 30

Db 1 ggattcaccctcagtagctatgacatgtct 30

RESULT 2

AAF28200

ID AAF28200 standard; DNA; 30 BP.

XX

AC AAF28200;

XX

DT 03-APR-2001 (first entry)

XX

DE DNA encoding LM609 VH CDR1 peptide.

XX

XX LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX

XX Unidentified.

OS

XX WO200078815-A1.

PN

XX 28-DEC-2000.

PD

XX

PF 23-JUN-2000; 2000WO-US17454.

XX

PR 24-JUN-1999; 99US-0339922.

XX

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA

XX

PI Huse WD, Wu H;

XX

XX WPI; 2001-050110/06.

DR

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX

PS Claim 16; Page 40; 132pp; English.

XX

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

SQ Sequence 30 BP; 7 A; 7 C; 6 G; 10 T; 0 other;

Query Match 100.0%; Score 30; DB 22; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00042;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ggattcaccctcagtagctatgacatgtct 30

Db 1 ggattcaccctcagtagctatgacatgtct 30

RESULT 3

AAV49825/c

ID AAV49825 standard; DNA; 84 BP.

XX

AC AAV49825;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody variable region oligonucleotide #2.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; ss.

XX

OS Synthetic.

OS Mus sp.

XX

XX WO9833919-A2.

PN

XX 06-AUG-1998.

PD

XX 30-JAN-1998; 98WO-US01826.

PF

XX 30-JAN-1997; 97US-0791391.

PR

XX (IXSY-) IXSYS INC.

FA

XX Glaser SM, Huse WD;

PI

XX WPI; 1998-437472/37.

DR

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Example 2; Page 65; 129pp; English.

XX

CC AAV49824-V49833 are oligonucleotides used in the construction of grafted

CC LM609 monoclonal antibody heavy and light chain variable regions. LM609

CC and the antibody vitaxin bind selectively to integrin alphavbeta3 and

CC can be used to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX SQ Sequence 84 BP; 22 A; 27 C; 20 G; 15 T; 0 other;

Query Match 100.0%; Score 30; DB 19; Length 84;  
Best Local Similarity 100.0%; Pred. No. 0.0005;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggattcaaccttcagtagcatgacatgtct 30  
| | | | | | | | | | | | | | | | | | | | | |  
Db 78 GGATTCACCTTCAGTAGCATGATGATGCT 49

RESULT 4  
AAH74628/c  
ID AAH74628 standard; DNA; 84 BP.  
XX  
AC AAH74628;  
XX  
DT 15-OCT-2001 (first entry)  
XX

PCR primer for heavy chain variable region of LM609 antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
KW cancer; PCR primer; ss.

XX Mus sp.

XX US2001011125-A1.

XX 02-AUG-2001.

XX 30-JAN-1997; 97US-0790540.

XX 30-JAN-1997; 97US-0790540.

XX (HUSE/) HUSE W D.

XX Huse WD;

XX WPI; 2001-496171/54.

XX New LM609 grafted antibody exhibiting selective binding affinity to  
PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
PT disorders or cancer -

XX Example 2; Page 16; 25pp; English.

XX PCR primers AAH74627-31 were used to amplify DNA encoding fragments  
CC of the heavy chain variable region of the monoclonal antibody LM609.  
CC LM609 is a murine antibody which specifically recognises the integrin  
CC alphavbeta3, and inhibits its functional activity. The specification  
CC describes a LM609 grafted antibody which has the complementarity  
CC determining regions (CDRs) substituted into a non-murine framework.  
CC Nucleic acids encoding LM609 grafted heavy and light chain polypeptides  
CC and fragments are useful in diagnostic and therapeutic purposes, such  
CC as in the production of LM609 grafted antibodies and fragments having  
CC binding specificity and inhibitory activity against the integrin  
CC alphavbeta3. The antibody can be used for the diagnosis or treatment  
CC of alphavbeta3-mediated diseases (e.g. inflammatory disorders, chronic  
CC articular rheumatism, psoriasis, disorders associated with inappropriate  
CC or inopportune invasion of vessels such as diabetic retinopathy,  
CC neovascular glaucoma and capillary proliferation in atherosclerotic  
CC plaques, or cancers), and to inhibit binding activity of alphavbeta3  
CC that are necessary for progression of an alphavbeta3-mediated disease.

XX Sequence 84 BP; 22 A; 27 C; 20 G; 15 T; 0 other;

Query Match 100.0%; Score 30; DB 22; Length 84;

Best Local Similarity 100.0%; Pred. No. 0.0005;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggattcaaccttcagtagcatgacatgtct 30  
| | | | | | | | | | | | | | | | | | | | | |  
Db 78 GGATTCACCTTCAGTAGCATGATGATGCT 49

RESULT 5  
AAF28180/c  
ID AAF28180 standard; DNA; 84 BP.  
XX  
AC AAF28180;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE Oligonucleotide #2.  
XX  
KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis -

XX Example 2; Page 67; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies  
CC exhibiting selective binding affinity to alphaVbeta3 integrin or  
CC their functional fragments. The antibodies or their functional  
CC fragments can be used in the diagnosis and treatment of  
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory  
CC diseases (such as psoriasis and chronic articular rheumatism),  
CC disorders associated with inappropriate or inopportune invasion of  
CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
CC diseases (such as macular degeneration), restenosis and  
CC osteoporosis.

XX Sequence 84 BP; 22 A; 27 C; 20 G; 15 T; 0 other;

Query Match 100.0%; Score 30; DB 22; Length 84;  
Best Local Similarity 100.0%; Pred. No. 0.0005;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggattcaaccttcagtagcatgacatgtct 30  
| | | | | | | | | | | | | | | | | | | | | |  
Db 78 GGATTCACCTTCAGTAGCATGATGATGCT 49

RESULT 6  
AAV49820  
ID AAV49820 standard; DNA; 351 BP.

XX AAV49820;



DE	XX	DNA encoding heavy chain variable region of LM609 grafted antibody.
KW	XX	Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW	KW	chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW	KW	neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW	XX	cancer; ss.
OS	XX	Synthetic.
OS	OS	Mus sp.
XX	XX	US20031011125-A1.
PN	XX	02-AUG-2001.
PD	XX	30-JAN-1997; 97US-0790540.
PF	XX	30-JAN-1997; 97US-0790540.
PR	XX	(HUSE/) HUSE W D.
PA	XX	Huse WD;
PI	XX	WPI; 2001-496171/54.
XX	XX	P-PSDB; AAG63587.
XX	XX	New LM609 grafted antibody exhibiting selective binding affinity to
PT	XX	alphavbeta3, comprising at least one LM609 grafted heavy and light
PT	XX	chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT	XX	disorders or cancer -
XX	XX	Claim 3; Fig 1A; 25pp; English.
XX	XX	The present sequence encodes the heavy chain variable region of the
CC	XX	grafted monoclonal antibody LM609. LM609 is a murine antibody which
CC	XX	specifically recognises the integrin alphavbeta3, and inhibits its
CC	XX	functional activity. The LM609 grafted antibody has the
CC	XX	complementarity determining regions (CDRs) substituted into a non-murine
CC	XX	framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC	XX	polypeptides and fragments are useful in diagnostic and therapeutic
CC	XX	purposes, such as in the production of LM609 grafted antibodies and
CC	XX	fragments having binding specificity and inhibitory activity against
CC	XX	the integrin alphavbeta3. The antibody can be used for the diagnosis
CC	XX	or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC	XX	disorders, chronic articular rheumatism, psoriasis, disorders
CC	XX	associated with inappropriate or inopportune invasion of vessels such
CC	XX	as diabetic retinopathy, neovascular glaucoma and capillary
CC	XX	proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC	XX	binding activity of alphavbeta3 that are necessary for progression of
CC	XX	an alphavbeta3-mediated disease.
XX	XX	Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;
SQ	XX	
Query Match	100.0%;	Score 30; DB 22; Length 351;
Best Local Similarity	100.0%;	Pred. No. 0.00063;
Matches	30; Conservative	0; Mismatches 0; Indels 0; Gaps
QY	1 ggattcacccttcagtagcatgacatgtctt 30	
Db	76 ggattcacccttcagtagcatgacatgtctt 105	
RESULT	8	
AAF28175		
ID	AAF28175 standard; DNA; 351 BP.	
XX	AAF28175;	
AC		
XX		
DT	03-APR-2001 (first entry)	
XX	Vitaxin heavy chain variable region DNA..	
DE		
XX	LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;	
KW		

KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.

OS Unidentified.

XX WO200078815-A1.

PN 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT osteoporosis -  
PT osteoporosis -

XX Disclosure; Fig 1; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies  
CC exhibiting selective binding affinity to alphavbeta3 integrin or  
CC their functional fragments. The antibodies or their functional  
CC fragments can be used in the diagnosis and treatment of  
CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory  
CC diseases (such as psoriasis and chronic articular rheumatism),  
CC disorders associated with inappropriate or inopportune invasion of  
CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
CC diseases (such as macular degeneration), restenosis and  
CC osteoporosis.

XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match 100.0%; Score 30; DB 22; Length 351;

Best Local Similarity 100.0%; Pred. No. 0.00063;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatgtct 30

Db 76 ggattcaccttcagtagctatgacatgtct 105

RESULT 9

AAV24268/c

ID AAV24268 standard; DNA; 132 BP.

XX AAV24268;

XX 03-SEP-1998 (first entry)

XX Chimeric antibody against hTPRP human H chain PCR primer MBCLHGP2.

XX Chimeric; antibody; human parathormone related peptide; hTPRP; mouse;  
KW L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;  
KW hypophosphemia; pathogen; vitamin D resistance; V region; C region;  
XX humanised; PCR primer ss.

XX Synthetic.

XX Homo sapiens.

XX WO9813388-A1.

XX 02-APR-1998.

XX 24-SEP-1997; 97WO-JP03382.

XX

PR 24-JUL-1997; 97JP-0214168.

PR 26-SEP-1996; 96JP-0255196.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Sato K, Wakahara Y, Yabuta N;

XX WPI; 1998-230640/20.

XX New chimeric antibodies against human parathormone related

PT peptide(s) - useful for, e.g. treatment of hypercalcaemia and other  
PT disorders caused by malignant neoplasm(s)

XX Example 3; Page 104; 182pp; Japanese.

XX New antibodies have been developed which are specific for human  
CC parathormone related peptides (hTPRP). The antibodies comprise chimeric  
CC L and/or H chains, where the C region is of human and L region of mouse,  
CC origin. The present sequence represents a PCR primer used in an example  
CC of the present invention. Host cells, transformed with vectors  
CC containing DNA encoding antibodies of the invention, can be used to  
CC produce the antibodies. The antibodies may be used to treat  
CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of  
CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,  
CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They  
CC pathogens or to vitamin D resistance.

XX Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;

Query Match 94.7%; Score 28.4; DB 19; Length 132;

Best Local Similarity 96.7%; Pred. No. 0.0028;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatgtct 30

Db 92 GGATTCACCTTCAGTAGCTATGCGCATGTCT 63

RESULT 10

AAAX00112/c

ID AAX00112 standard; DNA; 132 BP.

XX AAX00112;

XX 14-APR-1999 (first entry)

XX Human antibody PCR antisense primer MBCLHGP2.

XX Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;  
KW inhibitor; humanised; PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9851329-A1.

XX 19-NOV-1998.

XX 13-MAY-1998; 98WO-JP02116.

XX 18-JUL-1997; 97JP-0194445.

XX 15-MAY-1997; 97JP-0125505.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Ishii K, Sato K, Tunenari T;

XX WPI; 1999-070101/06.

XX Inhibitors of binding of parathyroid hormone related peptide to its  
PT receptor - useful for, e.g. treatment of cachexia arising from

PT cancer or other diseases  
 PS Example 4; Page 65; 125pp; Japanese.  
 XX

The present invention describes compositions for the treatment of cachexia containing a substance which inhibits the binding of a parathyroid hormone related peptide (PTHrP) to its receptor, as an active component. This substance may be an antagonist to the receptor, or an antibody (preferably monoclonal) or antibody fragment, recognising PTHrP. The antibody is preferably humanised or chimeric. The present invention also describes a humanised antibody prepared by hybridoma 23-57-137-1 (FERM Bp-5631). The composition is used for the treatment of cachexia arising in connection with diseases such as cancer, thereby improving the quality of life of the patient. The present sequence represents a PCR primer used in an example from the present invention.

XX Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;  
 SQ

Query Match 94.7%; Score 28.4; DB 20; Length 132;  
 Best Local Similarity 96.7%; Pred. NO. 0.0028;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30  
 |||||  
 Db 92 GGATTCACCTTCAGTAGCTATGGCATGTCT 63

RESULT 11  
 AAZ58893/C  
 ID AAZ58893 standard; DNA; 132 BP.  
 XX  
 AC AAZ58893;  
 XX  
 DT 26-APR-2000 (first entry)  
 XX  
 DE PCR primer MBC1HG2P.  
 XX  
 KW Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP;  
 KW human; tumour; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200000219-A1.  
 XX  
 PD 06-JAN-2000.  
 XX  
 PF 25-JUN-1999; 99WO-JP03433.  
 XX  
 PR 26-JUN-1998; 98JP-0180143.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Sato K, Tsunenari T;  
 XX  
 DR WPI; 2000-117115/10.  
 XX  
 PT Treatment of hypercalcemic crisis with a substance inhibiting binding  
 PT of parathyroid hormone related peptide to its receptor -  
 XX  
 PS Example 4; Page 79; 120pp; Japanese.  
 XX

The invention relates to a method of treatment of hypercalcemic crisis. A composition for the treatment of hypercalcemic crisis contains as active component a substance which inhibits the binding of parathyroid hormone related peptide (PTHrP) to its receptor. The inhibitor is used for the treatment of hypercalcemic crisis, such as that associated with a malignant tumour.

XX  
 SQ Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;

Query Match 94.7%; Score 28.4; DB 21; Length 132;  
 Best Local Similarity 96.7%; Pred. NO. 0.0028;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30  
 |||||  
 Db 92 GGATTCACCTTCAGTAGCTATGGCATGTCT 63

RESULT 12  
 AAH75086/C  
 ID AAH75086 standard; DNA; 132 BP.  
 XX  
 AC AAH75086;  
 XX  
 DT 13-NOV-2001 (first entry)  
 XX  
 DE Nucleotide sequence of a PCR primer.  
 XX  
 KW Tissue decomposition inhibitor; parathyroid hormone; cancer cachexia;  
 KW septicemia; injury; muscular dystrophy; cytokine; interleukin-6;  
 KW granulocyte colony stimulating factor; interleukin-11;  
 KW leukemia inhibitory factor; weight loss; PCR primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200164249-A1.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 30-AUG-2000; 2000WO-JP05886.  
 XX  
 PR 28-FEB-2000; 2000JP-0052414.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Saito H, Tsunenari T, Onuma E, Sato K;  
 XX  
 DR WPI; 2001-550131/61.  
 XX  
 PT Tissue decomposition inhibitor that prevents parathyroid hormone  
 PT associated proteins from binding to its receptor -  
 XX  
 PS Example 1; Page 87; 132pp; Japanese.  
 XX

The specification describes a tissue decomposition inhibitor, which comprises a substance that inhibits peptides associated with parathyroid hormone (PTH) from binding with their receptor. The method is used to inhibit tissue decomposition caused by cancer cachexia, septicemia, heavy external injury or muscular dystrophy, and for treating patients with elevated cytokine (Interleukin-6, Granulocyte colony stimulating factor, Interleukin-11 and Leukemia inhibitory factor) levels. It may also be used for preventing weight loss caused by cancer cachexia. PCR primers AAH75086-87 were used in the course of the invention.

XX  
 SQ Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;

Query Match 94.7%; Score 28.4; DB 22; Length 132;  
 Best Local Similarity 96.7%; Pred. NO. 0.0028;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30  
 |||||  
 Db 92 GGATTCACCTTCAGTAGCTATGGCATGTCT 63

RESULT 13  
 AAH74265/C  
 ID AAH74265 standard; DNA; 132 BP.  
 XX  
 AC AAH74265;

```
XX 15-OCT-2001 (first entry)
XX
XX Nucleotide sequence of an oligonucleotide.
DE
XX Parathyroid hormone-associated peptide; PTHrP; dental disease; primer;
KW ss.
XX
XX Synthetic.
OS
XX WO200154725-A1.
XX
XX 02-AUG-2001.
XX
XX 14-DEC-2000; 2000WO-JP08875.
XX
XX 25-JAN-2000; 2000JP-0083034.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Kato A, Suzuki M, Sugimoto T;
XX
XX WPI; 2001-465459/50.
XX
XX Parathyroid hormone-associated peptide binding inhibitors useful for
PT treating dental disease
PT
XX
XX Example 4; Page 91; 140pp; Japanese.
XX
XX The present oligonucleotide was used in the course of the invention.
CC The specification describes a treatment for dental diseases. The
CC treatment comprises a substance that inhibits binding between
CC parathyroid hormone-associated peptide and its receptor.
XX
XX Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;
SQ

Query Match          94.7%; Score 28.4; DB 22; Length 132;
Best Local Similarity 96.7%; Pred. No. 0.0028;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatgtct 30
   |||||
DB 92 GGATTCACCTTCAGTACGTATGGCATGTCT 63

RESULT 14
AAH76624/c
ID AAH76624 standard; DNA; 132 BP.
XX
XX AC AAH76624;
XX
XX 08-OCT-2001 (first entry)
XX
XX Humanised anti-PTHrP Ab VH CDR PCR primer MBC1HGP2, SEQ ID NO:25.
DE
XX Parathyroid hormone-related peptide; PTHrP; antagonist; antibody;
KW calcium regulation disorder; serum calcium concentration;
KW humoral hypercalcaemia of malignancy; cytostatic; analgesic;
KW PCR primer; ss.
XX
XX Synthetic.
OS
XX WO200147554-A1.
XX
XX 05-JUL-2001.
XX
XX 27-DEC-2000; 2000WO-JP09339.
XX
XX 28-DEC-1999; 99JP-0375203.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
```

```
PI Yamazaki T, Hayasaka A, Koga A;
XX
XX WPI; 2001-425590/45.
XX
XX Composition for treating diseases of calcium regulation and for use as
PT an analgesic, comprises an antibody recognizing parathyroid hormone
PT related peptide
XX
XX Examples; Page 86; 128pp; Japanese.
XX
XX The invention relates to a stabilised composition of an antibody which
CC recognises parathyroid hormone-related peptide (PTHrP) - see AAG64793.
CC The composition consists of a solution of the antibody in a buffer of pH
CC 5-8 containing one or more of acetic acid, phosphoric acid, citric acid
CC and their salts. The composition has increased storage stability,
CC especially at elevated temperatures. The composition antagonises the
CC action of PTHrP, and may be used in the treatment of diseases involving
CC disturbances of calcium regulation (high or low serum calcium
CC concentration) such as humoral hypercalcaemia of malignancy and as an
CC analgesic. The present sequence represents a PCR primer used in the
CC exemplifications of the invention in the construction of polynucleotides
CC encoding humanised versions of the anti-human PTHrP murine monoclonal
CC antibody 23-57-137-1.
XX
XX Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;
SQ

Query Match          94.7%; Score 28.4; DB 22; Length 132;
Best Local Similarity 96.7%; Pred. No. 0.0028;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatgtct 30
   |||||
DB 92 GGATTCACCTTCAGTACGTATGGCATGTCT 63

RESULT 15
AAF69109/c
ID AAF69109 standard; DNA; 132 BP.
XX
XX AC AAF69109;
XX
XX 12-APR-2001 (first entry)
XX
XX Human H chain V region PCR primer MBC1HGP2 SEQ ID NO:25.
DE
XX Human; mouse; parathyroid hormone-related peptide; PTHrP; vasopressin;
KW monoclonal antibody; antidiarrheic; antiemetic; antidiabetic;
KW antipyretic; cancer; dehydration; excessive urination; thirst;
KW vomiting; diarrhoea; fever; perspiration; diabetes; diabetes; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX WO200102010-A1.
XX
XX 11-JAN-2001.
XX
XX 03-JUL-2000; 2000WO-JP04413.
XX
XX 02-JUL-1999; 99JP-0189322.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Ogata E, Onuma E, Tsunenari T, Saito H, Azuma Y;
XX
XX WPI; 2001-112507/12.
XX
XX Inhibitor of parathyroid hormone related peptide binding to its
PT receptor can ameliorate symptoms caused by a decrease in vasopressin
PT level due to cancer
XX
XX Example 2; Page 71; 114pp; Japanese.
XX
```

SQ Sequence 132 BP; 31 A; 45 C; 34 G; 22 T; 0 other;

Qy 1 ggattcaccttcagtagctatgacatgtct 30  
|||  
Db 92 GGATTCACCTTCAGTAGCTATGGCATGTCT 63

Search completed: August 21, 2002, 10:08:24  
Job time: 10042 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 08:11:20 ; Search time 174.26 Seconds  
(without alignments)  
42.287 Million cell updates/sec

Title: US-09-339-922A-33  
Perfect score: 30  
Sequence: 1 gattacatttcagtagatgacatgtct 30

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26.8	89.3	354	5	PCT-US93-08435-9 Sequence 9, Appl
2	26.8	89.3	357	5	PCT-US94-07659-5 Sequence 5, Appl
3	26.8	89.3	519	1	US-08-339-582-1 Sequence 1, Appl
4	26.8	89.3	717	2	US-08-553-497A-17 Sequence 17, Appl
5	26.8	89.3	783	4	US-08-487-283A-19 Sequence 19, Appl
6	26.8	89.3	923	5	PCT-US94-07659-1 Sequence 1, Appl
7	25.4	84.7	335	5	US-08-477-553A-55 Sequence 55, Appl
8	25.4	84.7	342	2	US-08-477-553A-51 Sequence 51, Appl
9	25.4	84.7	378	4	US-09-240-274-94 Sequence 94, Appl
10	25.4	84.7	378	4	US-09-240-274-95 Sequence 95, Appl
11	25.4	84.7	378	4	US-09-240-274-192 Sequence 192, App
12	25.4	84.7	378	4	US-09-240-274-196 Sequence 196, App
13	25.4	84.7	453	3	US-08-724-752-12 Sequence 12, Appl
14	25.4	84.7	512	3	US-08-545-809A-30 Sequence 30, Appl
15	25.4	84.7	583	3	US-08-545-809A-33 Sequence 33, Appl
16	25.2	84.0	96	4	US-08-976-183A-52 Sequence 52, Appl
17	25.2	84.0	318	1	US-08-129-930B-94 Sequence 94, Appl
18	25.2	84.0	318	4	US-08-976-288A-94 Sequence 94, Appl
19	25.2	84.0	339	1	US-07-789-344A-9 Sequence 9, Appl
20	25.2	84.0	345	3	US-08-483-749A-5 Sequence 5, Appl
21	25.2	84.0	348	2	US-08-888-366-9 Sequence 9, Appl
22	25.2	84.0	354	4	US-08-487-761-14 Sequence 14, Appl
23	25.2	84.0	369	1	US-08-356-272-2 Sequence 2, Appl
24	25.2	84.0	394	4	US-08-134-346A-14 Sequence 14, Appl
25	25.2	84.0	405	4	US-08-579-378A-15 Sequence 15, Appl
26	25.2	84.0	405	4	US-08-579-378A-19 Sequence 19, Appl
27	25.2	84.0	413	1	US-08-253-877C-56 Sequence 56, Appl

Sequence 56, Appl  
Sequence 30, Appl  
Sequence 49, Appl  
Sequence 27, Appl  
Sequence 27, Appl  
Sequence 5, Appl  
Sequence 9, Appl  
Patent No. 5455030  
Sequence 3, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Patent No. 5455030  
Patent No. 5455030  
Sequence 3, Appl  
Patent No. 5455030

## ALIGNMENTS

RESULT 1  
PCT-US93-08435-9  
; Sequence 9, Application PC/TUS9308435  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham, Corporation  
; APPLICANT: U. S. Government, Secretary of  
; APPLICANT: the Navy  
; APPLICANT: U. S. Government, Secretary of  
; APPLICANT: the Army  
; TITLE OF INVENTION: Novel Antibodies for Conferring Passive  
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Box 457, 321 Norristown Road  
; CITY: Spring House  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08435  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/941,654  
; FILING DATE: 09-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: SBC P50107  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 540-9200  
; TELEFAX: (215) 540-5818  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 354 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..354  
PCT-US93-08435-9

Query Match 89.3%; Score 26.8; DB 5; Length 354;  
 Best Local Similarity 93.3%; Pred. No. 0.0015;  
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagcatgtct 30  
 ||||| ||||| ||||| ||||| |||||  
 Db 64 GGATTCACCTTCAGTAGCATGTCT 93

RESULT 2  
 PCT-US94-07659-5  
 ; Sequence 5, Application PC/TUS9407659  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Peter  
 ; APPLICANT: Gross, Mitchell  
 ; APPLICANT: Jonak, Zdenka L.  
 ; APPLICANT: Theisen, Timothy  
 ; APPLICANT: Hurle, Mark  
 ; APPLICANT: Jackson, Jeffrey R.  
 ; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta  
 ; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory  
 ; TITLE OF INVENTION: Disorders in Man  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporation - Corp.  
 ; ADDRESSEE: Intellectual Property  
 ; STREET: 709 Swedeland Road  
 ; CITY: King of Prussia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19406-2799  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/07659  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/090,534  
 ; FILING DATE: 09-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sutton, Jeffrey A.  
 ; REGISTRATION NUMBER: 34,028  
 ; REFERENCE/DOCKET NUMBER: P50171-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (610) 270-5024  
 ; TELEFAX: (610) 270-5090  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 357 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..357  
 PCT-US94-07659-5

Query Match 89.3%; Score 26.8; DB 5; Length 357;  
 Best Local Similarity 93.3%; Pred. No. 0.0015;  
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagcatgtct 30  
 ||||| ||||| ||||| ||||| |||||  
 Db 76 GGATTCACCTTCAGTAGCATGTCT 105

RESULT 3  
 US-08-339-582-1  
 ; Sequence 1, Application US/08339582  
 ; Patent No. 555852  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bigner, Darell D.  
 ; APPLICANT: Zalutsky, Michael R.  
 ; APPLICANT: Carrel, Stefan  
 ; TITLE OF INVENTION: METHOD OF TREATMENT  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kenneth D. Sibley  
 ; STREET: P.O. Drawer 34009  
 ; CITY: Charlotte  
 ; STATE: No. 555852th Carolina  
 ; COUNTRY: USA  
 ; ZIP: 28234  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/339,582  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/033,864  
 ; FILING DATE: 19-MAR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sibley, Kenneth D.  
 ; REGISTRATION NUMBER: 31,665  
 ; REFERENCE/DOCKET NUMBER: 5405-89  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 919-420-2200  
 ; TELEFAX: 919-881-3175  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 519 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 157..519  
 US-08-339-582-1

Query Match 89.3%; Score 26.8; DB 1; Length 519;  
 Best Local Similarity 93.3%; Pred. No. 0.0016;  
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagcatgtct 30  
 ||||| ||||| ||||| ||||| |||||  
 Db 244 GGATTCACCTTCAGTAGCATGTCT 273

RESULT 4  
 US-08-553-497A-17  
 ; Sequence 17, Application US/08553497A  
 ; Patent No. 584093  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KETLEBOROUGH, C. A.  
 ; APPLICANT: BENDIG, MARY M.  
 ; APPLICANT: ANSELL, KEITH H.  
 ; APPLICANT: GUSOW, DETLEF  
 ; APPLICANT: ADAN, JAUME  
 ; APPLICANT: MITJANS, FRANCES  
 ; APPLICANT: ROSELL, ELISABET  
 ; APPLICANT: BLASCO, FRANCES  
 ; APPLICANT: PIULATS, JAUME  
 ; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR

;; TITLE OF INVENTION: ANTIBODIES  
;; NUMBER OF SEQUENCES: 30  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTIGAN, P.C.  
;; STREET: 2200 CLARENDON BLVD. SUITE 1400  
;; CITY: ARLINGTON  
;; STATE: VA  
;; COUNTRY: US  
;; ZIP: 22201  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/553,497A  
;; FILING DATE: 17-NOV-1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/EP95/00978  
;; FILING DATE: 16-MAR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 94104160.0  
;; FILING DATE: 17-MAR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 94118970.6  
;; FILING DATE: 02-DEC-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: HAMLET-KING, DIANA  
;; REGISTRATION NUMBER: 33,302  
;; REFERENCE/DOCKET NUMBER: MERCK 1726  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-243-6333  
;; TELEFAX: 703-243-6410  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 717 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; HYPOTHEICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: N-terminal  
;; ORIGINAL SOURCE:  
;; ORGANISM: mouse  
;; STRAIN: Balb/c  
;; DEVELOPMENTAL STAGE: adult  
;; TISSUE TYPE: splenocytes  
;; IMMEDIATE SOURCE:  
;; CLONE: 4 B 2  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..717  
;;  
US-08-553-497A-17

Query Match 89.3%; Score 26.8; DB 2; Length 717;  
Best Local Similarity 93.3%; Pred. No. 0.0017;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30  
||||| ||||| ||||| ||||| |||||  
Db 76 GGATTCACCTTCAGTAGCTATGGCATGTCT 105

## RESULT 5

US-08-487-283A-19  
; Sequence 19, Application US/08487283A  
; Patent No. 6355245  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Mark J.  
; ADDRESSEE: Matis, Louis A.

;; APPLICANT: Mueller, Eileen Elliott  
;; APPLICANT: Nye, Steven H.  
;; APPLICANT: Rollins, Scott  
;; APPLICANT: Rother, Russell P.  
;; APPLICANT: Springhorn, Jeremy P.  
;; APPLICANT: Squinto, Stephen P.  
;; APPLICANT: Thomas, Thomas C.  
;; APPLICANT: Wilkins, James A.  
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT  
;; OF INFLAMMATORY DISEASES  
;; NUMBER OF SEQUENCES: 26  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Seth A. Fidel  
;; STREET: 25 Science Park (Alexion)  
;; CITY: New Haven  
;; STATE: Connecticut  
;; COUNTRY: USA  
;; ZIP: 06511  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch, 1.4mb storage  
;; COMPUTER: Macintosh Cetrus 610  
;; OPERATING SYSTEM: System 7  
;; SOFTWARE: WordPerfect 3.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/487,283A  
;; FILING DATE: June 7, 1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/236,208  
;; FILING DATE: 02-MAY-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seth A. Fidel  
;; REGISTRATION NUMBER: 38,449  
;; REFERENCE/DOCKET NUMBER: ALX-152.1 CIP  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (203)776-1790  
;; TELEFAX: (203)772-3655  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 783 base pairs  
;; TYPE: Nucleic Acid  
;; STRANDEDNESS: Double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: Other nucleic acid  
;; DESCRIPTION: N19/8 scFv (His Tagged)  
;;  
US-08-487-283A-19

Query Match 89.3%; Score 26.8; DB 4; Length 783;  
Best Local Similarity 93.3%; Pred. No. 0.0017;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ggattcaccttcagtagctatgacatgtct 30  
||||| ||||| ||||| ||||| |||||  
Db 466 GGATTCACCTTCAGTAGCTATTATATGTCT 495

## RESULT 6

PCT-US94-07659-1  
; Sequence 1, Application PC/TUS9407659  
; GENERAL INFORMATION:  
; APPLICANT: Young, Peter  
; APPLICANT: Gross, Mitchell  
; APPLICANT: Jonak, Zdenka L.  
; APPLICANT: Theisen, Timothy  
; APPLICANT: Hurle, Mark  
; APPLICANT: Jackson, Jeffrey R.  
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta  
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory  
; TITLE OF INVENTION: Disorders in Man  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation - Corp.  
; ADDRESSEE: Intellectual Property



STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07659  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/090,534  
FILING DATE: 09-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50171-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5024  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 923 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 169..909  
PCT-US94-07659-1

Query Match 89.3%; Score 26.8; DB 5; Length 923;  
Best Local Similarity 93.3%; Pred. No. 0.0018;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggattcccttcagtagcatgtct 30  
||||| | ||||| ||||| ||||| |||||

Db 301 GGATTCCTTCAGTAGCATGTCT 330

RESULT 7  
US-08-477-553A-55  
Sequence 55, Application US/08477553A  
Patent No. 5919910  
GENERAL INFORMATION:  
APPLICANT: HUGHES-JONES, Nevin C  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,553A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,034  
FILING DATE: 23-JUNE-1992

CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8925590.5  
FILING DATE: 13-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 007330-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..335  
OTHER INFORMATION: /note= "Nucleotides 1-375 corres.  
to nucleotides 24-359 of Fig. 14/14. Nucleotides  
1-23 and 360-375 represent PCR primers."  
US-08-477-553A-55

Query Match 84.7%; Score 25.4; DB 2; Length 335;  
Best Local Similarity 96.3%; Pred. No. 0.0063;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcccttcagtagcatgtcatg 27  
||||| | ||||| ||||| ||||| |||||

Db 52 GGATTCACCTTCAGTAGCTATGCGCATG 78

RESULT 8  
US-08-477-553A-51  
Sequence 51, Application US/08477553A  
Patent No. 5919910  
GENERAL INFORMATION:  
APPLICANT: HUGHES-JONES, Nevin C  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,553A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,034  
FILING DATE: 23-JUNE-1992  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8925590.5  
FILING DATE: 13-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 007330-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620

```
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..342
; OTHER INFORMATION: /note= "Nucleotides 1-381 corres.
; OTHER INFORMATION: to nucleotides 24-365 of Fig. 10/14. Nucleotides
; OTHER INFORMATION: 1-23 and 366-381 represent PCR primers."
US-08-477-553A-51

Query Match      84.7%; Score 25.4; DB 2; Length 342;
Best Local Similarity 96.3%; Pred. No. 0.0064;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
   |||||
DB 53 GGATTCACCTTCAGTAGCTATGGCATG 79

RESULT 9
US-09-240-274-94
; Sequence 94, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D30
US-09-240-274-94

Query Match      84.7%; Score 25.4; DB 4; Length 378;
Best Local Similarity 96.3%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
   |||||
DB 76 ggattcaccttcagtagctatggcatg 102

RESULT 10
US-09-240-274-95
; Sequence 95, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
```

```
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-95

Query Match      84.7%; Score 25.4; DB 4; Length 378;
Best Local Similarity 96.3%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
   |||||
DB 76 ggattcaccttcagtagctatggcatg 102

RESULT 11
US-09-240-274-192
; Sequence 192, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 192
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH39
US-09-240-274-192

Query Match      84.7%; Score 25.4; DB 4; Length 378;
Best Local Similarity 96.3%; Pred. No. 0.0065;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27
   |||||
DB 79 ggattcaccttcagtagctatggcatg 105

RESULT 12
US-09-240-274-196
; Sequence 196, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
```

NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 196  
LENGTH: 378  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH56  
US-09-240-274-196

Query Match 84.7%; Score 25.4; DB 4; Length 378;  
Best Local Similarity 96.3%; Pred. No. 0.0065;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27  
|||||  
Db 76 ggattcaccttcagtagctatgacatg 102

RESULT 13  
US-08-724-752-12  
Sequence 12, Application US/08724752  
Patent No. 6150584  
GENERAL INFORMATION:  
APPLICANT: Kucherlapati, Raju  
APPLICANT: Jakobovits, Aya  
APPLICANT: Brenner, Daniel G.  
APPLICANT: Capon, Daniel J.  
APPLICANT: Klapholz, Sue  
TITLE OF INVENTION: HUMAN ANTIBODIES DERIVED FROM IMMUNIZED  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,752  
FILING DATE: 02-DEC-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/05928  
FILING DATE: 29-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: Cell 4.17  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-724-752-12

Query Match 84.7%; Score 25.4; DB 3; Length 453;  
Best Local Similarity 96.3%; Pred. No. 0.0067;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27  
|||||  
Db 31 GGATTACCTTCAGTAGCTATGGCATG 57

RESULT 14  
US-08-545-809A-30  
Sequence 30, Application US/08545809A  
Patent No. 6096878  
GENERAL INFORMATION:  
APPLICANT: Honjo, Tasuku  
APPLICANT: Matsuda, Fumihiko  
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 512 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: human lymphoblast  
CELL LINE: CGM1  
US-08-545-809A-30

Query Match 84.7%; Score 25.4; DB 3; Length 512;  
Best Local Similarity 96.3%; Pred. No. 0.0059;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggattcaccttcagtagctatgacatg 27  
|||||  
Db 243 GGATTACCTTCAGTAGCTATGGCATG 269

RESULT 15  
US-08-545-809A-33  
Sequence 33, Application US/08545809A  
Patent No. 6096878  
GENERAL INFORMATION:  
APPLICANT: Honjo, Tasuku  
APPLICANT: Matsuda, Fumihiko  
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 512 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: human lymphoblast  
CELL LINE: CGM1  
US-08-545-809A-30

Query Match 84.7%; Score 25.4; DB 3; Length 512;  
Best Local Similarity 96.3%; Pred. No. 0.0059;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545.809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 583 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: human lymphoblast  
CELL LINE: CGM1  
US-08-545-809A-33

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|  
Db 254 GGATTACCTTCAGTAGCTATGGCATG 280

Search completed: August 21, 2002, 10:52:11  
Job time: 9651 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:48:56 ; Search time 2408.76 Seconds  
(without alignments)  
234.567 Million cell updates/sec

Title: US-09-339-922A-89  
Perfect score: 27  
Sequence: 1 caacagatggcagctggcctctgacg 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 ; Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vl.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	27	100.0	27	6	AX060868	AX060868 Sequence
2	25.4	94.1	27	6	AX060870	AX060870 Sequence
3	23.8	88.1	27	6	AX060824	AX060824 Sequence
4	23.8	88.1	57	6	AX060797	AX060797 Sequence
5	23.8	88.1	57	6	AX060806	AX060806 Sequence
6	23.8	88.1	321	6	AX060782	AX060782 Sequence
7	23.8	88.1	321	6	AX060786	AX060786 Sequence
8	23.8	88.1	321	6	AX060810	AX060810 Sequence
9	22.2	82.2	228	10	MDIGKVAV	Z22073 M.domesticu
10	22.2	82.2	236	10	MDIGKVAV	Z22072 M.domesticu
11	22.2	82.2	297	10	AF137617	AF137617 Mus muscu
12	22.2	82.2	306	10	MMVL3B6	X86546 M.musculus
13	22.2	82.2	317	10	MMIG1KL4	X02556 Mouse mRNa
14	22.2	82.2	321	10	AF163757	AF163757 Mus muscu
15	22.2	82.2	420	10	MUSIGKCKN	M16162 Mouse Ig ka
16	22.2	82.2	5238	6	A07699	A07699 Synthetic p
17	21.2	78.5	253	9	HS426269	AJ426269 Homo sapi
18	21.2	78.5	318	10	MMIGKVR4	X02234 Mouse mRNa
19	21.2	78.5	361	10	MMIGKBP5	X00652 Mouse DNA f
20	21.2	78.5	181088	2	AC097733	AC097733 Rattus no
21	20.8	77.0	101447	2	AC097994	AC097994 Rattus no
22	20.6	76.3	243	10	MMU19309	U19309 Mus musculu
23	20.6	76.3	300	10	MUSIGKABJ	M34528 Mouse Ig ka
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25	20.6	76.3	313	10	MUSIGVABW	L09021 Mus musculu
26	20.6	76.3	317	10	MMIG1KL3	X02555 Mouse mRNa
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31	20.6	76.3	324	10	AF087031	AF087031 Mus muscu
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35	20.6	76.3	324	10	AF139847	AF139847 Mus muscu
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42	20.6	76.3	582	10	MMU26998	U26998 Mus musculu
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44	20.2	74.8	52809	2	AC100034	AC100034 Mus muscu
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ALIGNMENTS

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DEFINITION	AX060868	Sequence	89	from Patent	WO0078815.	linear
ACCESSION	AX060868	Sequence	89	from Patent	WO0078815.	PAT 22-JAN-2001
VERSION	AX060868.1	GI:12406246				
KEYWORDS		synthetic construct.				
SOURCE		synthetic construct				
ORGANISM		artificial sequence.				
REFERENCE		1 (bases 1 to 27)				
AUTHORS		Huse,W.D. and Wu,H.				
TITLE		Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids				
JOURNAL		encoding same and methods of use				
FEATURES		Patent: WO 0078815-A 89 28-DEC-2000;				
source		Applied Molecular Evolution (US)				
		Location/Qualifiers				
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		/organism="synthetic construct"				
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Db 1 CAACAGAGTGGCAGCTGGCCTCAGC 27

RESULT 2
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DEFINITION Sequence 91 from Patent WO0078815.
ACCESSION AX060870
VERSION AX060870.1 GI:12406248
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial construct.
artificial sequence.
1 (bases 1 to 27)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 91 28-DEC-2000;
Applied Molecular Evolution (US)
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Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 caacagagtgccagctgacctgtgacg 27
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Db 1 CAACAGAGTGGCAGCTGGCCTCAGC 27

RESULT 3
AX060824 LOCUS AX060824 27 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 45 from Patent WO0078815.
ACCESSION AX060824
VERSION AX060824.1 GI:12406202
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 45 28-DEC-2000;
Applied Molecular Evolution (US)
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|||||
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DEFINITION Sequence 18 from Patent WO0078815.
ACCESSION AX060797
VERSION AX060797.1 GI:12406177
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial construct.
artificial sequence.
1 (bases 1 to 57)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 18 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
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Best Local Similarity 92.6%; Pred. No. 1.7;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 5
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DEFINITION Sequence 27 from Patent WO0078815.
ACCESSION AX060806
VERSION AX060806.1 GI:12406186
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial construct.
artificial sequence.
1 (bases 1 to 57)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 27 28-DEC-2000;
Applied Molecular Evolution (US)
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Applied Molecular Evolution (US)  
Location/Qualifiers  
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AX060782  
LOCUS AX060782 321 bp DNA linear PAT 22-JAN-2001  
DEFINITION Sequence 3 from Patent WO0078815.  
ACCESSION AX060782  
VERSION AX060782.1 GI:12406162  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequence.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Huse, W.D. and Wu, H.  
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
Patent: WO 0078815-A 3 28-DEC-2000;  
Applied Molecular Evolution (US)  
JOURNAL  
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BASE COUNT 78 a 93 c 79 g 71 t  
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Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27  
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DB 265 CAACAGAGTGGCAGCTGGCCTCACAG 291

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LOCUS AX060786 321 bp DNA linear PAT 22-JAN-2001  
DEFINITION Sequence 7 from Patent WO0078815.  
ACCESSION AX060786  
VERSION AX060786.1 GI:12406166  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 321)

Applied Molecular Evolution (US)  
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RESULT 6  
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DEFINITION Sequence 3 from Patent WO0078815.  
ACCESSION AX060782  
VERSION AX060782.1 GI:12406162  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequence.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Huse, W.D. and Wu, H.  
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
Patent: WO 0078815-A 3 28-DEC-2000;  
Applied Molecular Evolution (US)  
JOURNAL  
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BASE COUNT 78 a 93 c 79 g 71 t  
ORIGIN

Query Match 88.1%; Score 23.8; DB 6; Length 321;  
Best Local Similarity 92.6%; Pred. No. 1.4;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION Sequence 7 from Patent WO0078815.  
ACCESSION AX060786  
VERSION AX060786.1 GI:12406166  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 321)

Huse, W.D. and Wu, H.  
Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
Patent: WO 0078815-A 7 28-DEC-2000;  
Applied Molecular Evolution (US)  
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QY 1 caacagagtggcagctggcctctgacg 27  
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DB 265 CAACAGAGTGGCAGCTGGCCTCACAG 291

RESULT 8  
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LOCUS AX060810 321 bp DNA linear PAT 22-JAN-2001  
DEFINITION Sequence 31 from Patent WO0078815.  
ACCESSION AX060810  
VERSION AX060810.1 GI:12406189  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequence.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Huse, W.D. and Wu, H.  
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
Patent: WO 0078815-A 31 28-DEC-2000;  
Applied Molecular Evolution (US)  
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BASE COUNT 76 a 93 c 78 g 71 t 3 others  
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Best Local Similarity 92.6%; Pred. No. 1.4;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27  
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DB 265 CAACAGAGTGGCAGCTGGCCTCACAG 291

RESULT 9  
MDIGKVAW  
LOCUS MDIGKVAW 228 bp mRNA linear ROD 05-NOV-1994  
DEFINITION M.domesticus Igk variable region.  
ACCESSION Z22073  
VERSION Z22073.1 GI:297639  
KEYWORDS anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin.

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SOURCE      western European house mouse.
ORGANISM    Mus musculus domesticus
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE      1 (bases 1 to 228)
JOURNAL     Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.
MEDLINE    Both IgM and IgG anti-DNA antibodies are the products of clonally
REFERENCE   selective B cell stimulation in (NZB x NZW)F1 mice
AUTHORS    J. Exp. Med. 176 (3), 761-779 (1992)
TITLE      92381444
JOURNAL     2 (bases 1 to 228)
MEDLINE    Marion,T.N.
AUTHORS    Direct Submission
TITLE      Submitted (23-MAR-1993) Tony N. Marion, Microbiology and
JOURNAL     Immunology, University of, Tennessee, Memphis, 858 Madison Avenue,
            Memphis, TN, 38163, USA
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            /dev_stage="somatic variant"
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RESULT 10
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LOCUS M.domesticus Igk variable region.
ACCESSION 22072
VERSION 22072.1 GI:297637
KEYWORDS anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin.
SOURCE western European house mouse.
ORGANISM Mus musculus domesticus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 236)
JOURNAL Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.
MEDLINE Both IgM and IgG anti-DNA antibodies are the products of clonally
REFERENCE selective B cell stimulation in (NZB x NZW)F1 mice
AUTHORS J. Exp. Med. 176 (3), 761-779 (1992)
TITLE 92381444
JOURNAL 2 (bases 1 to 236)
MEDLINE Marion,T.N.
AUTHORS Direct Submission
TITLE Submitted (23-MAR-1993) Tony N. Marion, Microbiology and
JOURNAL Immunology, University of, Tennessee, Memphis, 858 Madison Avenue,
            Memphis, TN, 38163, USA
FEATURES    Location/Qualifiers
            1..236
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            /strain="(NZB x NZW)F1"
            /isolate="mouse #165"
            /db_xref="taxon:10092"
            /chromosome="6"
            /sex="Female"
            /cell_line="165.6"
            /cell_type="hybridoma"
            /tissue_type="spleen"
            /dev_stage="somatic variant"
            1..236
            /gene="Igk"
            <1..>236
            /gene="Igk"
            /function="kappa light chain variable region for anti-DNA
            antibody; Vκ23 family"
            /codon_start=1
            /product="immunoglobulin variable region"
            /protein_id="CAA80046.1"
            /db_xref="GI:297638"
            /translation="LATYTGINKNHSMLQGFSSMLPSPSLGSPPGSVAVDQGQISL
            SVSTVRLKILCEISVARVTAGLRVSVEAPSWSK"
BASE COUNT  68 a 57 c 53 g 58 t
ORIGIN
||||||| ||||||| |||
Query Match      82.2%; Score 22.2; DB 10; Length 236;
Best Local Similarity 88.9%; Pred. No. 8.2;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27
||||||| ||||||| |||
Db 180 CAACAGAGTAACAGCTGGCCTCAGCG 206

RESULT 11
AF137617 AF137617 297 bp mRNA linear ROD 03-JUN-1999
LOCUS Mus musculus clone 6C10F12 anti-fluorescein immunoglobulin light
ACCESSION chain mRNA, partial cds.
VERSION AF137617
KEYWORDS AF137617.1 GI:4972840
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 297)
JOURNAL van der Keyl,H., Gellad,Z.F. and Owen,J.A.
MEDLINE Disparity in the kinetics of onset of hypermutation in
REFERENCE immunoglobulin heavy and light chains
AUTHORS Unpublished
TITLE 2 (bases 1 to 297)
JOURNAL van der Keyl,H., Gellad,Z.F. and Owen,J.A.
AUTHORS Direct Submission
TITLE Submitted (25-MAR-1999) Biology, Haverford College, 370 Lancaster
JOURNAL Avenue, Haverford, PA 19041-1392, USA
FEATURES    Location/Qualifiers
            1..297
            /organism="Mus musculus"
            /strain="Balb/c"
            /db_xref="taxon:10090"
            /clone="6C10F12"
            /cell_type="hybridoma"
            <1..>297
            /note="from primary IgM antibody"
            /codon_start=1
            /product="anti-fluorescein immunoglobulin light chain"

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/protein_id="AAD34812.1"
/db_xref="GI:4972841"
/translation="QSPATLSVTPGDSVLSCRASQISNNLHWYQKSHSPRLLIK"
YASQISGIPSRFSGSGGDTLSINSVEXEDFGMYFCQDSNWPQTFFGGTKL"
BASE COUNT      76 a      69 g      72 t      2 others
ORIGIN

Query Match      82.2%; Score 22.2; DB 10; Length 297;
Best Local Similarity 88.9%; Pred. No. 8;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 caacagagtggcagctgcctctgacg 27
|||||  |||||  |||||  |||||  |||||
Db 250 CAACAGAGTAACAGCTGCCCTCAGC 276

RESULT 12
MMVL3E6
LOCUS      306 bp      mRNA      linear      ROD 26-JAN-1998
DEFINITION M.musculus mRNA for immunoglobulin light chain variable region
(VL3E6).
ACCESSION X86546
VERSION   X86546
KEYWORDS  immunoglobulin; immunoglobulin light chain; kappa chain; light
chain; variable region.
SOURCE    house mouse.
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 306)
AUTHORS  Cerato,E., Birkle,S., Portoukalian,J., Mezazigh,A., Chatal,J.F. and
Aubry,J.
TITLE     Variable region gene segments of nine monoclonal antibodies
specific to disialogangliosides (GD2, GD3) and their O-acetylated
derivatives
JOURNAL   Hybridoma 16 (4), 307-316 (1997)
MEDLINE   97455038
REFERENCE 2 (bases 1 to 306)
AUTHORS  Cerato,E.M.
TITLE     Direct Submission
JOURNAL   Submitted (24-APR-1995) E.M. Cerato, INSERM U211, Institut de
Biologie, 9 quai Moncousu, 44035 Nantes Cedex 01, FRANCE
FEATURES
source
1..306
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/chromosome="12"
/rearranged
/dev_stage="adult"
/tissue_type="spleen"
/cell_type="B cell hybridoma"
/cell_line="3E6 hybridoma"
V_region 16..306
/notes="anti-ganglioside GD3 immunoglobulin"
/product="immunoglobulin light chain variable region VL
3E6"
BASE COUNT      79 a      79 c      71 g      77 t
ORIGIN

Query Match      82.2%; Score 22.2; DB 10; Length 306;
Best Local Similarity 88.9%; Pred. No. 8;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 caacagagtggcagctgcctctgacg 27
|||||  |||||  |||||  |||||  |||||
Db 250 CAACAGAGTAACAGCTGCCCTCAGC 276

RESULT 13
MMIG1KL4

```

```

LOCUS      MMIG1KL4      317 bp      mRNA      linear      ROD 04-AUG-1992
DEFINITION Mouse mRNA fragment for Gl kappa immunoglobulin A 20/44 light chain
(V-J).
ACCESSION X02556
VERSION   X02556
KEYWORDS  Ig kappa light chain; immunoglobulin; joining region; variable
region.
SOURCE    house mouse.
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 317)
AUTHORS  Sablitzky,F. and Rajewsky,K.
TITLE     Molecular basis of an isogeneic anti-idiotypic response
JOURNAL   EMBO J. 3 (12), 3005-3012 (1984)
MEDLINE   85126904
FEATURES
Location/Qualifiers
1..317
/organism="Mus musculus"
/db_xref="taxon:10090"
misc_feature 1..285
/notes="V(K) region"
mRNA <1..>317
/notes="light chain fragment of A20/44"
misc_feature 286..317
/notes="J(K) region"
BASE COUNT      80 a      84 c      70 g      82 t      1 others
ORIGIN

Query Match      82.2%; Score 22.2; DB 10; Length 317;
Best Local Similarity 88.9%; Pred. No. 8;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 caacagagtggcagctgcctctgacg 27
|||||  |||||  |||||  |||||  |||||
Db 265 CAACAGAGTAACAGCTGCCCTCAGC 291

RESULT 14
AF163757
LOCUS      AF163757      321 bp      mRNA      linear      ROD 20-JUL-2001
DEFINITION Mus musculus mAb 101.4.1 immunoglobulin light chain variable region
mRNA, partial cds.
ACCESSION AF163757
VERSION   AF163757
KEYWORDS  house mouse.
SOURCE    house mouse.
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 321)
AUTHORS  Mertens,N.M., Galvin,J.E., Adderson,E.E. and Cunningham,M.W.
TITLE     Molecular analysis of cross-reactive anti-myoisin/anti-streptococcal
mouse monoclonal antibodies
JOURNAL   Mol. Immunol. 37 (15), 901-913 (2000)
MEDLINE   21179651
PUBMED    11282394
REFERENCE 2 (bases 1 to 321)
AUTHORS  Mertens,N.M. and Cunningham,M.W.
TITLE     Direct Submission
JOURNAL   Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma
University Health Sciences Center, 940 St. Young Blvd, Oklahoma
City, OK 73190, USA
FEATURES
Location/Qualifiers
1..321
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/notes="mAb 101.4.1"
<1..>321
/codon_start=1
CDS

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BASE COUNT83 a83 c73 g82 t

ORIGIN

/product="immunoglobulin light chain variable region"  
/protein\_id="AAD47036.1"  
/db\_xref="GI:5690321"  
/translation="DIVLTQSPATLSVTFPGDSVLSCSRASQISNNLHWYQQKSHESP  
RLIKYASQISGIPSFSGSGTDTLTLSINSVETEDFGMYFCQQSNSWPLTFGAGT  
KLELK"

Query Match82.2%; Score 22.2; DB 10; Length 321;  
Best Local Similarity88.9%; Pred. No. 8;  
Matches24; Conservative0; Mismatches3; Indels0; Gaps0;

QY1caacagagtggcagctggcctctgacg27  
||||||| ||||||| |||

Db265CAACAGAGTAACAGCTGGCCTCTCACG291

RESULT15

MUSIGKCKN420 bp mRNA linear ROD 27-APR-1993  
LOCUSMouse Ig kappa-chain mRNA VC-region (VJ5C) from hybridoma MAK33.  
DEFINITIONM16162  
ACCESSIONM16162  
VERSIONM16162.1 GI:196893  
KEYWORDSC-region; J-region; V-region; immunoglobulin kappa-chain;  
immunoglobulin light chain; processed gene.  
SOURCEMouse creatine kinase-specific monoclonal antibody producing  
hybridoma (MAK33), cDNA to mRNA.  
ORGANISMMus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE1 (bases 1 to 420)  
AUTHORSBuckel,P.; Huebner-Parajsz,C.; Mattes,R.; Lenz,H.; Haug,H. and  
Beaucamp,K.  
TITLECloning and nucleotide sequence of heavy- and light-chain cDNAs  
from a creatine-kinase-specific monoclonal antibody  
JOURNALGene 51, 13-19 (1987)  
MEDLINE87248058  
COMMENTDraft entry for [1] kindly provided by P.Buckel, 31-JUL-1987.  
FEATURES  
source  
1..420  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
sig\_peptide7..66  
CDS7..>420  
/note="Ig-kappa chain signal peptide"  
/note="Ig-kappa-chain (VJ5C) precursor"  
/codon\_start=1  
/protein\_id="AAA38823.1"  
/db\_xref="GI:196894"  
/translation="MVETPQILGLMFWISASRGDIVLTQSPATLSVTPRDSVSLSCR  
ASQSLSNLHWYQQKSHESPRLLIKYASQISGIPSFSGSGTDTLTLSINSVETED  
FGMYFCQQSNSWPLTFGAGTKLELKRAADAAPIVSIF"  
mat\_peptide67..>420  
/product="Ig-kappa chain"  
BASE COUNT105 a107 c93 g115 t  
ORIGINChromosome 6.

Query Match82.2%; Score 22.2; DB 10; Length 420;  
Best Local Similarity88.9%; Pred. No. 7.8;  
Matches24; Conservative0; Mismatches3; Indels0; Gaps0;

QY1caacagagtggcagctggcctctgacg27  
||||||| ||||||| |||

Db331CAACAGAGTAACAGCTGGCCTCTCACG357

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: August 21, 2002, 09:55:34 ; Search time 6260.2 seconds  
(without alignments)  
58.212 Million cell updates/sec

Title: US-09-339-922a-89  
Perfect score: 27  
Sequence: 1 caacagatggcagctgcctctgacg 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22.2	82.2	772	10	BI105452
2	22.2	82.2	833	10	BG966582
3	21.8	80.7	961	12	CNS031KL
4	20.6	76.3	835	10	BI083006
5	20.6	76.3	868	10	BG539952
6	20.6	76.3	874	10	BG539326
7	20.6	76.3	1138	10	BG536825
8	20.4	75.6	385	12	AZ311061
9	20.2	74.8	191	12	AZ309067
10	20.2	74.8	558	12	AZ304616
11	19.8	73.3	477	9	AW035934
12	19.8	73.3	611	12	AZ018356
13	19.8	73.3	662	10	BF232947
14	19.6	72.6	711	10	BG484755
15	19.6	72.6	1035	12	CNS054YD
16	19.6	72.6	1077	10	BF569518
17	19.4	71.9	846	10	BI555572
					BI555572 603239386
					BI105452 602891971
					BG966582 602834412
					AL223662 Tetraodon
					BI083006 602874524
					BG539952 602567464
					BG539326 602567937
					BG536825 602566362
					AZ311061 IM0026L13
					AZ309067 IM0012G13
					AZ304616 IM0004G13
					AW035934 EST282793
					AZ018356 RPCI-23-2
					BF232947 602023450
					BG484755 602505642
					AL321358 Tetraodon
					BF569518 602186012

18	19.2	71.1	234	9	AI103024
19	19.2	71.1	389	9	AW786966
20	19.2	71.1	389	9	AW786967
21	19.2	71.1	473	12	AQ633034
22	19.2	71.1	530	12	BH118115
23	19.2	71.1	645	12	AG059962
24	19.2	71.1	738	10	BF582153
25	19.2	71.1	791	9	AL576123
26	19	70.4	519	9	AW405183
27	19	70.4	600	10	BF031314
28	19	70.4	1043	10	BI869360
29	18.8	69.6	311	12	AZ902801
30	18.6	68.9	166	9	AA066242
31	18.6	68.9	166	9	AI614002
32	18.6	68.9	272	9	AW186570
33	18.6	68.9	331	9	AA062406
34	18.6	68.9	342	10	BG937558
35	18.6	68.9	362	10	T97665
36	18.6	68.9	383	9	AA118430
37	18.6	68.9	390	9	AA475298
38	18.6	68.9	396	9	AI036201
39	18.6	68.9	406	12	AQ174932
40	18.6	68.9	414	9	AI596454
41	18.6	68.9	414	9	AV664865
42	18.6	68.9	418	9	AA832758
43	18.6	68.9	434	9	AA238817
44	18.6	68.9	438	9	AV753666
45	18.6	68.9	449	12	AF046306

## ALIGNMENTS

## RESULT 1

BI105452  
LOCUS 602891971p1 NCI\_CGAP\_Lu29 Mus musculus cdna clone IMAGE:5037137 5',  
DEFINITION mRNA sequence.  
ACCESSION BI105452  
VERSION BI105452.1 GI:14556345  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 772)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1102 row: n column: 18  
High quality sequence stop: 771.  
Location/Qualifiers  
1..772

## FEATURES source

/organism="Mus musculus"  
/strain="C57BL/6J (fetal)"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5037137"  
/clone\_lib="NCI\_CGAP\_Lu29"  
/tissue\_type="spontaneous tumor, metastatic to mammary.  
stem cell origin."  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site: 1; SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator

```

BASE COUNT      214 a 208 c 173 g 177 t
ORIGIN
    providing samples: Gilbert Smith, NIH"

Query Match      82.2%; Score 22.2; DB 10; Length 772;
Best Local Similarity 88.9%; Pred. No. 38;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27
    ||||| ||||| ||||| ||||| |||||
Db 330 CAACAGAGTAACAGCTGGCGCTCGGACG 356.

RESULT 2
LOCUS      BG966582      833 bp mRNA linear EST 12-JUN-2001
DEFINITION 602834412F1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4988955 5',
    mRNA sequence.
ACCESSION  BG966582
VERSION     BG966582.1 GI:14354219
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 833)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-remail.nih.gov
    Tissue Procurement: Jeffrey E. Green, M.D.
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLAM1002 row: g column: 04
    High quality sequence stop: 830.
FEATURES   Location/Qualifiers
    source          1..833
    /organism="Mus musculus"
    /strain="FVB/N"
    /db_xref="taxon:10090"
    /clone_lib="NCI_CGAP_C024"
    /lab_host="DH10B (T1 phage-resistant)"
    /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
    Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
    Average insert size 1.6 kb. Constructed by Life
    Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      227 a 227 c 186 g 193 t
ORIGIN
    providing samples: Gilbert Smith, NIH"

Query Match      82.2%; Score 22.2; DB 10; Length 833;
Best Local Similarity 88.9%; Pred. No. 39;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27
    ||||| ||||| ||||| ||||| |||||
Db 329 CAACAGAGTGACAGCTGGCGCGCTCAGC 355.

RESULT 3
LOCUS      CNS031KL      961 bp DNA linear GSS 15-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
    205K05 of library G from Tetraodon nigroviridis, genomic survey
    sequence.
ACCESSION  AL223662

```

---

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VERSION      AL223662.1 GI:7882493
KEYWORDS     GSS; genome survey sequence.
SOURCE       Tetraodon nigroviridis.
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
    Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
    Tetraodontidae; Tetraodon.
REFERENCE    1 (bases 1 to 961)
AUTHORS     Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
    Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
    Weissenbach,J.
TITLE       Characterization and repeat analysis of the compact genome of the
    freshwater pufferfish Tetraodon nigroviridis
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 961)
AUTHORS     Roest-Crollius H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
    Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
    Saurin,W. and Weissenbach,J.
TITLE       Human gene number estimate provided by genome wide analysis using
    Tetraodon nigroviridis DNA sequence
JOURNAL      Unpublished
REFERENCE    3 (bases 1 to 961)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL      Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
    scale clone-end sequencing project of the Tetraodon nigroviridis
    genome. For more information, please take a look at
    http://www.genoscope.cns.fr/tetraodon.
FEATURES     Location/Qualifiers
    source          1..961
    /organism="Tetraodon nigroviridis"
    /db_xref="taxon:99883"
    /clone="205K05"
    /notes_lib="G"
    /note="Genoscope sequence ID : COAG205AF03SP1-end :
    PUC-Ori"
BASE COUNT    230 a 204 c 241 g 284 t 284 t 2 others
ORIGIN
    Query Match      80.7%; Score 21.8; DB 12; Length 961;
    Best Local Similarity 92.0%; Pred. No. 61;
    Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctga 25
    ||||| ||||| ||||| ||||| |||||
Db 515 CAACAGAGTGGCAGCTACCCCTCGA 539

RESULT 4
LOCUS      BI083006      835 bp mRNA linear EST 20-JUN-2001
DEFINITION 602874524F2 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5006453 5',
    mRNA sequence.
ACCESSION  BI083006
VERSION     BI083006.1 GI:14501336
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 835)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-remail.nih.gov
    Tissue Procurement: Gilbert Smith, Ph.D.
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLAM11047 row: p column: 06  
 High quality sequence row: 769.

FEATURES  
SOURCE

```

BASE COUNT
ORIGIN
225 a      229 c      186 g      195 t
Location/Qualifiers
1. 835
/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone_image="IMAGE:5006453"
/clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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Query Match	76.3%	Score 20.6;	DB 10;	Length 835;
Best Local Similarity	85.3%;	Pred. No.	1.8e+02;	
Matches 23;	Conservative	0;	Mismatches 4;	Indels 0; Gaps 0;
OY	1	cacagagtggcagctggccctcgacg	27	
Dd	343	CACAGAGTAACAGCTGGCGGCTCAGC	369	

RESULT	5
GC339952	
LOCUS	868 bp. mRNA linear EST 03-APR-2001
DEFINITION	G025674.64F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4692326 5', mRNA sequence.
ACCESSION	BC539952
VERSION	BC539952.1 GI:13532185
KEYWORDS	EST.
SOURCE	human.

SOURCE: Homo sapiens  
ORGANISM: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE: 1 (bases 1 to 868)  
AUTHORS: NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE: National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL: Unpublished (1999)  
COMMENT: Contact: Robert Strausberg, Ph.D.

Contact: Robert B. Edwards, Jr., Ph.D.  
 Email: rgeb@u.washington.edu  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: L1CM1512 row: 0 column: 15  
 High quality sequence stop: 707.

```

FEATURES
source
      1. .868
      Location/Qualifiers
        organism="Homo sapiens"
        db_xref="taxon:9606"
        clone="IMAGE:4692326"
        clone_lib="NIH_MGC_77"
        lab_host="DH10B (T1 phage-resistant)"
        note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1:
              SfiI (ggcgctgcgc); Site:2: SfiI (ggccattatgcgc); 5' and
              3' adaptors used in cloning as follows: 5' adaptor
              sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
              5'-ATTCTAGAGCCGACGGCGGCACATG-DT(30)BN-3' (where B = A,
              C, or G and N = A, C, G, or T). Average insert size 1.9
              kb (range 0.5-4.0 kb). 12/15 colonies contained inserts

```

by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

BASE COUNT	218 a	247 c	222 g	181 t
ORIGIN				

```
Query Match          76.3% Score 20.6 DB 10 Length 868;
Best Local Similarity 85.2%; Pred. No. 1.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0 Gaps 0;
```

---

```
QY      1 caacagagtggcagctgacctgtgacy 27  
        ||| |||| | |||| |||||  
Db     359 CAGCAGCGCTGGCACGTGCCCTCCGAGG 385
```

RESULT	6
BG539326	
LOCUS	874 bp mRNA linear EST 03-APR-2001
DEFINITION	G02567937F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4692361 5', mRNA sequence.
ACCESSION	BG539326
VERSION	BG539326
KEYWORDS	BG539326.1 GI:13531559
SOURCE	EST.
	human.

ORGANISM	<p>Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 (bases 1 to 874)</p>
REFERENCE	<p>NIH-MGC <a href="http://mgc.ncbi.nlm.nih.gov/">http://mgc.ncbi.nlm.nih.gov/</a>.</p>
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	Unpublished (1999)
JOURNAL	
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: [cqabps-r@mail.nih.gov](mailto:cqabps-r@mail.nih.gov)  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCMI513 row: 1 column: 10  
High quality sequence stop: 588.

```

FEATURES                                source
Location/Qualifiers
1. .874
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4692561"
/clonelib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggcgctctggccc); Site_2: SfiI (ggcgattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
211 a 270 c 213 g 180 t

```

Query Match	76.3%	Score 20.6;	'DB 10;	Length 874;
Best Local Similarity	85.2%;	Pred. No. 1.9e+02;		
Matches 23;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	1	caacagagtggcgactgacctgcagc	27	
DG	358	CAGCAGCGTGGCAGCTGCCTCCGAGG	384	

[illegible]

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dduan@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0004 row: G column: 13  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 558.

JRES  
source

source

BASE COUNT  
ORIGIN

Query Match  
Best Local  
Matches

QY	2	88
Db	1	88

RESULT 11  
AW035934/C  
LOCUS  
DEFINITION  
  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

SOURCE  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

## Lycopersicon.

REFERENCE 1 (bases 1 to 477)  
 AUTHORS Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D., and Giovannoni, J.  
 TITLE Generation of ESTs from tomato callus tissue  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: CUGI  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.

## FEATURES

source

1. .477  
 Location/Qualifiers  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="cLEG37J24"  
 /tissue\_type="callus"  
 /dev\_stage="25-40 days old"  
 /lab\_host="X11-Blue MRP"  
 /note="Vector: pBlueScript SK(-); Site\_1: EcoRI; Site\_2: XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"

BASE COUNT 134 a 97 c 105 g 141 t  
 ORIGIN

Query Match 73.3%; Score 19.8; DB 9; Length 477;  
 Best Local Similarity 91.3%; Pred. No. 3.2e+02;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 aacagagtgcagctggcctctg 24

|||||  
 Db 291 AACAGAGTGGCAGGACCTCTG 269

## RESULT 12

AZ018356  
 LOCUS AZ018356 611 bp DNA linear GSS 25-FEB-2000  
 DEFINITION RPCI-23-298M6.TJ RPCI-23 Mus musculus genomic clone RPCI-23-298M6, DNA sequence.  
 ACCESSION AZ018356  
 VERSION AZ018356.1 GI:7093740  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 611)  
 AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.  
 TITLE Mouse BAC End Sequences from Library RPCI-23

## JOURNAL

COMMENT Unpublished (1999)  
 Other\_GSSs: RPCI-23-298M6.TV  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: [szhao@tigr.org](mailto:szhao@tigr.org)  
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong ([pieterdejong.med.buffalo.edu](mailto:pieterdejong.med.buffalo.edu)). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC end page:

[http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
 Plate: 298 row: M column: 6  
 Seq primer: SP6  
 Class: BAC ends.

## FEATURES

source

Location/Qualifiers  
 1. .611  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-298M6"  
 /clone\_lib="RPCI-23"  
 /sex="Female"  
 /lab\_host="DHI0B"  
 /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DHI0B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 158 a 98 c 141 g 214 t  
 ORIGIN

Query Match 73.3%; Score 19.8; DB 12; Length 611;  
 Best Local Similarity 91.3%; Pred. No. 3.5e+02;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 acagagtgcagctggcctctga 25

|||||  
 Db 431 AGACAGTGGCAGCTGGCCTCTGA 453

## RESULT 13

BF232947  
 LOCUS BF232947 662 bp mRNA linear EST 14-NOV-2000  
 DEFINITION 602023450F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:4158685 5', mRNA sequence.  
 ACCESSION BF232947  
 VERSION BF232947.1 GI:11142629  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 662)  
 REFERENCE 1 (bases 1 to 662)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution by: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM9435 row: d column: 14  
 High quality sequence start: 2  
 High quality sequence stop: 650.

## FEATURES

source

Location/Qualifiers  
 1. 662  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4158685"  
 /clone\_lib="NCI\_CGAP\_L19"  
 /lab\_host="DHI0B (T1 phage-resistant)"  
 /note="Organ: liver; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."



BASE COUNT 139 a 143 c 209 g 171 t

ORIGIN

Query Match 73.3%; Score 19.8; DB 10; Length 662;  
Best Local Similarity 91.3%; Pred. No. 3.6e+02;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 cagagtggtggcagctggtcctgac 26

||||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 349 CAGGGTCCAGCTGGCCTCTGAC 371

RESULT 14

LOCUS BG484755

DEFINITION BG484755 711 bp mRNA linear EST 21-MAR-2001  
602505642F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4619074 5',  
mRNA sequence.

ACCESSION BG484755

VERSION BG484755.1 GI:13417034

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 711)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CMI378 row: c column: 11

High quality sequence stop: 564.

Location/Qualifiers

FEATURES

source

1. .711

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4619074"

/lab\_host="NIH\_MGC\_77"

/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site.1:

SfiI (ggcgctcgcc); Site.2: SfiI (ggcattatggcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CAGCGCCATATGGCC-3' and 3' adaptor sequence:

5'-ATTCTAGAGCGGCGGCGGCGCATG-dt(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.9

kb (range 0.5-4.0 kb). 12/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH\_MGC Library."

BASE COUNT 177 a 206 c 192 g 136 t

ORIGIN

Query Match 72.6%; Score 19.6; DB 10; Length 711;  
Best Local Similarity 84.6%; Pred. No. 4.5e+02;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgac 26

||||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 310 CAGCAGCGTCGAGCTGGCCTCTCAC 335

RESULT 15

LOCUS CNS054YD/c

CNS054YD

1035 bp DNA linear GSS 26-JUL-2000

DEFINITION

Tetraodon nigroviridis genome survey sequence T7 end of clone  
041J22 of library A from Tetraodon nigroviridis, genomic survey  
sequence.

ACCESSION AL321358

VERSION AL321358.1 GI:9554242

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis.

ORGANISM

Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 1035)

AUTHORS

Roest Crollius,H., Jaillon,O., Dasilva,C., Bounneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.

TITLE Estimate of human gene number provided by genome-wide analysis

using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL 20296633

MEDLINE 2 (bases 1 to 1035)

AUTHORS

Crollius,H.R., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C.,  
Fischer,C., Bounneau,L., Billault,A., Quetier,F., Saurin,W.,  
Bernot,A. and Weissenbach,J.

TITLE Characterization and repeat analysis of the compact genome of the

freshwater pufferfish tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

JOURNAL 20359837

MEDLINE 3 (bases 1 to 1035)

AUTHORS

Genoscope.

TITLE Direct Submission

Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at

<http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source

1. .1035

/organism="Tetraodon nigroviridis"

/db\_xref="taxon:99883"

/clone="041J22"

/clone\_lib="A"

/notes="Genoscope sequence ID : COM0041DE11C1-end : T7"

BASE COUNT 247 a 266 c 241 g 228 t

ORIGIN

Query Match 72.6%; Score 19.6; DB 12; Length 1035;

Best Local Similarity 84.6%; Pred. No. 5.3e+02;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgac 26

||||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 420 CAACAGAGTGGCAGTTGGCTCGGCC 395

Search completed: August 21, 2002, 09:55:42

Job time: 9305 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:24 ; Search time 754.01 Seconds  
(without alignments)  
61.480 Million cell updates/sec

Title: US-09-339-922a-89  
Perfect score: 27  
Sequence: 1 caacagagtggcagctgcctctgacg 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_032802.\*  
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	19	AAV49872
2	27	100.0	27	22	AAV28228
3	25.4	94.1	27	19	AAV49873
4	25.4	94.1	27	22	AAV28229
5	23.8	88.1	27	19	AAV49850
6	23.8	88.1	27	22	AAV28206
7	23.8	88.1	57	19	AAV49842
8	23.8	88.1	57	19	AAV49833
9	23.8	88.1	57	22	AAH74636

10	23.8	88.1	57	22	AAF28188	Oligonucleotide #1
11	23.8	88.1	57	22	AAF28197	Grafted light chain
12	23.8	88.1	321	19	AAV49843	LM609 antibody lig
13	23.8	88.1	321	19	AAV49821	Vitaxin antibody l
14	23.8	88.1	321	19	AAV49823	LM609 antibody lig
15	23.8	88.1	321	22	AAH74624	DNA encoding light
16	23.8	88.1	321	22	AAH74626	DNA encoding light
17	23.8	88.1	321	22	AAF28176	Vitaxin light chain
18	23.8	88.1	321	22	AAF28178	Antibody LM609 lig
19	23.8	88.1	321	22	AAF28199	DNA encoding light
20	22.2	82.2	5238	11	AAQ04654	Plasmid pBT111 enc
21	20.6	76.3	69	20	AAV59221	PCR primer CR510 u
22	20.6	76.3	72	20	AAV59220	PCR primer CR508 u
23	20.6	76.3	73	20	AAV59218	PCR primer CR503 u
24	20.6	76.3	98	20	AAV71819	Alpha-v beta-3 MAB
25	20.6	76.3	321	20	AAV71800	Humanised anti-alp
26	20.6	76.3	324	20	AAV71798	Murine vitronectin
27	20.6	76.3	338	20	AAV71802	Vitronectin alpha-
28	20.6	76.3	381	15	AAQ64167	Sequence of mouse
29	20.6	76.3	381	21	AAZ35242	Mouse anti-verotox
30	20.6	76.3	381	21	AAZ35244	Humanised anti-ver
c 31	19.2	71.1	276	22	ABA53976	Human foetal liver
c 32	19.2	71.1	276	22	ABA23726	Probe #2192 for ge
c 33	19.2	71.1	276	22	AAK02242	Human brain expres
c 34	19.2	71.1	276	22	AAK27692	Human bone marrow
c 35	19.2	71.1	276	22	AAI33626	Probe #2312 used t
c 36	19.2	71.1	276	22	AAI02187	Probe #2178 used t
c 37	19.2	71.1	424	22	ABA44443	Human breast cell
c 38	19.2	71.1	424	22	ABA54890	Human foetal liver
c 39	19.2	71.1	424	22	ABA24656	Probe #3122 for ge
c 40	19.2	71.1	424	22	AAK03166	Human brain expres
c 41	19.2	71.1	424	22	AAK28616	Human bone marrow
c 42	19.2	71.1	424	22	AAI13190	Probe #3123 for ge
c 43	19.2	71.1	424	22	AAI34542	Probe #3228 used t
c 44	19.2	71.1	424	22	AAI03095	Probe #3086 used t
c 45	19.2	71.1	566	22	ABA66550	Human foetal liver

#### ALIGNMENTS

RESULT 1

AAV49872  
ID AAV49872 standard; DNA; 27 BP.

XX AAV49872;

XX AAV49872;

DT 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-L region CDR3 DNA fragment #4.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;  
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
XX macular degeneration; osteoporosis; primer; V-L region; CDR;  
XX complementarity determining region; ss.

OS Mus sp.

XX WO9833919-A2.

PN PD

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSV-) IXSVS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR P-PSDB; AAW76035.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

XX Disclosure; Page 42; 129pp; English.

PS

XX AAV49844-V49877 are nucleotide fragments of the grafted monoclonal

CC antibody LM609 heavy and light chain variable region. LM609 and the

CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used

CC to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX

SQ Sequence 27 BP; 6 A; 8 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 27; DB 19; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.014; 0; Mismatches 0; Gaps 0;

Matches 27; Conservative 0;

QY 1 caacagagtggcagctggcctctgacg 27

|||||

Db 1 caacagagtggcagctggcctctgacg 27

|||||

RESULT 2

AAAF28228

ID AAF28228 standard; DNA; 27 BP.

XX

AC AAF28228;

DT 03-APR-2001 (first entry)

XX

DE DNA encoding mutant VL CDR3 peptide #3.

XX

XX LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX

XX Unidentified.

OS

PN WO200078815-A1.

XX

XX 28-DEC-2000.

XX

XX 23-JUN-2000; 2000WO-US17454.

PF

XX

XX 24-JUN-1999; 99US-0339922.

PR

XX

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA

XX

PI Huse WD, Wu H;

XX

XX WPI; 2001-050110/06.

XX

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX

XX Claim 16; Page 42; 132pp; English.

PS

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta\_3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

SQ Sequence 27 BP; 6 A; 8 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 27; DB 22; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.014; 0; Mismatches 0; Gaps 0;

Matches 27; Conservative 0;

QY 1 caacagagtggcagctggcctctgacg 27

|||||

Db 1 caacagagtggcagctggcctctgacg 27

|||||

RESULT 3

AAV49873

ID AAV49873 standard; DNA; 27 BP.

XX

AC AAV49873;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody V-L region CDR3 DNA fragment #5.

XX

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-L region; CDR;

KW complementarity determining region; ss.

XX

OS Mus sp.

XX

XX WO9833919-A2.

PN

XX

XX 06-AUG-1998.

PD

XX

XX 30-JAN-1998; 98WO-US01826.

PF

XX

XX 30-JAN-1997; 97US-0791391.

PR

XX

XX (IXSY-) IXSYS INC.

PA

XX

XX Glaser SM, Huse WD;

PI

XX

XX WPI; 1998-437472/37.

DR

XX

XX P-PSDB; AAW76036.

DR

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

XX Disclosure; Page 42; 129pp; English.

PS

XX AAV49844-V49877 are nucleotide fragments of the grafted monoclonal

CC antibody LM609 heavy and light chain variable region. LM609 and the

CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used

CC to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX

CC greater than that of parent the parent antibody.  
 XX  
 SQ Sequence 27 BP; 7 A; 8 C; 9 G; 3 T; 0 other;

Query Match 94.1%; Score 25.4; DB 19; Length 27;  
 Best Local Similarity 96.3%; Pred. No. 0.067;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27  
 |||||  
 Db 1 caacagagtggcagctggcctctgacg 27

## RESULT 4

AAAF28229  
 ID AAF28229 standard; DNA; 27 BP.

XX AC AAF28229;

XX DT 03-APR-2001 (first entry)

XX DE DNA encoding mutant VL CDR3 peptide #4.

XX KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 XX KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX PS WPI; 2001-050110/06.

XX CC Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 XX CC to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 XX CC angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 XX CC osteoporosis -

XX PS Disclosure; Page 42; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies  
 XX CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 XX CC their functional fragments. The antibodies or their functional  
 XX CC fragments can be used in the diagnosis and treatment of  
 XX CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 XX CC diseases (such as psoriasis and chronic articular rheumatism),  
 XX CC disorders associated with inappropriate or inopportune invasion of  
 XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 XX CC diseases (such as macular degeneration), restenosis and  
 XX CC osteoporosis.

XX SQ Sequence 27 BP; 7 A; 8 C; 9 G; 3 T; 0 other;

Query Match 94.1%; Score 25.4; DB 22; Length 27;  
 Best Local Similarity 96.3%; Pred. No. 0.067;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27  
 |||||  
 Db 1 caacagagtggcagctggcctctgacg 27

## RESULT 5

AAV49850

ID AAV49850 standard; DNA; 27 BP.

XX AC AAV49850;

XX DT 02-NOV-1998 (first entry)

XX DE LM609 grafted antibody V-L region CDR2 DNA fragment #1.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 XX KW macular degeneration; osteoporosis; primer; V-L region; CDR;  
 XX KW complementarity determining region; ss.

XX OS Mus sp.

XX PN WO9833919-A2.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US01826.

XX PR 30-JAN-1997; 97US-0791391.

XX PA (IXSY-) IXSYS INC.

XX PI Glaser SM, Huse WD;

XX XX WPI; 1998-437472/37.

XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 XX PT integrin - and related antibodies based on murine monoclonal  
 XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 XX PT angiogenesis or restenosis

XX PS Disclosure; Page 40; 129pp; English.

XX CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal  
 XX CC antibody LM609 heavy and light chain variable region. LM609 and the  
 XX CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used  
 XX CC to inhibit binding of alphavbeta3 to a ligand and thus block  
 XX CC integrin-mediated signal transduction. This is useful in the treatment,  
 XX CC prevention and diagnosis of alphavbeta3-mediated disease, specifically  
 XX CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
 XX CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
 XX CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
 XX CC antibodies contain non-murine framework regions so are suitable for use  
 XX CC in humans. Enhanced types of LM609 have affinity more than 90 times  
 XX CC greater than that of parent the parent antibody.

XX SQ Sequence 27 BP; 7 A; 9 C; 8 G; 3 T; 0 other;

Query Match 88.1%; Score 23.8; DB 19; Length 27;  
 Best Local Similarity 92.6%; Pred. No. 0.33;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27  
 |||||  
 Db 1 caacagagtggcagctggcctctgacg 27

## RESULT 6

AAF28206

ID AAF28206 standard; DNA; 27 BP.

XX AC AAF28206;

XX DT 03-APR-2001 (first entry)

XX DNA encoding LM609 VL CDR3 peptide.  
 DE LM609; grafted antibody; alphaVbeta<sub>3</sub> integrin; angiogenesis;  
 XX inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
 KW Unidentified.  
 OS WO200078815-A1.  
 XX 28-DEC-2000.  
 PN 23-JUN-2000; 2000WO-US17454.  
 XX 24-JUN-1999; 99US-0339922.  
 PF (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX Huse WD, Wu H;  
 PI WPI; 2001-050110/06.  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 CC to alpha(V)beta<sub>3</sub> integrin, useful in the diagnosis and treatment of  
 CC angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 CC osteoporosis -  
 XX Disclosure; Page 40; 132pp; English.  
 PS The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX Sequence 27 BP; 7 A; 9 C; 8 G; 3 T; 0 other;  
 SQ

Query Match 88.1%; Score 23.8; DB 22; Length 27;  
 Best Local Similarity 92.6%; Pred. No. 0.33;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 caacagagtggcagctggcctctgacg 27  
 Db 1 caacagagtggcagctggcctctgacg 27  
 |||||

RESULT 7  
 AAV49842  
 ID AAV49842 standard; DNA; 57 BP.  
 XX AAV49842;  
 AC  
 XX 02-NOV-1998 (first entry)  
 DT LM609 grafted antibody light chain variable region oligonucleotide #5.  
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 XX LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; primer; ss.  
 XX Synthetic.  
 OS Mus sp.  
 XX WO9833919-A2.  
 PN

XX 06-AUG-1998.  
 PD 30-JAN-1998; 98WO-US01826.  
 XX 30-JAN-1997; 97US-0791391.  
 PR (IXSY-) IXSYS INC.  
 XX Glaser SM, Huse WD;  
 XX WPI; 1998-437472/37.  
 DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta<sub>3</sub>  
 XX integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX Example 5; Page 80; 129pp; English.  
 PS AAV49838-V49842 are oligonucleotides used in the construction of grafted  
 XX LM609 monoclonal antibody light chain variable regions. LM609 and the  
 CC antibody vitaxin bind selectively to integrin alphaVbeta<sub>3</sub> and can be  
 CC used to inhibit binding of alphaVbeta<sub>3</sub> to a ligand and thus block  
 CC integrin-mediated signal transduction. This is useful in the treatment,  
 CC prevention and diagnosis of alphaVbeta<sub>3</sub>-mediated disease, specifically  
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
 CC antibodies contain non-murine framework regions so are suitable for use  
 CC in humans. Enhanced types of LM609 have affinity more than 90 times  
 CC greater than that of parent the parent antibody.  
 XX Sequence 57 BP; 16 A; 12 C; 21 G; 8 T; 0 other;  
 SQ

Query Match 88.1%; Score 23.8; DB 19; Length 57;  
 Best Local Similarity 92.6%; Pred. No. 0.37;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 caacagagtggcagctggcctctgacg 27  
 Db 1 caacagagtggcagctggcctctgacg 27  
 |||||

RESULT 8  
 AAV49833  
 ID AAV49833 standard; DNA; 57 BP.  
 XX AAV49833;  
 AC  
 XX 02-NOV-1998 (first entry)  
 DT LM609 grafted antibody variable region oligonucleotide #10.  
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 XX LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; primer; ss.  
 XX Synthetic.  
 OS Mus sp.  
 XX WO9833919-A2.  
 PN 06-AUG-1998.  
 PD 30-JAN-1998; 98WO-US01826.  
 PF 30-JAN-1997; 97US-0791391.  
 PR (IXSY-) IXSYS INC.  
 XX

XX PI Glaser SM, Huse WD;  
 XX WPI; 1998-437472/37.  
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX Example 2; Page 65; 129pp; English.  
 XX AAV49824-V49833 are oligonucleotides used in the construction of grafted  
 CC LM609 monoclonal antibody heavy and light chain variable regions. LM609  
 CC and the antibody vitaxin bind selectively to integrin alphavbeta3 and  
 CC can be used to inhibit binding of alphavbeta3 to a ligand and thus block  
 CC integrin-mediated signal transduction. This is useful in the treatment,  
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,  
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
 CC antibodies contain non-murine framework regions so are suitable for use  
 CC in humans. Enhanced types of LM609 have affinity more than 90 times  
 CC greater than that of parent the parent antibody.  
 XX Sequence 57 BP; 16 A; 12 C; 21 G; 8 T; 0 other;  
 SQ

Query Match 88.1%; Score 23.8; DB 19; Length 57;  
 Best Local Similarity 92.6%; Pred. No. 0.37;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtgccagctggcctctgacg 27  
 |||||  
 Db 1 caacagagtgccagctggcctcacag 27

RESULT 9  
 AAH74636  
 ID AAH74636 standard; DNA; 57 BP.  
 XX AC  
 XX AAH74636;  
 XX 15-OCT-2001 (first entry)  
 XX PCR primer for light chain variable region of LM609 antibody.  
 DE Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer; PCR primer; ss.  
 XX Mus sp.  
 XX OS  
 XX US2001011125-A1.  
 XX PN  
 XX 02-AUG-2001.  
 XX 30-JAN-1997; 97US-0790540.  
 XX PF  
 XX 30-JAN-1997; 97US-0790540.  
 XX PR  
 XX (HUSE/) HUSE W D.  
 XX PA  
 XX Huse WD;  
 XX PI  
 XX WPI; 2001-496171/54.  
 XX New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer -  
 XX

PS Example 2; Page 17; 25pp; English.  
 XX PCR primers AAH74632-36 were used to amplify DNA encoding fragments  
 CC of the light chain variable region of the monoclonal antibody LM609.  
 CC LM609 is a murine antibody which specifically recognises the integrin  
 CC alphavbeta3, and inhibits its functional activity. The specification  
 CC describes a LM609 grafted antibody which has the complementarity  
 CC determining regions (CDRs) substituted into a non-murine framework.  
 CC Nucleic acids encoding LM609 substituted heavy and light chain polypeptides  
 CC and fragments are useful in diagnostic and therapeutic purposes, such  
 CC as in the production of LM609 grafted antibodies and fragments having  
 CC binding specificity and inhibitory activity against the integrin  
 CC alphavbeta3. The antibody can be used for the diagnosis or treatment  
 CC of alphavbeta3-mediated diseases (e.g. inflammatory disorders, chronic  
 CC articular rheumatism, psoriasis, disorders associated with inappropriate  
 CC or inopportune invasion of vessels such as diabetic retinopathy,  
 CC neovascular glaucoma and capillary proliferation in atherosclerotic  
 CC plaques, or cancers), and to inhibit binding activity of alphavbeta3  
 CC that are necessary for progression of an alphavbeta3-mediated disease.  
 XX Sequence 57 BP; 16 A; 12 C; 21 G; 8 T; 0 other;  
 SQ

Query Match 88.1%; Score 23.8; DB 22; Length 57;  
 Best Local Similarity 92.6%; Pred. No. 0.37;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtgccagctggcctctgacg 27  
 |||||  
 Db 1 caacagagtgccagctggcctcacag 27

RESULT 10  
 AAF28188  
 ID AAF28188 standard; DNA; 57 BP.  
 XX AC  
 XX AAF28188;  
 XX 03-APR-2001 (first entry)  
 XX Oligonucleotide #10.  
 XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
 XX Unidentified.  
 XX OS  
 XX WO200078815-A1.  
 XX PN  
 XX 28-DEC-2000.  
 XX PD  
 XX 23-JUN-2000; 2000WO-US17454.  
 XX PF  
 XX 24-JUN-1999; 99US-0339922.  
 XX PR  
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX PA  
 XX Huse WD, Wu H;  
 XX PI  
 XX WPI; 2001-050110/06.  
 XX DR  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX Example 2; Page 67; 132pp; English.  
 XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 57 BP; 16 A; 12 C; 21 G; 8 T; 0 other;

Query Match 88.1%; Score 23.8; DB 22; Length 57;  
 Best Local Similarity 92.6%; Pred. No. 0.37;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27  
 |||||  
 Db 1 caacagagtggcagctggcctcacg 27

RESULT 11  
 AAF28197  
 ID AAF28197 standard; DNA; 57 BP.  
 XX  
 AC AAF28197;

XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Grafted light chain variable region oligonucleotide #5.

XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
 KW  
 XX Unidentified.

XX WO200078815-A1.  
 FN  
 XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.  
 XX 24-JUN-1999; 99US-0339922.  
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;  
 PI  
 XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX

PS Example 4; Page 81; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX Sequence 57 BP; 16 A; 12 C; 21 G; 8 T; 0 other;

Query Match 88.1%; Score 23.8; DB 22; Length 57;  
 Best Local Similarity 92.6%; Pred. No. 0.37;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27  
 |||||  
 Db 1 caacagagtggcagctggcctcacg 27

RESULT 12  
 AAV49843  
 ID AAV49843 standard; DNA; 321 BP.  
 XX  
 AC AAV49843;

XX  
 DT 02-NOV-1998 (first entry)  
 XX  
 DE LM609 antibody light chain variable region DNA grafted fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; ss.

XX Mus sp.

XX Key Location/Qualifiers  
 FH CDS 1..321  
 FT /\*tag= a  
 FT /product= "LM609 grafted antibody light chain variable  
 FT region"  
 FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX P-PSDB; AAW76006.

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis

XX Claim 24; Fig 7; 129pp; English.

XX This sequence encodes a LM609 grafted antibody variable light chain  
 CC region. LM609 and the antibody vitaxin bind selectively to integrin  
 CC alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a ligand  
 CC and thus block integrin-mediated signal transduction. This is useful in  
 CC the treatment, prevention and diagnosis of alphaVbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
 CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match 88.1%; Score 23.8; DB 19; Length 321;  
 Best Local Similarity 92.6%; Pred. No. 0.46;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctggcctctgacg 27

Db 265 caacagagtgccagctggcctcacgc 291

## RESULT 13

AAV49821  
ID AAV49821 standard; DNA; 321 BP.

XX AAV49821;

XX 02-NOV-1998 (first entry)

XX Vitaxin antibody light chain variable region DNA.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
LM609; inhibitor; integrin-mediated signal transduction; treatment;  
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
macular degeneration; osteoporosis; ss.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 1..321  
FT /\*tag= a  
FT /product= "vitaxin antibody light chain variable region"  
FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX P-PSDB; AAW76002.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
integrin - and related grafted antibodies based on murine monoclonal  
LM609, also related nucleic acid, used to treat, prevent or diagnose  
angiogenesis or restenosis

XX Claim 6; Fig 1b; 129pp; English.

XX This sequence encodes the vitaxin antibody variable light chain region.  
CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3  
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
CC block integrin-mediated signal transduction. This is useful in the  
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
CC etc.). The antibodies contain non-murine framework regions so are  
CC suitable for use in humans. Enhanced types of LM609 have affinity more  
CC than 90 times greater than that of parent the parent antibody.

XX Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;

Query Match 88.1%; Score 23.8; DB 19; Length 321;

Best Local Similarity 92.6%; Pred. No. 0.46; 2; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0

Qy 1 caacagagtgccagctggcctctgacg 27

|||||

Db 265 caacagagtgccagctggcctcacgc 291

## RESULT 14

AAV49823

ID AAV49823 standard; DNA; 321 BP.

XX AAV49823;

XX 02-NOV-1998 (first entry)

XX LM609 antibody light chain variable region DNA fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
LM609; inhibitor; integrin-mediated signal transduction; treatment;  
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
macular degeneration; osteoporosis; ss.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 1..321  
FT /\*tag= a  
FT /product= "LM609 antibody light chain variable region"  
FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX P-PSDB; AAW75004.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
integrin - and related grafted antibodies based on murine monoclonal  
LM609, also related nucleic acid, used to treat, prevent or diagnose  
angiogenesis or restenosis

XX Claim 40; Fig 2b; 129pp; English.

XX This sequence encodes the LM609 antibody variable light chain region.  
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3  
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
CC block integrin-mediated signal transduction. This is useful in the  
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
CC etc.). The antibodies contain non-murine framework regions so are  
CC suitable for use in humans. Enhanced types of LM609 have affinity more  
CC than 90 times greater than that of parent the parent antibody.

XX Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 88.1%; Score 23.8; DB 19; Length 321;

Best Local Similarity 92.6%; Pred. No. 0.46; 2; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0

Qy 1 caacagagtgccagctggcctctgacg 27

|||||

Db 265 caacagagtgccagctggcctcacgc 291

## RESULT 15

AAH74624



Search completed: August 21, 2002, 10:08:26  
Job time: 10044 sec

AAH74624 standard; DNA; 321 BP.  
AAH74624;  
15-OCT-2001 (first entry)  
DNA encoding light chain variable region of LM609 grafted antibody.  
Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
chronic articular rheumatism; psoriasis; diabetic retinopathy;  
neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
cancer; ss.  
Synthetic.  
Mus sp.  
Key Location/Qualifiers  
CDS 1..321  
/\*tag= a  
/transl\_except= "(pos: 145..147, aa: Xaa)"  
/note= "Xaa is unspecified"  
US2001011125-A1.  
02-AUG-2001.  
30-JAN-1997; 97US-0790540.  
30-JAN-1997; 97US-0790540.  
(HUSE/) HUSE W D.  
Huse WD;  
WPI: 2001-496171/54.  
P-PSDB; AAC63588.  
New LM609 grafted antibody exhibiting selective binding affinity to  
alphavbeta3, comprising at least one LM609 grafted heavy and light  
chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
disorders or cancer -  
Claim 6: Fig 1B; 25pp; English.  
The present sequence encodes the light chain variable region of the  
grafted monoclonal antibody LM609. LM609 is a murine antibody which  
specifically recognises the integrin alphavbeta3, and inhibits its  
functional activity. The LM609 grafted antibody has the  
complementarity determining regions (CDRs) substituted into a non-murine  
framework. Nucleic acids encoding LM609 grafted heavy and light chain  
polypeptides and fragments are useful in diagnostic and therapeutic  
purposes, such as in the production of LM609 grafted antibodies and  
fragments having binding specificity and inhibitory activity against  
the integrin alphavbeta3. The antibody can be used for the diagnosis  
or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
disorders, chronic articular rheumatism, psoriasis, disorders  
associated with inappropriate or inopportune invasion of vessels such  
as diabetic retinopathy, neovascular glaucoma and capillary  
proliferation in atherosclerotic plaques, or cancers), and to inhibit  
binding activity of alphavbeta3 that are necessary for progression of  
an alphavbeta3-mediated disease.  
Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match 88.1%; Score 23.8; DB 22; Length 321;  
Best Local Similarity 92.6%; Pred. No. 0.46;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1- caacagagtggcagctgacctgtgacg 27  
Db 265 caacagagtggcagctgacctgtgacg 291

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:11 ; Search time 174.26 Seconds  
(without alignments)  
38.059 Million cell updates/sec

Title: US-09-339-922A-89

Perfect score: 27

Sequence: 1 caacagagtgccagctgcctctgacg 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_NA:\*

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22.2	82.2	5238	6	Patent No. 5453363
2	20.6	76.3	424	1	Sequence 3, Appli
3	19	70.4	27	2	Sequence 32, Appli
c 4	19	70.4	116	1	Sequence 93, Appli
c 5	19	70.4	116	1	Sequence 93, Appli
c 6	19	70.4	116	1	Sequence 93, Appli
c 7	19	70.4	116	1	Sequence 93, Appli
c 8	19	70.4	116	4	Sequence 93, Appli
9	19	70.4	321	2	Sequence 35, Appli
10	19	70.4	321	2	Sequence 36, Appli
11	19	70.4	321	2	Sequence 39, Appli
12	19	70.4	381	1	Sequence 82, Appli
13	19	70.4	381	1	Sequence 82, Appli
14	19	70.4	381	1	Sequence 82, Appli
15	19	70.4	381	1	Sequence 82, Appli
16	19	70.4	381	4	Sequence 82, Appli
c 17	17.6	65.2	2074	2	Sequence 11, Appli
c 18	17.6	65.2	2074	3	Sequence 11, Appli
c 19	17.6	65.2	2074	3	Sequence 11, Appli
c 20	17.6	65.2	2074	3	Sequence 11, Appli
21	17.4	64.4	3867	3	Sequence 7, Appli
22	17.4	64.4	4016	3	Sequence 23, Appli
23	17	63.0	2476	4	Sequence 23, Appli
c 24	17	63.0	2920	3	Sequence 1, Appli
c 25	17	63.0	2920	4	Sequence 1, Appli
c 26	16.8	62.2	26664	4	Sequence 28, Appli
c 27	16.6	61.5	516	2	Sequence 12, Appli

c 28	16.6	61.5	516	4	US-09-285-873-12	Sequence 12, Appli
c 29	16.6	61.5	568	3	US-08-985-950-9	Sequence 9, Appli
30	16.6	61.5	591	2	US-08-756-387B-10	Sequence 10, Appli
31	16.6	61.5	591	3	US-08-788-934-1	Sequence 1, Appli
32	16.6	61.5	591	4	US-09-285-873-10	Sequence 10, Appli
33	16.6	61.5	699	2	US-08-756-387B-7	Sequence 7, Appli
34	16.6	61.5	699	4	US-09-285-873-7	Sequence 7, Appli
35	16.6	61.5	713	2	US-08-238-027-3	Sequence 3, Appli
36	16.6	61.5	774	2	US-08-756-387B-4	Sequence 4, Appli
c 37	16.6	61.5	774	2	US-08-756-387B-5	Sequence 5, Appli
c 38	16.6	61.5	774	4	US-09-285-873-4	Sequence 4, Appli
c 39	16.6	61.5	774	4	US-09-285-873-5	Sequence 5, Appli
40	16.6	61.5	1174	1	US-07-869-933-10	Sequence 10, Appli
41	16.6	61.5	1174	4	US-09-103-663-10	Sequence 10, Appli
42	16.6	61.5	1198	2	US-08-756-387B-1	Sequence 1, Appli
c 43	16.6	61.5	1198	2	US-08-756-387B-3	Sequence 3, Appli
44	16.6	61.5	1198	4	US-09-285-873-1	Sequence 1, Appli
c 45	16.6	61.5	1198	4	US-09-285-873-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
5453363-1  
; Patent No. 5453363  
; APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MARTES, RALF  
; TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR  
; ING AFTER GENETIC EXPRESSION IN PROKARYOTES  
; NUMBER OF SEQUENCES: 4  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/206,044  
; FILING DATE: 02-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 942,370  
; FILING DATE: 09-SEP-1992  
; APPLICATION NUMBER: 498,500  
; FILING DATE: 23-MAR-1990  
; APPLICATION NUMBER: 76,207  
; FILING DATE: 23-OCT-1986  
; SEQ ID NO:1:  
; LENGTH: 5238  
5453363-1

Query Match 82.2%; Score 22.2; DB 6; Length 5238;  
Best Local Similarity 88.9%; Pred. No. 0.5;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 caacagagtgccagctgcctctgacg 27  
||||||| ||||||||| |||  
Db 271 caacagagtaacagctgcctctcacg 297

RESULT 2  
US-08-436-463-3  
; Sequence 3, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoto  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992.
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23..403
; US-08-436-463-3

Query Match 76.3%; Score 20.6; DB 1; Length 424;
Best Local Similarity 85.2%; Pred. No. 2;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 caacagagtgccagctgacctctgacg 27
||||| ||| ||| ||| ||| ||| |||
DB 347 CAACAGAGTAACAGCTGGCCTCACG 373

RESULT 3
US-08-232-081B-32
; Sequence 32, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WJDNES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
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;
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-232-081B-32

Query Match 70.4%; Score 19; DB 2; Length 27;
Best Local Similarity 81.5%; Pred. No. 8.2;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtgccagctgacctctgacg 27
||||| ||| ||| ||| ||| ||| |||
DB 1 CAACAAGTAGTAGCTGGCCTCAGC 27

RESULT 4
US-07-634-278-93/C
; Sequence 93, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLET, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
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US-07-634-278-93

Query Match 70.4%; Score 19; DB 1; Length 116;  
Best Local Similarity 81.5%; Pred. No. 9.1;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27  
||||| ||| ||||| |||  
Db 86 CAACAGAGTAACAGTTGGCCTCATACG 60

RESULT 5

US-08-477-728-93/c  
; Sequence 93, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:

; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111

; COMPUTER READABLE FORM:  
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; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 93:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (oligonucleotide)  
US-08-477-728-93

Query Match 70.4%; Score 19; DB 1; Length 116;  
Best Local Similarity 81.5%; Pred. No. 9.1;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27  
||||| ||| ||||| |||

Db 86 CAACAGAGTAACAGTTGGCCTCATACG 60

RESULT 6

US-08-474-040-93/c  
; Sequence 93, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:

; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 93:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 116 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (oligonucleotide)  
US-08-474-040-93

Query Match 70.4%; Score 19; DB 1; Length 116;  
Best Local Similarity 81.5%; Pred. No. 9.1;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27  
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Db 86 CAACAGAGTAACAGTTGGCCTCATACG 60

RESULT 7

US-08-487-200-93/c  
; Sequence 93, Application US/08487200  
; Patent No. 5693762

GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELING, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,200  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002610  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-08-487-200-93

Query Match 70.4%; Score 19; DB 1; Length 116;  
Best Local Similarity 81.5%; Pred. No. 9.1;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctgacctgacg 27  
||||||| ||| ||||| |||  
Db 86 CAACAGAGTAACAGTTGGCCTCATACG 60

RESULT 8  
US-08-484-537-93/c  
Sequence 93, Application US/08484537  
Patent No. 6180370  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELING, Kathleen L.

APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,537  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-08-484-537-93

Query Match 70.4%; Score 19; DB 4; Length 116;  
Best Local Similarity 81.5%; Pred. No. 9.1;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctgacctgacg 27  
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Db 86 CAACAGAGTAACAGTTGGCCTCATACG 60

RESULT 9  
US-08-232-081B-35  
Sequence 35, Application US/08232081B  
Patent No. 5886152  
GENERAL INFORMATION:  
APPLICANT: NAKATANI, TOMOYUKI  
APPLICANT: GOMI, HIDEYUKI  
APPLICANT: WIJDENES, JOHN  
APPLICANT: NOGUCHI, HIROSHI  
TITLE OF INVENTION: HUMANIZED B-B10  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA

ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,081B  
FILING DATE:

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SVENSSON, LEONARD R  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 20-3484  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-232-081B-35

Query Match 70.4%; Score 19; DB 2; Length 321;  
Best Local Similarity 81.5%; Pred. No. 9.7;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27  
||||| ||| ||||| || |||  
DB 265 CAACAAAGTAGTAGTGGCGCTCAGC 291

## RESULT 10

US-08-232-081B-36  
Sequence 36, Application US/082322081B  
Patent No. 5886152

GENERAL INFORMATION:  
APPLICANT: NAKATANI, TOMOYUKI  
APPLICANT: GOMI, HIDEYUKI  
APPLICANT: WIJDNES, JOHN  
TITLE OF INVENTION: HUMANIZED B-B10  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA

ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,081B  
FILING DATE:

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SVENSSON, LEONARD R  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 20-3484  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-232-081B-36

Query Match 70.4%; Score 19; DB 2; Length 321;  
Best Local Similarity 81.5%; Pred. No. 9.7;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27  
||||| ||| ||||| || |||  
DB 265 CAACAAAGTAGTAGTGGCGCTCAGC 291

## RESULT 11

US-08-232-081B-39  
Sequence 39, Application US/082322081B  
Patent No. 5886152

GENERAL INFORMATION:  
APPLICANT: NAKATANI, TOMOYUKI  
APPLICANT: GOMI, HIDEYUKI  
APPLICANT: WIJDNES, JOHN  
APPLICANT: NOGUCHI, HIROSHI  
TITLE OF INVENTION: HUMANIZED B-B10  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747

## COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,081B  
FILING DATE:

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SVENSSON, LEONARD R  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 20-3484  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..321  
US-08-232-081B-39

Query Match 70.4%; Score 19; DB 2; Length 321;  
Best Local Similarity 81.5%; Pred. No. 9.7;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27  
||||| ||| ||||| || |||  
DB 265 CAACAAAGTAGTAGTGGCGCTCAGC 291

## RESULT 12

US-07-634-278-82  
; Sequence 82, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourile and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381  
US-07-634-278-82

Query Match 70.4%; Score 19; DB 1; Length 381;  
Best Local Similarity 81.5%; Pred. No. 9.8;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27  
||||||| ||| ||||| |||  
Db 325 CAACAGAGTAACAGTTGGCCTCATACG 351

RESULT 13  
US-07-728-82  
; Sequence 82, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.

; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381  
US-08-477-728-82

Query Match 70.4%; Score 19; DB 1; Length 381;  
Best Local Similarity 81.5%; Pred. No. 9.8;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 caacagagtggcagctggcctctgacg 27  
||||||| ||| ||||| |||  
Db 325 CAACAGAGTAACAGTTGGCCTCATACG 351

RESULT 14  
US-08-474-040-82  
; Sequence 82, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
TELEPHONE: (415) 326-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-08-474-040-82

Query Match 70.4%; Score 19; DB 1; Length 381;
Best Local Similarity 81.5%; Pred. No. 9.8;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctgcctctgacg 27
||||| ||| ||| ||| |||
Db 325 CAACAGAGTAAACAGTTGGCCTCATACG 351

RESULT 15
US-08-487-200-82
Sequence 82, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELING, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto

STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..381
US-08-487-200-82

Query Match 70.4%; Score 19; DB 1; Length 381;
Best Local Similarity 81.5%; Pred. No. 9.8;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 caacagagtggcagctgcctctgacg 27
||||| ||| ||| ||| |||
Db 325 CAACAGAGTAAACAGTTGGCCTCATACG 351

Search completed: August 21, 2002, 10:52:13
Job time: 9653 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:48:59 ; Search time 2408.76 Seconds  
(without alignments)  
443.072 Million cell updates/sec

Title: US-09-339-922A-101

Perfect score: 51

Sequence: 1 aaagttagtggtggtgg.....atttagacactgtgcagggc 51

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sta:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sta:\*

28: em\_un:\*

29: em\_vi:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htgo\_inv:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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RESULT 1

AX060880

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

AX060880

Sequence 101 from Patent WO0078815.

AX060880

AX060880.1

GI:12406258

synthetic construct.

synthetic construct

artificial sequence.

1 (bases 1 to 51)

Huse, W.D. and Wu, H.

Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids

encoding same and methods of use

Patent: WO 0078815-A 101 28-DEC-2000;

Applied Molecular Evolution (US)

Location/Qualifiers

1..51

/organism="synthetic construct"

/db\_xref="taxon:32630"

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/note="Mutated complementarity determining region (CDR)"

/codon\_start=1

ALIGNMENTS

51 bp

DNA

Sequence 101 from Patent WO0078815.

AX060880

AX060880.1

GI:12406258

synthetic construct.

synthetic construct

artificial sequence.

1 (bases 1 to 51)

Huse, W.D. and Wu, H.

Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids

encoding same and methods of use

Patent: WO 0078815-A 101 28-DEC-2000;

Applied Molecular Evolution (US)

Location/Qualifiers

1..51

/organism="synthetic construct"

/db\_xref="taxon:32630"

<1..>51

/note="Mutated complementarity determining region (CDR)"

/codon\_start=1

/transl\_table=11  
/protein\_id="CAC24926.1"  
/db\_xref="GI:12406259"  
/translation="KVSSGGSTYYLDTVQG"  
13 a 8 c 16 g 14 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 51;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcaggc 51  
|||||

Db 1 AAAGTTAGTAGTGGTGGTAGCACCTACTATTATTAGACACTGTGCAGGC 51  
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## RESULT 2

AX060790 AX060790 87 bp DNA linear PAT 22-JAN-2001  
LOCUS Sequence 11 from Patent WO0078815.  
DEFINITION  
ACCESSION AX060790  
VERSION AX060790.1 GI:12406170  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 87)

AUTHORS Huse,W.D. and Wu,H.

TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids

JOURNAL encoding same and methods of use

PATENT: WO 0078815-A 11 28-DEC-2000;

APPLIED Molecular Evolution (US)

FEATURES Location/Qualifiers

1..87

source /organism="synthetic construct"

/db\_xref="taxon:32630"

/note="oligonucleotide"

23 a 18 c 24 g 22 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 87;  
Best Local Similarity 100.0%; Pred. No. 1.3e-10;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcaggc 51  
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Db 10 AAAGTTAGTAGTGGTGGTAGCACCTACTATTATTAGACACTGTGCAGGC 60  
|||||

## RESULT 3

AX060780 AX060780 351 bp DNA linear PAT 22-JAN-2001  
LOCUS Sequence 1 from Patent WO0078815.  
DEFINITION  
ACCESSION AX060780  
VERSION AX060780.1 GI:12406160  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 351)

AUTHORS Huse,W.D. and Wu,H.

TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids

JOURNAL encoding same and methods of use

PATENT: WO 0078815-A 1 28-DEC-2000;

APPLIED Molecular Evolution (US)

FEATURES Location/Qualifiers

1..351

source /organism="synthetic construct"

/db\_xref="taxon:32630"

<1..>351

/note="grafted antibody variable region"

## CDS

/codon\_start=1  
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/protein\_id="CAC24888.1"  
/db\_xref="GI:12406161"  
/translation="QVOLVESGGVWQPSRLSLSCAASGFTSSYDMSWVROIPKRG  
LEWVAKVSSGGSTYYLDTVQGRFTISRDNKNTLYLOMSSLNSEDATVYYCARHNYG  
SFAYWGGTIVTVSS"  
80 a 82 c 104 g 85 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 351;  
Best Local Similarity 100.0%; Pred. No. 1.3e-10;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcaggc 51  
|||||

Db 148 AAAGTTAGTAGTGGTGGTAGCACCTACTATTATTAGACACTGTGCAGGC 198  
|||||

## RESULT 4

AX060784 AX060784 351 bp DNA linear PAT 22-JAN-2001  
LOCUS Sequence 5 from Patent WO0078815.  
DEFINITION  
ACCESSION AX060784  
VERSION AX060784.1 GI:12406164  
KEYWORDS  
SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 351)

AUTHORS Huse,W.D. and Wu,H.

TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids

JOURNAL encoding same and methods of use

PATENT: WO 0078815-A 5 28-DEC-2000;

APPLIED Molecular Evolution (US)

FEATURES Location/Qualifiers

1..351

source /organism="Mus musculus"

/db\_xref="taxon:10090"

<1..>351

/note="unnamed protein product"

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/protein\_id="CAC24890.1"

/db\_xref="GI:12406165"

/translation="EVQLVESGGGLVQPSRLSLSCAASGFAFSSYDMSWVROIPKRG  
LEWVAKVSSGGSTYYLDTVQGRFTISRDNKNTLYLOMSSLNSEDATVYYCARHNYG  
SFAYWGGTIVTVSA"

83 a 81 c 102 g 85 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 351;  
Best Local Similarity 100.0%; Pred. No. 1.3e-10;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcacctactatttagacactgtgcaggc 51  
|||||

Db 148 AAAGTTAGTAGTGGTGGTAGCACCTACTATTATTAGACACTGTGCAGGC 198  
|||||

## RESULT 5

AX060882 AX060882 51 bp DNA linear PAT 22-JAN-2001  
LOCUS Sequence 103 from Patent WO0078815.  
DEFINITION  
ACCESSION AX060882  
VERSION AX060882.1 GI:12406260  
KEYWORDS  
SOURCE synthetic construct.

ORGANISM synthetic construct

artificial sequence.

REFERENCE 1 (bases 1 to 51)

AUTHORS Huse, W. D. and Wu, H.  
TITLE Anti-\_g(a) v2\_g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use  
JOURNAL Patent: WO 0078815-A 103 28-DEC-2000; Applied Molecular Evolution (US)  
FEATURES  
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/db\_xref="taxon:32630"  
CDS <1..>51  
/note="Mutated complementarity determining region (CDR)"  
/codon\_start=1  
/transl\_table=11  
/protein\_id="CAC24927.1"  
/db\_xref="GI:12406261"  
/translation="KVSSGGSTYPTVQV"  
BASE COUNT 13 a 10 c 16 g 12 t  
ORIGIN  
1 aaagttagtggtggtgtagcactatttagacactgtgcagggc 51  
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Db 1 AAGGTAGTAGTGGTGGTAGCACCCTACTATCCAGACACTGTGCAGGC 51  
RESULT 6  
LOCUS MMTGH4 339 bp mRNA linear ROD 12-OCT-1992  
DEFINITION M.musculus mRNA (L14-2G9) for IgH heavy chain V region.  
ACCESSION X59107  
VERSION X59107.1 GI:51944  
KEYWORDS Ig heavy chain; Ig variable region; immunoglobulin; rearranged.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 339)  
AUTHORS Kavalier, J.  
TITLE Direct Submission  
JOURNAL Submitted (15-APR-1991) J. Kavalier, Wistar Institute, 3601 Spruce Street, Philadelphia PA 19104, USA  
REFERENCE 2 (bases 1 to 339)  
AUTHORS Kavalier, J.  
JOURNAL Unpublished  
FEATURES  
source Location/Qualifiers  
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/organism="Mus musculus"  
/strain="BALB/c"  
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/tissue\_type="hybridoma"  
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/protein\_id="CAA41833.1"  
/db\_xref="GI:51945"  
/translation="VVSGLVKPGGSLKSCAASGAFSSYDMSWVROTPEKRLWV  
AVISSGGSTYPTVQVKGRTISRDNKNTLYLQMSLSKSDTAMYYCARHPVGNYYA  
MDYWGQTSVT"  
BASE COUNT 84 a 83 c 92 g 80 t  
ORIGIN  
Query Match 82.7%; Score 42.2; DB 10; Length 339;  
Best Local Similarity 93.6%; Pred. No. 6.4e-07;  
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
AUTHORS Huse, W. D. and Wu, H.  
TITLE Anti-\_g(a) v2\_g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use  
JOURNAL Patent: WO 0078815-A 103 28-DEC-2000; Applied Molecular Evolution (US)  
FEATURES  
source 1..51  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
CDS <1..>51  
/note="Mutated complementarity determining region (CDR)"  
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/transl\_table=11  
/protein\_id="CAC24927.1"  
/db\_xref="GI:12406261"  
/translation="KVSSGGSTYPTVQV"  
BASE COUNT 13 a 10 c 16 g 12 t  
ORIGIN  
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Db 1 AAGGTAGTAGTGGTGGTAGCACCCTACTATCCAGACACTGTGCAGGC 51  
RESULT 6  
LOCUS MMTGH4 339 bp mRNA linear ROD 12-OCT-1992  
DEFINITION M.musculus mRNA (L14-2G9) for IgH heavy chain V region.  
ACCESSION X59107  
VERSION X59107.1 GI:51944  
KEYWORDS Ig heavy chain; Ig variable region; immunoglobulin; rearranged.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 339)  
AUTHORS Kavalier, J.  
TITLE Direct Submission  
JOURNAL Submitted (15-APR-1991) J. Kavalier, Wistar Institute, 3601 Spruce Street, Philadelphia PA 19104, USA  
REFERENCE 2 (bases 1 to 339)  
AUTHORS Kavalier, J.  
JOURNAL Unpublished  
FEATURES  
source Location/Qualifiers  
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/strain="BALB/c"  
/db\_xref="taxon:10090"  
/cell\_line="L14-2G9"  
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/tissue\_type="hybridoma"  
CDS 1..339  
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/codon\_start=1  
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/protein\_id="CAA41833.1"  
/db\_xref="GI:51945"  
/translation="VVSGLVKPGGSLKSCAASGAFSSYDMSWVROTPEKRLWV  
AVISSGGSTYPTVQVKGRTISRDNKNTLYLQMSLSKSDTAMYYCARHPVGNYYA  
MDYWGQTSVT"  
BASE COUNT 84 a 83 c 92 g 80 t  
ORIGIN  
Query Match 82.7%; Score 42.2; DB 10; Length 339;  
Best Local Similarity 93.6%; Pred. No. 6.4e-07;  
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcactatttagacactgtgcagggc 51  
|||||  
Db 140 TTAGTAGTGGTGGTGGTAGCACCCTACTATCCAGACACTGTGAAGGC 186  
RESULT 7  
LOCUS MMAHCVR15 375 bp DNA linear ROD 31-AUG-1996  
DEFINITION M.musculus antibody heavy chain variable region (375bp).  
ACCESSION X90890  
VERSION X90890.1 GI:1518290  
KEYWORDS antibody heavy chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 375)  
AUTHORS Geiser, M. and Kretschmar, T.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 375)  
AUTHORS Geiser, M.  
TITLE Direct Submission  
JOURNAL Submitted (17-AUG-1995) M. Geiser, CIBA-GEIGY LTD, CDDT, K-681.5.46, CH-4002, Basel, SWITZERLAND  
FEATURES  
source Location/Qualifiers  
1..375  
/organism="Mus musculus"  
/strain="Balb/c"  
/db\_xref="taxon:10090"  
/cell\_type="lymphocytes"  
/tissue\_type="spleen"  
/dev\_stage="12 weeks old"  
CDS <1..>375  
/codon\_start=1  
/product="antibody heavy chain variable region"  
/protein\_id="CAA62398.1"  
/db\_xref="GI:1518291"  
/translation="EVKLESGLVKPGGSLKSCAASGAFSSYDMSWVROTPEKR  
LEWAYISSGGSTYPTVQVKGRTISRDNKNTLYLQMSLSKSDTAMYYCARQKGF  
YDYLTRNWFVDMGAGTLVTYSS"  
BASE COUNT 90 a 91 c 107 g 87 t  
ORIGIN  
Query Match 82.7%; Score 42.2; DB 10; Length 375;  
Best Local Similarity 93.6%; Pred. No. 6.4e-07;  
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 5 ttagtagtggtggtgtagcactatttagacactgtgcagggc 51  
|||||  
Db 152 TTAGTAGTGGTGGTGGTAGCACCCTACTATCCAGACACTGTGAAGGC 198  
RESULT 8  
LOCUS MMA229172 345 bp mRNA linear ROD 15-NOV-1999  
DEFINITION Mus musculus rearranged cDNA for VH region of anti arsonate antibody (B cell hybridoma A22).  
ACCESSION AJ229172  
VERSION AJ229172.1 GI:3135848  
KEYWORDS anti arsonate antibody; diversity segment; heavy chain; immunoglobulin; joining segment; variable segment.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 345)  
AUTHORS Ismaili, J., RazanaJaona, D., Van Acker, A., Wuilmart, C., Mancini, I., Heinen, E., Leo, O., Lebecque, S., Urbain, J., and Brait, M.  
TITLE Molecular and cellular basis of the altered immune response against arsonate in irradiated A/J mice autologously reconstituted  
JOURNAL Int. Immunol. 11 (7), 1157-1167 (1999)  
MEDLINE 99315320

```

REFERENCE 2 (bases 1 to 345)
AUTHORS Urban,J.J.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-1998) Urban J.J., Biologie moleculaire,
Universite Libre de Bruxelles, 67 rue des Chevaux, Rhode-St-Genese,
1640, BELGIUM
FEATURES
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                /db_xref="taxon:10090"
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                /cell_type="B cell hybridoma"
                /clone="A22"
                <1..276
                /gene="IGHF"
                /evidence=experimental
                /product="variable segment of immunoglobulin heavy chain"
                1..276
                /gene="IGHF"
                277..300
                /gene="DSP2.7"
                /evidence=experimental
                /product="diversity region of immunoglobulin heavy chain"
                277..300
                /gene="DSP2.7"
                301..345
                /gene="JH2"
                301..345
                /gene="JH2"
                /evidence=experimental
                /product="joining region of immunoglobulin heavy chain"
                80 a 92 c 89 g 81 t 3 others
BASE COUNT 80 a 92 c 89 g 81 t
ORIGIN
Query Match 80.8%; Score 41.2; DB 10; Length 345;
Best Local Similarity 91.5%; Pred. No. 1.7e-06;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccctactatttagacactgtgcagggc 51
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DB 134 TTAGTAGTGGTGGTGTAGCACCTACTATCCAGACACTGTGNAGGCG 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 9
A62608/c A62608 85 bp DNA linear PAT 12-MAR-1998
LOCUS Sequence 27 from Patent EP0781847.
DEFINITION A62608
ACCESSION A62608
VERSION A62608.1 GI:3716515
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 85)
AUTHORS Bendig,M.D., Saldana,J.D. and Jones,T.D.
TITLE Humanized monoclonal antibody
JOURNAL Patent: EP 0781847-A 27 02-JUL-1997;
COMMENT MERCK PATENT GMBH (DE)
OTHER publication JP 9183799 19970715.
FEATURES
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                1..85
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                /db_xref="taxon:32644"
BASE COUNT 19 a 23 c 21 g 22 t
ORIGIN
Query Match 79.6%; Score 40.6; DB 6; Length 85;
Best Local Similarity 91.5%; Pred. No. 3e-06;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 5 ttagtagtggtggtgtagcaccctactatttagacactgtgcagggc 51
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 73 TTAGTAGAGTGGTGGTAGCACCTACTATCCAGACACTGTGAAGGCG 27
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RESULT 10
MUSIGVAAS 345 bp mRNA linear ROD 27-APR-1993
LOCUS Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
DEFINITION sequence.
ACCESSION L08991
VERSION L08991.1 GI:197989
KEYWORDS V-region; Immunoglobulin V region; processed gene.
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 345)
AUTHORS Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
TITLE V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
mice
JOURNAL J. Immunol. 150, 1591-1610 (1993)
MEDLINE 93163585
FEATURES
    source      Location/Qualifiers
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                /cell_line="anti-Sm hybridoma 14C10"
                /cell_type="B-cell"
                /tissue_type="spleen"
                /dev_stage="adult"
BASE COUNT 80 a 85 c 102 g 78 t
ORIGIN
Query Match 79.6%; Score 40.6; DB 10; Length 345;
Best Local Similarity 91.5%; Pred. No. 3e-06;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccctactatttagacactgtgcagggc 51
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DB 151 TTAGTAGTGGTGGTGTAGCACCTACTATCCAGACACTGTGAAGGCG 197
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 11
MUSIGVAAS 345 bp mRNA linear ROD 27-APR-1993
LOCUS Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
DEFINITION sequence.
ACCESSION L08996
VERSION L08996.1 GI:197994
KEYWORDS V-region; Immunoglobulin V region; processed gene.
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 345)
AUTHORS Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
TITLE V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
mice
JOURNAL J. Immunol. 150, 1591-1610 (1993)
MEDLINE 93163585
FEATURES
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                /cell_line="anti-Sm hybridoma 22F6"
                /cell_type="B-cell"

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/tissue\_type="spleen"  
/dev\_stage="adult"  
80 a 86 c 102 g 77 t

Query Match 79.6%; Score 40.6; DB 10; Length 345;  
Best Local Similarity 91.5%; Pred. No. 3e-06;  
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51  
|||||  
Db 152 TTAGTAGTGGTGGTGTAGCACCTACTATCCACACAGTGTGAAGGC 198

RESULT 12  
MUSIGVABB  
LOCUS MUSIGVABB 348 bp mRNA linear ROD 27-APR-1993  
DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region  
sequence.  
ACCESSION L09000  
VERSION L09000.1 GI:197998  
KEYWORDS V-region; immunoglobulin V region; processed gene.  
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 348)  
Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,  
Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.  
V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr  
mice  
JOURNAL J. Immunol. 150, 1591-1610 (1993)  
MEDLINE 93163585  
FEATURES  
source  
1. 348  
/organism="Mus musculus"  
/strain="mrl/mp-lpr/lpr"  
/db\_xref="taxon:10090"  
/cell\_line="anti-Sm hybridoma 4D12"  
/cell\_type="B-cell"  
/tissue\_type="spleen"  
/dev\_stage="adult"  
80 a 87 c 102 g 79 t

Query Match 79.6%; Score 40.6; DB 10; Length 348;  
Best Local Similarity 91.5%; Pred. No. 3e-06;  
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51  
|||||  
Db 152 TTAGTAGTGGTGGTGTAGCACCTACTATCCACACAGTGTGAAGGC 198

RESULT 13  
MUSIGVAAV  
LOCUS MUSIGVAAV 351 bp mRNA linear ROD 27-APR-1993  
DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region  
sequence.  
ACCESSION L08997  
VERSION L08997.1 GI:197995  
KEYWORDS V-region; immunoglobulin V region; processed gene.  
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 351)  
Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,  
Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.  
V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr  
mice

J. Immunol. 150, 1591-1610 (1993)  
MEDLINE 93163585  
FEATURES  
source  
Location/Qualifiers  
1. 351  
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/cell\_type="B-cell"  
/tissue\_type="spleen"  
/dev\_stage="adult"  
82 a 87 c 103 g 79 t

BASE COUNT 82 a 87 c 103 g 79 t  
ORIGIN

Query Match 79.6%; Score 40.6; DB 10; Length 351;  
Best Local Similarity 91.5%; Pred. No. 3e-06;  
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51  
|||||  
Db 152 TTAGTAGTGGTGGTGTAGCACCTACTATCCACACAGTGTGAAGGC 198

RESULT 14  
A62623  
LOCUS A62623 441 bp DNA linear PAT 12-MAR-1998  
DEFINITION Sequence 42 from Patent EP0781847.  
ACCESSION A62623  
VERSION A62623.1 GI:3716530  
KEYWORDS unidentified.  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 441)  
AUTHORS Bendig,M.D., Saldana,J.D. and Jones,T.D.  
TITLE Humanized monoclonal antibody  
JOURNAL Patent: EP 0781847-A 42 02-JUL-1997;  
MERCK PATENT GMBH (DE)  
COMMENT Other publication JP 9183799 19970715.  
FEATURES  
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sig\_peptide  
12. 68  
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/product="CHIMERIC MAB 15, HEAVY CHAIN VARIABLE REGION"  
/protein\_id="CAA03670.1"  
/db\_xref="GI:4530024"  
/translation="MNRGLSLIFLVLPKGVKCEVQVVESSGGLVKGSGSLKLSCAAS  
GFAPSDYDMWVROTPEKRLWVAYLSRGGSTYPDPVKGKFTISRDNKKILFLQM  
TSLKSEDAAMYICARHGEEVRFDFWGQGLTVTSA"  
98 a 99 c 130 g 114 t

BASE COUNT 98 a 99 c 130 g 114 t  
ORIGIN

Query Match 79.6%; Score 40.6; DB 6; Length 441;  
Best Local Similarity 91.5%; Pred. No. 3e-06;  
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51  
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Db 220 TTAGTAGAGTGGTGGTGTAGCACCTACTATCCACACACTGTGAAGGC 266

RESULT 15  
A62635  
LOCUS A62635 445 bp DNA linear PAT 12-MAR-1998  
DEFINITION Sequence 54 from Patent EP0781847.  
ACCESSION A62635

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VERSION      A62635.1  GI:3716534
KEYWORDS     .
SOURCE       unidentified.
ORGANISM      unclassified.
REFERENCE    1 (bases 1 to 445)
AUTHORS      Bendig,M.D., Saldana,J.D. and Jones,T.D.
TITLE        Humanized monoclonal antibody
JOURNAL      Patent: EP 0781847-A 54 02-JUL-1997;
              MERCK PATENT GMBH (DE)
COMMENT      Other publication JP 9183799 19970715.
FEATURES
  source      1..445
              /organism="unidentified"
              /db_xref="taxon:32644"
  misc_signal 1..15
  sig_peptide 16..72
  CDS         16..>432
              /function="FR'S, CDR'S"
              /codon_start=1
              /product="RESHAPED MAB 15, HEAVY CHAIN VARIABLE REGION"
              /protein_id="CAA03672.1"
              /db_xref="GI:4530025"
              /translation="MEFGLSWLFVAILKGVCEVOLLESGGGLVOPGGSLRLSCAAS
GETFSDDMSWVRQAPGKRLRWVAILSRGGSTIYEDTVKGRFTISRDNKNTLILQM
NSLRAEDTAVYYCARHGEVRPEFDYWGQGLTVTVSS"
BASE COUNT   91 a 108 c 141 g 105 t
ORIGIN
```

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Query Match      79.6%; Score 40.6; DB 6; Length 445;
Best Local Similarity 91.5%; Pred. No. 3e-06;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  5 ttagttagtggtgtagcaccactatttagacactgtgcagggc 51
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  224 TTAGTAGAGGTGGTGTAGCACCTACTATCCAGACACTGTGAAGGCC 270
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Search completed: August 21, 2002, 10:49:01  
Job time: 9756 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: August 21, 2002, 09:55:42 ; Search time 6260.2 Seconds  
(without alignments)  
109.956 Million cell updates/sec

Title: US-09-339-922a-101  
Perfect score: 51  
Sequence: 1 aaagttagtagtggtggtg.....atttagacactgtgcagggc 51

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estinu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hct:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hct:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
1	37.4	73.3	861	10	BI455668	BI455668	603173862
2	35.8	70.2	333	10	BI336517	BI336517	AR097E07S
3	35.8	70.2	424	10	BI337375	BI337375	AR089G02P
4	35.8	70.2	469	9	AI645111	AI645111	ms87g10.y
5	35.8	70.2	650	10	BF579001	BF579001	602096117
6	35.8	70.2	823	9	AA170256	AA170256	ms87g10.r
7	35.8	70.2	837	10	BG966355	BG966355	602832843
8	35.2	69.0	662	10	BF163874	BF163874	601772386
9	35.2	69.0	883	10	BI151077	BI151077	602917012
10	35.2	69.0	908	10	BF161883	BF161883	601766819
11	35.2	69.0	913	10	BF162056	BF162056	601768714
12	34.8	68.2	338	9	BB868286	BB868286	BB868286
13	34.8	68.2	404	10	BF452207	BF452207	uz85h05.y
14	34.8	68.2	548	9	AW408295	AW408295	UI-HF-BKO
15	34.8	68.2	877	10	BF144493	BF144493	601790133
16	34.2	67.1	689	10	BF579926	BF579926	602095194
17	34.2	67.1	758	10	BM083708	BM083708	imageqc_2

18	33.6	65.9	898	10	BG757960		BG757960 602715003
19	33.2	65.1	342	9	BB869694		BB869694 BB869694
20	33.2	65.1	406	9	AW403983		AW403983 UI-HF-BKO
21	33.2	65.1	494	10	BG145342		BG145342 uu72905.y
22	32.6	63.9	308	10	BF844139		BF844139 PM2-HT034
23	32.6	63.9	330	10	F14516		F14516 SSC1D10.Por
24	32.6	63.9	332	10	BF155433		BF155433 PM2-HT034
25	32.6	63.9	367	10	BI305075		BI305075 ARO68E091
26	32.6	63.9	372	9	AA581192		AA581192 nd38b11.r
27	32.6	63.9	454	9	AW824857		AW824857 us08c01.y
28	32.6	63.9	648	10	BG340670		BG340670 602462250
29	32.6	63.9	652	10	BG965201		BG965201 602830954
30	32.6	63.9	718	10	BF136279		BF136279 601780988
31	32.6	63.9	735	10	BG745292		BG745292 602723604
32	32.6	63.9	737	10	BF974929		BF974929 602245594
33	32.6	63.9	774	10	BF581450		BF581450 602100853
34	32.6	63.9	862	10	BF143948		BF143948 601786493
35	32.6	63.9	875	10	BG340548		BG340548 602462113
36	32.6	63.9	954	10	BG963956		BG963956 602828679
37	32.6	63.9	966	10	BG745389		BG745389 602723728
38	32.6	63.9	1012	10	BF142302		BF142302 601791844
39	31.6	62.0	624	12	BH021317		BH021317 CT7-185G1
40	31.6	62.0	1559	10	BF138708		BF138708 601781893
41	31	60.8	294	9	AW606245		AW606245 PM2-HT035
42	31	60.8	406	9	AW401971		AW401971 UI-HF-BKO
43	31	60.8	412	9	AW800162		AW800162 MR2-UM006
44	31	60.8	434	9	AW630702		AW630702 hn86d11.y
45	31	60.8	440	9	AW408304		AW408304 UI-HF-BKO

ALIGNMENTS

RESULT 1  
BI455668 861 bp mRNA linear EST 21-AUG-2001  
LOCUS 603173862F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:5253279 5',  
DEFINITION mRNA sequence.  
ACCESSION BI455668  
VERSION BI455668.1 GI:15246324  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 861)  
AUTHORS NTH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11639 row: 1 column: 16  
High quality sequence stop: 780.  
FEATURES  
Location/Qualifiers  
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/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5253279"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1; Salt;  
Site:2; NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Robin Humphreys,

```

BASE COUNT      205 a      239 c      211 g      206 t
ORIGIN

Query Match      73.3%; Score 37.4; DB 10; Length 861;
Best Local Similarity 87.2%; Pred. No. 0.0015;
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 tttagtagtggtgtagcaccattatttagacactgtgcaggcc 51
||||| ||||||| ||||||| ||| ||||||| |||||
Db 279 TTAGTAATGGTGGTGGTAGCACCATTATATCCAGACACTGTAAAGGGC 325

RESULT 2
BI336517
LOCUS
DEFINITION AR037E07SPD09S Porcine Spleen cDNA library Sus scrofa cDNA, mRNA
sequence.
ACCESSION BI336517
VERSION BI336517.1 GI:15417813
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 333)
AUTHORS Rink A., Santschi, E.M. and Beattie, C.W.
TITLE Amplified, Normalized cDNA Libraries from a Porcine Model of
Orthopedic Implant Associated Staphylococcus aureus Infection
Unpublished (2001)
JOURNAL
COMMENT Contact: Rink A
Department of Animal Biotechnology
College of Agriculture, Biotechnology and Natural Resources,
University of Nevada, Reno
MS 202, FA 103, 1664 N Virginia St, Reno, NV 89557-0236, USA
Tel: 775 784 1705
Fax: 775 784 1375
Email: arink@cabnr.unr.edu
Tissues and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of Staphylococcus
aureus in a tibial transection, reduced and internally fixed with a
dynamic compression plate. NOTE: The sequences contain a 'cDNA
adapter' between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCACGAG'.
FEATURES
Location/Qualifiers
source
1..333
/organism="Sus scrofa"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone_lib="Porcine Spleen cDNA library"
/tissue_type="Spleen"
/cell_type="mixed"
/dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
/notes="Vector: pBSK; Site_1: Eco RI; Site_2: XhoI; Tissues
and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of
Staphylococcus aureus in a tibial transection, reduced and
internally fixed with a dynamic compression plate. NOTE:
The sequences contain a 'cDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
'AATTCGGCACGAG'."
BASE COUNT      69 a      84 c      101 g      69 t      10 others
ORIGIN

Query Match      70.2%; Score 35.8; DB 10; Length 333;
Best Local Similarity 85.1%; Pred. No. 0.0042;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 tttagtagtggtgtagcaccattatttagacactgtgcaggcc 51
||||| ||||||| ||||||| ||| ||||||| |||||
Db 236 TTAGTAATGGTGGTGGTAGCACCATTATATCCAGACACTGTGTGAAGGGC 194

RESULT 3
BI337375
LOCUS
DEFINITION AR089G02PBCG02S Porcine Peripheral Blood Cell cDNA library Sus
scrofa cDNA, mRNA sequence.
ACCESSION BI337375
VERSION BI337375.1 GI:15418671
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 424)
AUTHORS Rink A., Santschi, E.M. and Beattie, C.W.
TITLE Amplified, Normalized cDNA Libraries from a Porcine Model of
Orthopedic Implant Associated Staphylococcus aureus Infection
Unpublished (2001)
JOURNAL
COMMENT Contact: Rink A
Department of Animal Biotechnology
College of Agriculture, Biotechnology and Natural Resources,
University of Nevada, Reno
MS 202, FA 103, 1664 N Virginia St, Reno, NV 89557-0236, USA
Tel: 775 784 1705
Fax: 775 784 1375
Email: arink@cabnr.unr.edu
Tissues and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of Staphylococcus
aureus in a tibial transection, reduced and internally fixed with a
dynamic compression plate. NOTE: The sequences contain a 'cDNA
adapter' between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCACGAG'.
FEATURES
Location/Qualifiers
source
1..424
/organism="Sus scrofa"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone_lib="Porcine Peripheral Blood Cell cDNA library"
/tissue_type="Peripheral Blood Cell"
/cell_type="mixed"
/dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
/notes="Vector: pBSK; Site_1: Eco RI; Site_2: XhoI; Tissues
and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of
Staphylococcus aureus in a tibial transection, reduced and
internally fixed with a dynamic compression plate. NOTE:
The sequences contain a 'cDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
'AATTCGGCACGAG'."
BASE COUNT      88 a      101 c      133 g      92 t      10 others
ORIGIN

Query Match      70.2%; Score 35.8; DB 10; Length 424;
Best Local Similarity 85.1%; Pred. No. 0.0045;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 tttagtagtggtgtagcaccattatttagacactgtgcaggcc 51
||||| ||||||| ||||||| ||| ||||||| |||||
Db 236 TTAGTAATGGTGGTGGTAGCACCATTATATCCAGACACTGTGTGAAGGGC 282

RESULT 4
AI645111
LOCUS
DEFINITION ms87g10.y1 Soares mouse 3NDMS Mus musculus cDNA clone IMAGE:1618594
5' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-III REGION
(HUMAN); gb:U23089 Mus musculus CB17 SCID immunoglobulin heavy
chain V region mRNA, (MOUSE);, mRNA sequence.

```



Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
This read is a SEQUENCE of a previously sequenced mouse clone  
This read has been VERIFIED (found to hit its original self in the  
correct orientation)  
MGI:379418

WASHU-HIMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [mouseest@watson.wustl.edu](mailto:mouseest@watson.wustl.edu)  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:379418

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/lab_host="DH10B (T1 phage-resistant)"
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LOCUS BI151077 883 bp mRNA linear EST 05-JUL-2001  
 DEFINITION 602917012F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:5067314 5';  
 mRNA sequence.  
 ACCESSION BI151077  
 VERSION BI151077.1 GI:14611078  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 883)  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM1181 row: h column: 03  
 High quality sequence stop: 719.

#### FEATURES

##### source

1. .883  
 /organism="Mus musculus"  
 /strain="C57BL/6J (f1)"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5067314"  
 /clone\_lib="NCI\_CGAP\_Lu29"  
 /tissue\_type="spontaneous tumor, metastatic to mammary."  
 Stem cell origin.  
 /lab\_host="DH10B"  
 /note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Gilbert Smith, NIH"  
 BASE COUNT 211 a 268 c 217 g 187 t  
 ORIGIN

Query Match 69.0%; Score 35.2; DB 10; Length 883;  
 Best Local Similarity 83.3%; Pred. No. 0.0096;  
 Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 Qy 3 agttagtggtggtgtagcacttatttagacactgtgcagg 50  
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 Db 103 AGCCATTAGTGGTGGTAGCACCCTACTATCCAGACAGTGGAAGG 150

RESULT 10  
 BF161883  
 LOCUS 601766819F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3982828 5';  
 DEFINITION mRNA sequence.  
 ACCESSION BF161883  
 VERSION BF161883.1 GI:11042078  
 KEYWORDS EST.  
 SOURCE house mouse.

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 908)  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM9182 row: e column: 05  
 High quality sequence stop: 662.

#### FEATURES

##### source

1. .908  
 /organism="Mus musculus"  
 /strain="C57BL/6J (f1)"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:3982828"  
 /clone\_lib="NCI\_CGAP\_Lu29"  
 /tissue\_type="spontaneous tumor, metastatic to mammary."  
 Stem cell origin.  
 /lab\_host="DH10B"  
 /note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Gilbert Smith, NIH"  
 BASE COUNT 214 a 228 c 253 g 213 t  
 ORIGIN

#### FEATURES

Query Match 69.0%; Score 35.2; DB 10; Length 908;  
 Best Local Similarity 83.3%; Pred. No. 0.0097;  
 Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 Qy 3 agttagtggtggtgtagcacttatttagacactgtgcagg 50  
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 Db 265 AGCCATTAGTGGTGGTAGCACCCTACTATCCAGACAGTGGAAGG 312

#### RESULT 11

BF162056  
 LOCUS 601768714F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3987986 5';  
 DEFINITION mRNA sequence.  
 ACCESSION BF162056  
 VERSION BF162056.1 GI:11042257  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 913)  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM9195 row: l column: 03  
 High quality sequence stop: 581.

#### FEATURES

##### source

1. .913  
 /organism="Mus musculus"  
 /strain="C57BL/6J (f1)"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:3987986"  
 /clone\_lib="NCI\_CGAP\_Lu29"  
 /tissue\_type="spontaneous tumor, metastatic to mammary."  
 Stem cell origin.  
 /lab\_host="DH10B"  
 /note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Library constructed by Life Technologies. Investigator

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BASE COUNT      218 a      248 c      260 g      187 t
ORIGIN
    providing samples: Gilbert Smith, NIH"

Query Match      69.0%; Score 35.2; DB 10; Length 913;
Best Local Similarity 83.3%; Pred. No. 0.0097;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 agttagtggtggtgtagcaccctactatttagacactgtgcagg 50
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 273 AGCAATTAGTAGTGGTGGTACCACTACTATCCAGACAGTGTGAAGG 320

RESULT 12
LOCUS      BB868286      338 bp      mRNA      linear      EST 27-NOV-2001
DEFINITION BB868286 RIKEN full-length enriched, pooled tissues, intestinal
            mucosa, etc. Mus musculus cDNA clone G630003K04 5', mRNA sequence.
ACCESSION  BB868286
VERSION     BB868286.1 GI:17114496
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 338)
AUTHORS     Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
            Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
            Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
            Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
            Shibata,K., Shinaigawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
            A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
            Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
            RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
            2001)
TITLE       Unpublished (2001)
JOURNAL     Contact: Yoshihide Hayashizaki
COMMENT     Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center (GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
            S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            Y. and Hayashizaki,Y.
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
            e mouse tissues.
            Location/Qualifiers
            1. .338
            /organism="Mus musculus"
            /strain="C57BL/6"
            /db_xref="taxon:10090"
            /clone="G630003K04"

/clone_lib="RIKEN full-length enriched, pooled tissues,
intestinal mucosa, etc."
/note="pooled tissues", (tissue_type=intestinal mucosa,
dev_stage=adult, sex=male), (tissue_type=accessory
axillary lymph node, dev_stage=adult, sex=male),
(tissue_type=jejunal and colic lymph node, dev_stage=adult
sex=male), (tissue_type=gastric gland, dev_stage=adult,
sex=male), (tissue_type=vesicular gland, dev_stage=adult,
sex=male), (tissue_type=spinal cord, dev_stage=11 days
embryo), (tissue_type=brain, dev_stage=13 days embryo),
(tissue_type=spinal cord, dev_stage=13 days embryo),
(tissue_type=lung, dev_stage=14 days embryo),
(tissue_type=brain, dev_stage=15 days embryo),
(tissue_type=ovary and uterus, dev_stage=10 days pregnant
adult, sex=female), (tissue_type=cortex, dev_stage=0 day
neonate), (tissue_type=cerebellum, dev_stage=1 month
neonate), (tissue_type=diencephalon, dev_stage=16 days
neonate, sex=male), (tissue_type=medulla oblongata,
dev_stage=16 days neonate, sex=male),
(tissue_type=cerebellum, dev_stage=21 days neonate),
(tissue_type=testis, dev_stage=8 days neonate, sex=male)"
BASE COUNT      70 a      80 c      100 g      88 t
ORIGIN
    Query Match      68.2%; Score 34.8; DB 9; Length 338;
    Best Local Similarity 84.8%; Pred. No. 0.0098;
    Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccctactatttagacactgtgcagg 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 289 TCAGTAGTGGTGGTGGTTCACCGATTATTAGACAGTGTGAAGG 334

RESULT 13
LOCUS      BF452207      404 bp      mRNA      linear      EST 29-DEC-2000
DEFINITION BF452207 NCI-CCAP Lu29 Mus musculus cDNA clone IMAGE:3675897 5',
            similar to SW:HV55_MOUSE P18526 IG HEAVY CHAIN V REGION 345
            PRECURSOR. 1, mRNA sequence.
ACCESSION  BF452207
VERSION     BF452207.1 GI:11518376
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 404)
REFERENCE   1 (bases 1 to 404)
AUTHORS     NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: ccaps-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CCAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml

MGI:1436665
Seq primer: -40RP from Gibco
High quality sequence stop: 399.
Location/Qualifiers
1. .404
/organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:3675897"
/clone_lib="NCI-CCAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.

```

```
Stem cell origin."
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 96 a 94 c 109 g 105 t
ORIGIN

Query Match 68.2%; Score 34.8; DB 10; Length 404;
Best Local Similarity 84.8%; Pred. No. 0.01;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagg 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 257 TTAGTGATGTTGGTGTACCACTACTATCTAGACAGTGTGAAGG 302

RESULT 14
AW408295 548 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BK0-abj-d-12-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3056327 5', mRNA sequence.
ACCESSION AW408295
VERSION AW408295.1 GI:6927352
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 548)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.
FEATURES
Location/Qualifiers
source
1..548
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/db_xref="taxon:9606"
/clone="IMAGE:3056327"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/lab_host="DH10B (UTI)"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 109 a 148 c 156 g 135 t
ORIGIN

Query Match 68.2%; Score 34.8; DB 9; Length 548;
Best Local Similarity 84.8%; Pred. No. 0.012;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagg 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 276 TTAGTTGGATGTTGGTGTAGCACTACTATGCAGACTCTGTGAAGG 321
```

```
RESULT 15
BF144493 877 bp mRNA linear EST 24-OCT-2000
LOCUS 601790133F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4020753 5',
DEFINITION mRNA sequence.
ACCESSION BF144493
VERSION BF144493.1 GI:10983533
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 877)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9275 row: a column: 10
High quality sequence stop: 644.
FEATURES
Location/Qualifiers
source
1..877
/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4020753"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dt. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 198 a 233 c 254 g 192 t
ORIGIN

Query Match 68.2%; Score 34.8; DB 10; Length 877;
Best Local Similarity 84.8%; Pred. No. 0.013;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagg 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 245 TTAGTAGTGGTGTAGTTACCTACTATCCAGACAGTGTGAAGG 290

Search completed: August 21, 2002, 09:55:46
Job time: 9309 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:26 ; Search time 754.01 seconds  
(without alignments)  
116.129 Million cell updates/sec

Title: US-09-339-922A-101  
Perfect score: 51  
Sequence: 1 aaattagtagtggtggtg.....atttagacactgtgcaggcc 51

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_032802.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	51	22	AAF28234
2	51	100.0	87	19	AAV49826
3	51	100.0	87	22	AAH74629
4	51	100.0	87	22	AAF28181
5	51	100.0	351	19	AAV49820
6	51	100.0	351	19	AAV49822
7	51	100.0	351	22	AAH74623
8	51	100.0	351	22	AAH74625
9	51	100.0	351	22	AAF28175

10	51	100.0	351	22	AAF28177	Antibody LM609 hea
11	47.8	93.7	51	22	AAF28235	DNA encoding enhan
12	40.6	79.6	85	18	AAV72258	Mouse MAb 15 heavy
13	40.6	79.6	369	19	AAV07642	anti-CD22 monoclon
14	40.6	79.6	441	18	AAV72269	Chimeric MAB 15 PC
15	40.6	79.6	445	18	AAV72237	Humanised reshaped
16	40.6	79.6	457	18	AAV72267	Mouse MAB 15 heavy
17	40.6	79.6	923	16	AAV51436	Murine MAB SK48-E2
18	39	76.5	413	15	AAQ68650	MAB A33 heavy chai
19	39	76.5	482	11	AAQ55555	Sequence encoding
20	39	76.5	721	20	AAV99765	A33/212 single-cha
21	39	76.5	721	21	AAZ37397	Linked fusion prot
22	39	76.5	733	20	AAV99766	A33/218 single-cha
23	39	76.5	733	21	AAZ37398	Linked fusion prot
24	39	76.5	1938	19	AAV58929	A33 chimeric recep
25	38	74.5	51	19	AAV44992	15D3 antibody heav
26	38	74.5	51	20	AAZ10944	15D3 VH chain CDR2
27	38	74.5	357	19	AAV44997	15D3 antibody heav
28	38	74.5	357	20	AAZ10957	15D3 VH chain codi
29	38	74.5	357	20	AAV08933	Antibody 15D3 heav
30	38	74.5	480	13	AAQ20070	MRK16-H chain. Ch
31	37.4	73.3	97	22	AAF86879	Ganglioside GD3 sp
32	37.4	73.3	351	16	AAQ96282	Human Ige receptor
33	37.4	73.3	351	18	AAV90025	cDNA encoding heav
34	37.4	73.3	354	14	AAQ48765	Monoclonal antibod
35	37.4	73.3	357	17	AAV28000	B5 immunoglobulin
36	37.4	73.3	360	17	AAV33445	Egf receptor chime
37	37.4	73.3	363	18	AAV75583	Monoclonal antibod
38	37.4	73.3	363	18	AAV71325	Thyroid hormone sp
39	37.4	73.3	363	20	AAV81002	Murine 340 Vh DNA
40	37.4	73.3	363	24	AAV25246	Mouse monoclonal a
41	37.4	73.3	403	14	AAQ37057	Rat immunoglobulin
42	37.4	73.3	403	15	AAQ45439	KM641 L chain vari
43	37.4	73.3	403	20	AAV99482	pKM641 HA3 immunog
44	37.4	73.3	403	21	AAA51003	Murine immunoglobu
45	37.4	73.3	474	18	AAV70808	Mouse anti-idiotyp

#### ALIGNMENTS

RESULT 1  
AAF28234  
ID AAF28234 standard; DNA; 51 BP.  
XX AC  
XX AAF28234;  
DT 03-APR-2001 (first entry)  
XX  
DE DNA encoding enhanced 6H6LH heavy chain CDR2.  
XX  
KW LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
XX  
OS Unidentified.  
XX  
PN WO200078815-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 23-JUN-2000; 2000WO-US17454.  
XX  
PR 24-JUN-1999; 99US-0339922.  
XX  
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX  
PI Huse WD, Wu H;  
XX WPI; 2001-050110/06.  
XX  
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

PS Claim 16; Page 105; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta<sub>3</sub> integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

SQ Sequence 51 BP; 13 A; 8 C; 16 G; 14 T; 0 other;

Query Match 100.0%; Score 51; DB 22; Length 51;

Best Local Similarity 100.0%; Pred. No. 9.8e-11;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcacctactatttagacactgtgcagggc 51

|||||

DB 1 aaagttagtagtggtggtgtagcacctactatttagacactgtgcagggc 51

|||||

RESULT 2

AAV49826

ID AAV49826 standard; DNA; 87 BP.

XX

AC AAV49826;

XX

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody variable region oligonucleotide #3.

XX

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; ss.

XX

OS Synthetic.

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

PI

XX WPI; 1998-437472/37.

DR

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta<sub>3</sub>

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Example 2; Page 65; 129pp; English.

XX

CC AAV49824-V49833 are oligonucleotides used in the construction of grafted

CC LM609 monoclonal antibody heavy and light chain variable regions. LM609

CC and antibody vitaxin bind selectively to integrin alphavbeta<sub>3</sub> and

CC can be used to inhibit binding of alphavbeta<sub>3</sub> to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC

CC prevention and diagnosis of alphavbeta<sub>3</sub>-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX

SQ Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;

Query Match 100.0%; Score 51; DB 19; Length 87;

Best Local Similarity 100.0%; Pred. No. 1.1e-10;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcacctactatttagacactgtgcagggc 51

|||||

DB 10 aaagttagtagtggtggtgtagcacctactatttagacactgtgcagggc 60

|||||

RESULT 3

AAH74629

ID AAH74629 standard; DNA; 87 BP.

XX

AC AAH74629;

XX

DT 15-OCT-2001 (first entry)

XX

DE PCR primer for heavy chain variable region of LM609 antibody.

XX

KW Grafted antibody; LM609; integrin; alphavbeta<sub>3</sub>; inflammatory disorder;

KW chronic articular rheumatism; psoriasis; diabetic retinopathy;

KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;

KW cancer; PCR primer; ss.

XX

OS Mus sp.

XX

PN US2001011125-A1.

XX

PD 02-AUG-2001.

XX

PF 30-JAN-1997; 97US-0790540.

XX

PR 30-JAN-1997; 97US-0790540.

XX

PA (HUSE/) HUSE W D.

XX

PI Huse WD;

PI

XX WPI; 2001-496171/54.

DR

XX New LM609 grafted antibody exhibiting selective binding affinity to

PT alphavbeta<sub>3</sub>, comprising at least one LM609 grafted heavy and light

PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory

PT disorders or cancer

XX

PS Example 2; Page 16; 25pp; English.

XX

CC PCR primers AAH74627-31 were used to amplify DNA encoding fragments

CC of the heavy chain variable region of the monoclonal antibody LM609.

CC LM609 is a murine antibody which specifically recognises the integrin

CC alphavbeta<sub>3</sub>, and inhibits its functional activity. The specification

CC describes a LM609 grafted antibody which has the complementarity

CC determining regions (CDRs) substituted into a non-murine framework

CC Nucleic acids encoding LM609 grafted heavy and light chain polypeptides

CC and fragments are useful in diagnostic and therapeutic purposes, such

CC as in the production of LM609 grafted antibodies and fragments having

CC binding specificity and inhibitory activity against the integrin

CC alphavbeta<sub>3</sub>. The antibody can be used for the diagnosis or treatment

CC of alphavbeta<sub>3</sub>-mediated diseases (e.g. inflammatory disorders, chronic

CC articular rheumatism, psoriasis, disorders associated with inappropriate

CC or inopportune invasion of vessels such as diabetic retinopathy,

CC neovascular glaucoma and capillary proliferation in atherosclerotic

CC plaques, or cancers), and to inhibit binding activity of alphavbeta3  
CC that are necessary for progression of an alphavbeta3-mediated disease.  
XX  
SQ Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;

Query Match 100.0%; Score 51; DB 22; Length 87;  
Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 51  
|||||  
Db 10 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 60

RESULT 4  
AAAF28181  
ID AAF28181 standard; DNA; 87 BP.  
XX  
AC AAF28181;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE Oligonucleotide #3.  
XX  
XX LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
XX  
OS Unidentified.  
XX  
PN WO200078815-A1.  
XX  
XX 28-DEC-2000.  
PD  
PF 23-JUN-2000; 2000WO-US17454.  
XX  
PR 24-JUN-1999; 99US-0339922.  
XX  
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX  
PI Huse WD, Wu H;  
DR WPI; 2001-050110/06.  
XX  
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis -  
XX  
PS Example 2; Page 67; 132pp; English.  
XX  
XX The present invention relates to enhanced LM609 grafted antibodies  
CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
CC their functional fragments. The antibodies or their functional  
CC fragments can be used in the diagnosis and treatment of  
CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
CC diseases (such as psoriasis and chronic articular rheumatism),  
CC disorders associated with inappropriate or inopportune invasion of  
CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
CC diseases (such as macular degeneration), restenosis and  
CC osteoporosis.  
XX  
SQ Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;

Query Match 100.0%; Score 51; DB 22; Length 87;  
Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 51  
|||||  
Db 10 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 60

RESULT 5  
AAV49820  
ID AAV49820 standard; DNA; 351 BP.  
XX  
AC AAV49820;  
XX  
DT 02-NOV-1998 (first entry)  
XX  
DE Vitaxin antibody heavy chain variable region DNA.  
XX  
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis; ss.  
XX  
OS Mus sp.  
XX  
XX  
FH Key Location/Qualifiers  
CDS 1..351  
FT /\*tag= a  
FT /product= "vitaxin antibody heavy chain variable region"  
FT /note= "partial sequence, no start or stop codon given"  
XX  
PN WO9833919-A2.  
XX  
XX 06-AUG-1998.  
PD  
XX 30-JAN-1998; 98WO-US01826.  
PF  
XX 30-JAN-1997; 97US-0791391.  
PR  
XX (IXSY-) IXSYS INC.  
PA  
XX Glaser SM, Huse WD;  
PI  
XX WPI; 1998-437472/37.  
DR  
XX P-PSDB; AAW76001.  
XX  
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
PT integrin - and related grafted antibodies based on murine monoclonal  
PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
PT angiogenesis or restenosis  
XX  
PS Claim 3; Fig 1a; 129pp; English.  
XX  
XX This sequence encodes the vitaxin antibody variable heavy chain region.  
CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3  
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
CC block integrin-mediated signal transduction. This is useful in the  
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
CC etc.). The antibodies contain non-murine framework regions so are  
CC suitable for use in humans. Enhanced types of LM609 have affinity more  
CC than 90 times greater than that of parent the parent antibody.  
XX  
SQ Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match 100.0%; Score 51; DB 19; Length 351;  
Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 51  
|||||  
Db 148 aaagttagtagtggtggtgtagcactactatttagacactgtgcaggc 198

RESULT 6



```

AAV49822
ID  AAV49822 standard; DNA; 351 BP.
XX
AC  AAV49822;
XX
DT  02-NOV-1998  (first entry)
XX
DE  LM609 antibody heavy chain variable region DNA fragment.
XX
KW  Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX  LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX  diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX  neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX  macular degeneration; osteoporosis; ss.
OS  Mus sp.
XX
FH  Location/Qualifiers
FT  1..351
FT  /*tag= a
FT  /product= "LM609 antibody heavy chain variable region"
FT  /note= "partial sequence, no start or stop codon given"
XX
PN  WO9833919-A2.
XX
PD  06-AUG-1998.
XX
PF  30-JAN-1998; 98WO-US01826.
XX
PR  30-JAN-1997; 97US-0791391.
XX
PA  (IXSY-) IXSYS INC.
XX
PI  Glaser SM, Huse WD;
XX
DR  WPI; 1998-437472/37.
XX
PT  Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT  integrin - and related grafted antibodies based on murine monoclonal
PT  LM609, also related nucleic acid, used to treat, prevent or diagnose
PT  angiogenesis or restenosis
XX
PS  Claim 37; Fig 2a; 129pp; English.
XX
CC  This sequence encodes the LM609 antibody variable heavy chain region.
CC  LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC  and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC  block integrin-mediated signal transduction. This is useful in the
CC  treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC  specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC  inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC  psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC  etc.). The antibodies contain non-murine framework regions so are
CC  suitable for use in humans. Enhanced types of LM609 have affinity more
CC  than 90 times greater than that of parent the parent antibody.
XX
SQ  Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

Query Match      100.0%; Score 51; DB 19; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 aaagttagtggtggtgtagcacctactatttagacactgtgcagggc 51
    |||||||
DB  148 aaagttagtggtggtgtagcacctactatttagacactgtgcagggc 198

RESULT  17
AAH74623
ID  AAH74623 standard; DNA; 351 BP.
XX
AC  AAH74623;
XX
DT  15-OCT-2001  (first entry)
XX
DE  DNA encoding heavy chain variable region of LM609 grafted antibody.
XX
KW  Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
XX  chronic articular rheumatism; psoriasis; diabetic retinopathy;
XX  neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
XX  cancer; ss.
OS  Synthetic.
XX
OS  Mus sp.
XX
PN  US2001011125-A1.
XX
PD  02-AUG-2001.
XX
PF  30-JAN-1997; 97US-0790540.
XX
PR  30-JAN-1997; 97US-0790540.
XX
PA  (HUSE/) HUSE W D.
XX
PI  Huse WD;
XX
DR  WPI; 2001-496171/54.
XX
DR  P-PSDB; AAG63587.
XX
PT  New LM609 grafted antibody exhibiting selective binding affinity to
PT  alphavbeta3, comprising at least one LM609 grafted heavy and light
PT  chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT  disorders or cancer
XX
PS  Claim 3; Fig 1A; 25pp; English.
XX
CC  The present sequence encodes the heavy chain variable region of the
CC  grafted monoclonal antibody LM609. LM609 is a murine antibody which
CC  specifically recognises the integrin alphavbeta3, and inhibits its
CC  functional activity. The LM609 grafted antibody has the
CC  complementarity determining regions (CDRs) substituted into a non-murine
CC  framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC  polypeptides and fragments are useful in diagnostic and therapeutic
CC  purposes, such as in the production of LM609 grafted antibodies and
CC  fragments having binding specificity and inhibitory activity against
CC  the integrin alphavbeta3. The antibody can be used for the diagnosis
CC  or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC  disorders, chronic articular rheumatism, psoriasis, disorders
CC  associated with inappropriate or inopportune invasion of vessels such
CC  as diabetic retinopathy, neovascular glaucoma and capillary
CC  proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC  binding activity of alphavbeta3 that are necessary for progression of
CC  an alphavbeta3-mediated disease.
XX
SQ  Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match      100.0%; Score 51; DB 22; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 aaagttagtggtggtgtagcacctactatttagacactgtgcagggc 51
    |||||||
DB  148 aaagttagtggtggtgtagcacctactatttagacactgtgcagggc 198

RESULT  8
AAH74625
ID  AAH74625 standard; DNA; 351 BP.
XX
AC  AAH74625;
XX
DT  15-OCT-2001  (first entry)
XX

```

DE DNA encoding heavy chain variable region of LM609 antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;

KW chronic articular rheumatism; psoriasis; diabetic retinopathy;

KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;

KW cancer; ss.

XX Mus sp.

OS US200101125-A1.

XX 02-AUG-2001.

PD 30-JAN-1997; 97US-0790540.

XX 30-JAN-1997; 97US-0790540.

PF (HUSE/) HUSE W D.

XX Huse WD;

PI WPI; 2001-496171/54.

DR P-PSDB; AAG63589.

XX New LM609 grafted antibody exhibiting selective binding affinity to

PT alphavbeta3, comprising at least one LM609 grafted heavy and light

PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory

PT disorders or cancer -

XX Disclosure; Fig 2A; 25pp; English.

PS The present sequence encodes the heavy chain variable region of the

XX monoclonal antibody LM609. LM609 is a murine antibody which specifically

CC recognises the integrin alphavbeta3, and inhibits its functional activity.

CC The specification describes a LM609 grafted antibody which has the

CC complementarity determining regions (CDRs) substituted into a non-murine

CC framework. Nucleic acids encoding LM609 grafted heavy and light chain

CC polypeptides and fragments are useful in diagnostic and therapeutic

CC purposes, such as in the production of LM609 grafted antibodies and

CC fragments having binding specificity and inhibitory activity against

CC the integrin alphavbeta3. The antibody can be used for the diagnosis

CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory

CC disorders, chronic articular rheumatism, psoriasis, disorders

CC associated with inappropriate or inopportune invasion of vessels such

CC as diabetic retinopathy, neovascular glaucoma and capillary

CC proliferation in atherosclerotic plaques, or cancers), and to inhibit

CC binding activity of alphavbeta3 that are necessary for progression of

CC an alphavbeta3-mediated disease.

XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

SQ

Query Match 100.0%; Score 51; DB 22; Length 351;

Best Local Similarity 100.0%; Pred. No. 1.5e-10;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcaccctatttagacactgtgcaggcc 51

|||||

Db 148 aaagttagtggtggtgtagcaccctatttagacactgtgcaggcc 198

|||||

RESULT 9

AAF28175

ID AAF28175 standard; DNA; 351 BP.

XX

AC AAF28175;

XX

DT 03-APR-2001 (first entry)

XX

DE Vitaxin heavy chain variable region DNA.

XX LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.

XX Unidentified.

OS WO200078815-A1.

PN 28-DEC-2000.

PD 23-JUN-2000; 2000WO-US17454.

PF 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA Huse WD, Wu H;

PI WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

XX to alpha(V)beta(3) integrin; useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX Disclosure; Fig 1; 132pp; English.

PS The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta\_3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

SQ

Query Match 100.0%; Score 51; DB 22; Length 351;

Best Local Similarity 100.0%; Pred. No. 1.5e-10;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaagttagtggtggtgtagcaccctatttagacactgtgcaggcc 51

|||||

Db 148 aaagttagtggtggtgtagcaccctatttagacactgtgcaggcc 198

|||||

RESULT 10

AAF28177

ID AAF28177 standard; DNA; 351 BP.

XX

AC AAF28177;

XX

DT 03-APR-2001 (first entry)

XX

DE Antibody LM609 heavy chain variable region DNA.

XX LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.

XX Unidentified.

OS WO200078815-A1.

PN 28-DEC-2000.

PD 23-JUN-2000; 2000WO-US17454.

PF 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA

XX

PI Huse WD, Wu H;  
 DR WPI; 2001-050110/06.  
 XX  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Fig 2; 132pp; English.  
 XX  
 XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;  
 Query Match 100.0%; Score 51; DB 22; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 aaagttagtagtggtggtgtagcactactatttagacactgtgcagggc 51  
 |||||  
 Db 148 aaagttagtagtggtggtgtagcactactatttagacactgtgcagggc 198  
 |||||  
 RESULT 11  
 AAF28235  
 ID AAF28235 standard; DNA; 51 BP.  
 XX  
 AC AAF28235;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE DNA encoding enhanced 2236-38/ 6H6LH heavy chain CDR2.  
 XX  
 KW LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 XX WPI; 2001-050110/06.  
 DR  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Claim 14; Page 105; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or

CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 51 BP; 13 A; 10 C; 16 G; 12 T; 0 other;  
 Query Match 93.7%; Score 47.8; DB 22; Length 51;  
 Best Local Similarity 96.1%; Pred. No. 1.8e-09;  
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 aaagttagtagtggtggtgtagcactactatttagacactgtgcagggc 51  
 |||||  
 Db 1 aaagttagtagtggtggtgtagcactactatccagacactgtgcagggc 51  
 |||||  
 RESULT 12  
 AAT72258/C  
 ID AAT72258 standard; DNA; 85 BP.  
 XX  
 AC AAT72258;  
 XX  
 DT 03-JAN-1998 (first entry)  
 XX  
 DE Mouse Mab 15 heavy chain backward PCR primer 4.  
 XX  
 KW Humanised antibody; monoclonal antibody; Mab 15; tumour;  
 KW lung cancer; therapy; polymerase chain reaction; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN EP781847-A1.  
 XX  
 PD 02-JUL-1997.  
 XX  
 PF 25-OCT-1996; 96EP-0117154.  
 XX  
 PR 06-NOV-1995; 95EP-0117407.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 PI Bendig M, Jones T, Saldana J;  
 XX  
 XX WPI; 1997-334904/31.  
 DR  
 XX Humanised form of murine monoclonal antibody Mab 15 - useful for  
 PT treating lung cancer  
 XX  
 PS Disclosure; Page 27; 71pp; English.  
 XX  
 XX This synthetic oligonucleotide comprises backward PCR primer 4  
 CC that was used with other sense and antisense primers (AAT72255-60)  
 CC to produce a sequence encoding a reshaped humanised monoclonal  
 CC antibody (Mab) 15 heavy chain variable region VH sequence (see  
 CC AAT72237). The full-length product was then amplified with external  
 CC primers (see AAT72261-62) and subcloned into HCMV expression vector  
 CC containing human heavy chain gamma-1 constant region. Humanised  
 CC reshaped Mab 15 is claimed for use in the treatment of human  
 CC tumours, especially lung cancer.  
 XX  
 SQ Sequence 85 BP; 19 A; 23 C; 21 G; 22 T; 0 other;  
 Query Match 79.6%; Score 40.6; DB 18; Length 85;  
 Best Local Similarity 91.5%; Pred. No. 1.3e-06;  
 Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ttatgtagtgtgtggtagcacctactatttagacactgtgcaggc 51  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 73 TTAGTAGAGGTGGTGTAGCACCTACTATCCAGACACTGTGAAGGC 27

RESULT 13  
 AAV07642  
 ID AAV07642 standard; DNA; 369 BP.  
 XX  
 AC AAV07642;  
 XX  
 DT 10-DEC-1998 (first entry)  
 XX  
 DE anti-CD22 monoclonal antibody heavy chain variable region DNA sequence.  
 XX  
 KW anti-CD22 monoclonal antibody heavy chain variable region; VL;  
 KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;  
 KW malignant B-cell; immunodiagnosis; RFB4 IgG; ss.  
 XX  
 OS Mammalia.

XX Key Location/Qualifiers  
 FH CDS 1..369  
 FT /tag= a  
 FT /transl\_except= (pos:361..363, aa:Thr)  
 FT /note= "CDS does not contain a stop codon"  
 XX  
 PN WO9841641-AL.

XX 24-SEP-1998.  
 XX 19-MAR-1998; 98WO-US05453.  
 XX 20-MAR-1997; 97US-0041437.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Fitzgerald D, Kreitman R, Mansfield E, Pastan I;  
 XX WPI; 1998-521227/44.  
 DR P-PSDB; AAW66099.

XX Recombinant anti-CD22 antibodies and immuno-conjugates - of  
 PT antibodies linked to a therapeutic agent, e.g. Pseudomonas exotoxin  
 PT or a label; for inhibiting malignant B-cells  
 XX Claim 15; Fig 1; 71pp; English.  
 PS The present sequence represents the anti-CD22 monoclonal antibody  
 CC (RFB4 IgG) heavy chain variable region DNA sequence. The invention  
 CC claims for a recombinant immunoconjugate comprising of a therapeutic  
 CC agent (e.g. Pseudomonas exotoxin) or a detectable label peptide bonded  
 CC to a recombinant anti-CD22 antibody having a variable heavy (VH;  
 CC AAW66099) chain with a cysteine residue at amino acid 44 and a variable  
 CC light (VL; AAW66098) chain with a cysteine residue at amino acid 100.  
 CC The immunoconjugate is claimed to inhibit the growth of malignant  
 CC B-cells in vivo, such as rodent, canine or primate B-cells. The  
 CC anti-CD22 antibody is claimed useful for detecting CD22 protein in a  
 CC sample or in vivo in a mammal, and can be used in diagnostic kits.  
 XX

XX Sequence 369 BP; 83 A; 85 C; 110 G; 91 T; 0 other;  
 SQ Query Match 79.6%; Score 40.6; DB 19; Length 369;  
 Best Local Similarity 91.5%; Pred. No. 1.8e-06;  
 Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 5 ttatgtagtgtgtggtagcacctactatttagacactgtgcaggc 51  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 152 ttatgtagtgtgtgtaccactactatccagacactgtgaaggc 198

RESULT 14

AAT72269  
 ID AAT72269 standard; cDNA; 441 BP.  
 XX  
 AC AAT72269;  
 XX  
 DT 03-JAN-1998 (first entry)  
 XX  
 DE Chimeric MAB 15 PCR-modified heavy chain variable region cDNA.  
 XX  
 KW Humanised antibody; monoclonal antibody; MAB 15; tumour;  
 KW lung cancer; therapy; ds.  
 XX  
 OS Chimeric Mus musculus.  
 OS Chimeric synthetic.

XX Key Location/Qualifiers  
 FH sig\_peptide 12..68  
 FT /tag= a  
 FT mat\_peptide 69..428  
 FT /tag= b

XX EP781847-AL.  
 XX  
 PD 02-JUL-1997.  
 XX  
 PF 25-OCT-1996; 96EP-0117154.  
 XX  
 PR 06-NOV-1995; 95EP-0117407.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.

XX Bendig M, Jones T, Saldana J;  
 XX WPI; 1997-334904/31.  
 DR P-PSDB; AAW21656.

XX Humanised form of murine monoclonal antibody MAB 15 - useful for  
 PT treating lung cancer  
 PT Disclosure; Fig 5; 71pp; English.  
 XX This cDNA sequence comprises the heavy chain variable region VH  
 CC sequence of murine monoclonal antibody (MAB) 15 (DSM ACC2117),  
 CC modified for the expression of chimeric 15 antibody. The 5' and  
 CC 3' ends of the VH sequence (see also AAT72267) were modified by  
 CC PCR (see AAT72245-46) to provide a Kozak sequence for efficient  
 CC translation, a 5' HindIII site for cloning into HCMV vectors, a  
 CC 3' splice donor site at the J-C junction for splicing the mouse  
 CC variable regions to human constant regions and a 3' BamHI site for  
 CC cloning into HCMV vectors. The VL sequence was similarly modified  
 CC (see AAT72268). The modified VH and VL sequences were used in a  
 CC claimed process to model and design novel humanised, reshaped MAB  
 CC 15 having humanised, reshaped VH and VL sequences (see AAW21652 and  
 CC AAW21651), which can be used for treating tumours, especially lung  
 CC cancer, and for the manufacture of a drug related to tumours,  
 CC especially lung cancer.  
 XX Sequence 441 BP; 98 A; 99 C; 130 G; 114 T; 0 other;

XX Query Match 79.6%; Score 40.6; DB 18; Length 441;  
 Best Local Similarity 91.5%; Pred. No. 1.9e-06;  
 Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ttatgtagtgtgtggtagcacctactatttagacactgtgcaggc 51  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 220 ttatgagagggtgtggtgtagcacctactatccagacactgtgaaggc 266

RESULT 15  
 AAT72237  
 ID AAT72237 standard; cDNA; 445 BP.  
 XX

17

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:13 ; Search time 174.26 Seconds  
(without alignments)  
71.889 Million cell updates/sec

Title: US-09-339-922A-101  
Perfect score: 51  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
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5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40.6	79.6	923	5	PCT-US94-07659-1
2	39	76.5	413	1	US-08-253-877C-56
3	39	76.5	413	2	US-08-452-164A-56
4	39	76.5	416	4	US-08-976-183A-30
5	39	76.5	721	2	US-08-224-591-15
6	39	76.5	721	2	US-08-926-789-15
7	39	76.5	733	2	US-08-224-591-17
8	39	76.5	733	2	US-08-926-789-17
9	38	74.5	51	1	US-08-475-000-2
10	38	74.5	51	2	US-08-483-199-2
11	38	74.5	51	2	US-08-484-508-2
12	38	74.5	90	1	US-08-253-877C-70
13	38	74.5	90	2	US-08-452-164A-70
14	38	74.5	90	4	US-08-976-183A-49
15	38	74.5	357	1	US-08-475-000-15
16	38	74.5	357	2	US-08-483-199-15
17	38	74.5	357	2	US-08-484-508-15
18	37.4	73.3	354	1	US-08-326-362-1
19	37.4	73.3	357	1	US-08-331-398A-21
20	37.4	73.3	357	2	US-08-331-397B-21
21	37.4	73.3	357	2	US-08-759-804A-21
22	37.4	73.3	357	2	US-09-227-693-21
23	37.4	73.3	375	1	US-08-331-398A-59
24	37.4	73.3	375	2	US-08-331-397B-59
25	37.4	73.3	375	2	US-08-759-804A-58
26	37.4	73.3	403	1	US-08-408-133-4
27	37.4	73.3	403	1	US-08-454-683-4

28	37.4	73.3	403	2	US-08-116-778E-20	Sequence 20, Appli
29	37.4	73.3	403	2	US-08-454-680-4	Sequence 4, Appli
30	37.4	73.3	403	2	US-08-438-582-20	Sequence 20, Appli
31	37.4	73.3	403	2	US-08-483-528B-20	Sequence 20, Appli
32	37.4	73.3	403	3	US-08-673-799C-20	Sequence 5, Appli
33	37.4	73.3	474	2	US-08-653-402B-5	Sequence 9, Appli
34	37.4	73.3	474	2	US-08-653-402B-9	Sequence 19, Appli
35	35.8	70.2	783	4	US-08-487-283A-19	Sequence 5, Appli
36	34.2	67.1	357	5	PCT-US94-07659-5	Sequence 43, Appli
37	34.2	67.1	870	3	US-08-545-809A-43	Sequence 17, Appli
38	34	66.7	51	5	PCT-US93-08435-17	Sequence 48, Appli
39	34	66.7	102	5	PCT-US93-08435-48	Sequence 94, Appli
40	34	66.7	318	1	US-08-129-930B-94	Sequence 94, Appli
41	34	66.7	318	4	US-08-976-288A-94	Sequence 9, Appli
42	34	66.7	354	5	PCT-US93-08435-9	Sequence 11, Appli
43	34	66.7	389	5	PCT-US93-08435-11	Sequence 13, Appli
44	34	66.7	389	5	PCT-US93-08435-13	Sequence 14, Appli
45	34	66.7	394	4	US-08-134-346A-14	

ALIGNMENTS

RESULT 1

PCT-US94-07659-1

: Sequence 1, Application PC/TUS9407659

: GENERAL INFORMATION:

: APPLICANT: Young, Peter

: APPLICANT: Gross, Mitchell

: APPLICANT: Jonak, Zdenka L.

: APPLICANT: Theisen, Timothy

: APPLICANT: Hurle, Mark

: APPLICANT: Jackson, Jeffrey R.

: TITLE OF INVENTION: Recombinant and Humanized Il-1 beta

: TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory Disorders in Man

: NUMBER OF SEQUENCES: 21

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Smithline Beecham Corporation - Corp.

: ADDRESSEE: Intellectual Property

: STREET: 709 Swedeland Road

: CITY: King of Prussia

: STATE: PA

: COUNTRY: USA

: ZIP: 19406-2799

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: PCT/US94/07659

: FILING DATE:

: CLASSIFICATION:

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 08/090,534

: FILING DATE: 09-JUL-1993

: ATTORNEY/AGENT INFORMATION:

: NAME: Sutton, Jeffrey A.

: REGISTRATION NUMBER: 34,028

: REFERENCE/DOCKET NUMBER: P50171-1

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (610) 270-5024

: TELEFAX: (610) 270-5090

: INFORMATION FOR SEQ ID NO: 1:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 923 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: double

: TOPOLOGY: unknown

: MOLECULE TYPE: DNA (genomic)

: FEATURE:

: NAME/KEY: CDS

; LOCATION: 169..909  
PCT-US94-07659-1

Query Match 79.6%; Score 40.6; DB 5; Length 923;  
Best Local Similarity 91.5%; Pred. No. 4.1e-07;  
Matches 43; Conservative 0; Mismatches 4; Indels

Qy 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagggc 51  
|||||  
Db 377 TTAGTAGTGGTGGTGGCACCTACTATCCAGACACTGTGAAGGGC 423

```

RESULT      2
US-08-253-877C-56
; Sequence 56, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Phillip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426

```

Query Match 76.5%; Score 39; DB 1; Length 413;  
Best Local Similarity 89.4%; Pred. No. 1.4e-06;  
Matches 42; Conservative 0; Mismatches 5; Indels

Qy 5 ttagttagtggtggtggtagcacactactatatttagacactgtgcaggcc 51  
† ||||| ||||| || ||||| ||||| ||||| ||||| |||||  
pb 214 TTACTAGTGGTGGTAGTTACACTACTATTATGACAGTGTAAGGCC 260

```

RESULT 3
US-08-452-164A-56
; Sequence 56, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methytrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6..413
; US-08-452-164A-56

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Query Match	76.5%	Score 39	DB 2	Length 413
Best Local Similarity	89.4%	Pred. No. 1.4e-06		
Matches 42	Conservative 0	Mismatches 5	Indels 0	Gaps 0
QY	5	ttagtagtggctggctagcacctactatttagacacactgtcagggc	51	
Db	214	TTAGTAGTGGTGTAGTTACACCTACTATTATAGACACTGTGAAGGC	260	

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RESULT      4
US-08-976-183A-30
; Sequence 30, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANT
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
;

```

;; STREET: 3000 K. Street, N.W., Suite 500  
;; CITY: Washington, D.C.  
;; COUNTRY: USA  
;; ZIP: 20007  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/976.183A  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/595.848  
;; FILING DATE: 02-FEB-1996  
;; APPLICATION NUMBER: PCT/GB93/02529  
;; FILING DATE: 10-DEC-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: GB 9225853.2  
;; FILING DATE: 10-DEC-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 9315249.4  
;; FILING DATE: 22-JUL-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bernhard D. Saxe  
;; REGISTRATION NUMBER: 28.665  
;; REFERENCE/DOCKET NUMBER: 40283/151/CARA  
;; TELEPHONE: (202) 672-5300  
;; TELEX: 904136  
;; INFORMATION FOR SEQ ID NO: 30:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 416 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 6..416  
US-08-976-183A-30  
  
Query Match 76.5%; Score 39; DB 4; Length 416;  
Best Local Similarity 89.4%; Pred. No. 1.4e-06;  
Matches 42; Conservative 0; Mismatches 5; Indels 0;  
  
Qy 5 ttagtgtggtgtagcacctactatttagacactgtgcaggc 51  
|||||  
Db 214 TTAGTAGTGGTGTAGTTACACCTACTATTATAGACAGTGTGAAGGC 260  
  
RESULT 5  
US-08-224-591-15  
; Sequence 15, Application US/08224591  
; Patent No. 5856456  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/926.789  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/224,591  
; FILING DATE:  
; APPLICATION NUMBER: US 08/002,845  
; FILING DATE: 15-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/980,529  
; FILING DATE: 20-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.

;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/224.591  
;; FILING DATE: Herewith  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/002.845  
;; FILING DATE: 15-JAN-1993  
;; APPLICATION NUMBER: US 07/980.529  
;; FILING DATE: 20-NOV-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldstein, Jorge A.  
;; REGISTRATION NUMBER: 29,021  
;; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 721 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: both  
;; TOPOLOGY: both  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: join(1..711)  
US-08-224-591-15  
  
Query Match 76.5%; Score 39; DB 2; Length 721;  
Best Local Similarity 89.4%; Pred. No. 1.6e-06;  
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 5 ttagtgtggtgtagcacctactatttagacactgtgcaggc 51  
|||||  
Db 515 TTAGTAGTGGTGTAGTTACACCTACTATTATAGACAGTGTGAAGGC 561  
  
RESULT 6  
US-08-926-789-15  
; Sequence 15, Application US/08926789  
; Patent No. 5990275  
; GENERAL INFORMATION:  
; APPLICANT: Whitlow, Marc  
; APPLICANT: Filpula, David  
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/926.789  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/224,591  
; FILING DATE:  
; APPLICATION NUMBER: US 08/002,845  
; FILING DATE: 15-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/980,529  
; FILING DATE: 20-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.



```
;
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..711)
US-08-926-789-15

Query Match 76.5%; Score 39; DB 2; Length 721;
Best Local Similarity 89.4%; Pred. No. 1.6e-06;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
|||||
DB 515 TTAGTAGTGGTGGTAGTTACCTACTATTATTTAGACAGTGTGAAGGCC 561

RESULT 7
US-08-224-591-17
; Sequence 17, Application US/08224591
; Patent No. 5856456
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,591
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..723)
US-08-224-591-17
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;
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..711)
US-08-926-789-15

Query Match 76.5%; Score 39; DB 2; Length 733;
Best Local Similarity 89.4%; Pred. No. 1.6e-06;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
|||||
DB 527 TTAGTAGTGGTGGTAGTTACCTACTATTATTTAGACAGTGTGAAGGCC 573

RESULT 8
US-08-926-789-17
; Sequence 17, Application US/08926789
; Patent No. 5990275
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,789
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/224,591
; FILING DATE:
; APPLICATION NUMBER: US 08/002,845
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,529
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..723)
US-08-926-789-17

Query Match 76.5%; Score 39; DB 2; Length 733;
Best Local Similarity 89.4%; Pred. No. 1.6e-06;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 51
|||||
DB 527 TTAGTAGTGGTGGTAGTTACCTACTATTATTTAGACAGTGTGAAGGCC 573

RESULT 9
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US-08-475-000-2  
; Sequence 2, Application US/08475000  
; Patent No. 5811267  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,000  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0850.007  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 51 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-475-000-2

Query Match 74.5%; Score 38; DB 1; Length 51;  
Best Local Similarity 89.1%; Pred. No. 2.3e-06;  
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 tttagtggtggtgtagcacctactatttagacactgtgcagg 50  
|||||  
DB 5 TTAGTAGTGGTGGTGAACACCTACTATCCAGACAGTGTGAAGG 50

RESULT 10  
US-08-483-199-2  
; Sequence 2, Application US/08483199  
; Patent No. 5849877  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,199  
; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0850.009  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 51 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-483-199-2

Query Match 74.5%; Score 38; DB 2; Length 51;  
Best Local Similarity 89.1%; Pred. No. 2.3e-06;  
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 tttagtggtggtgtagcacctactatttagacactgtgcagg 50  
|||||  
DB 5 TTAGTAGTGGTGGTGAACACCTACTATCCAGACAGTGTGAAGG 50

RESULT 11  
US-08-484-508-2  
; Sequence 2, Application US/08484508  
; Patent No. 5948647  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,508  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0850.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 51 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-484-508-2

Query Match 74.5%; Score 38; DB 2; Length 51;  
Best Local Similarity 89.1%; Pred. No. 2.3e-06;  
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 5 TTAGTAGTGGTGGTAAACCTACTATTCCAGACAGTGTGAAGG 50

## RESULT 12

US-08-253-877C-70  
; Sequence 70, Application US/08253877C  
; Patent No. 5773001

; GENERAL INFORMATION:

; APPLICANT: Hamann, Philip R.  
; APPLICANT: Hinman, Lois  
; APPLICANT: Hollander, Irwin  
; APPLICANT: Holcomb, Ryan  
; APPLICANT: Hallett, William  
; APPLICANT: Tsou, Hwei-Ru  
; APPLICANT: Weiss, Martin J.

; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
; Agents and Intermediates for Their Synthesis

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/253,877C

; FILING DATE: 03-JUN-1994

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 32,368

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-831-3246

; TELEFAX: 201-831-3305

; INFORMATION FOR SEQ ID NO: 70:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 90 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-253-877C-70

Query Match 74.5%; Score 38; DB 1; Length 90;

Best Local Similarity 89.1%; Pred. No. 2.6e-06;

Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 11 TTAGTAGTGGTGGTAAACCTACTATTCCAGACAGTGTGAAGG 56

## RESULT 13

US-08-452-164A-70

; Sequence 70, Application US/08452164A

; Patent No. 5877296

; GENERAL INFORMATION:

; APPLICANT: Hamann, Philip R.

; APPLICANT: Hinman, Lois

; APPLICANT: Hollander, Irwin

; APPLICANT: Holcomb, Ryan

; APPLICANT: Hallett, William

; APPLICANT: Tsou, Hwei-Ru

; APPLICANT: Weiss, Martin J.

; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor

; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis  
; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Home Products Corporation

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 07054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/452,164A

; FILING DATE: 26-MAY-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 32,368-04

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-683-2158

; TELEFAX: 201-683-4117

; INFORMATION FOR SEQ ID NO: 70:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 90 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-452-164A-70

Query Match 74.5%; Score 38; DB 2; Length 90;

Best Local Similarity 89.1%; Pred. No. 2.6e-06;

Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 11 TTAGTAGTGGTGGTAAACCTACTATTCCAGACAGTGTGAAGG 56

## RESULT 14

US-08-976-183A-49

; Sequence 49, Application US/08976183A

; Patent No. 6307026

; GENERAL INFORMATION:

; APPLICANT: King, David J.

; APPLICANT: Adair, John R.

; APPLICANT: Owens, Raymond J.

; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33

; TITLE OF INVENTION: ANTIGEN

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER

; STREET: 3000 K. Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/976,183A

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/595,848

; FILING DATE: 02-FEB-1996

; APPLICATION NUMBER: PCT/GB93/02529

; FILING DATE: 10-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9225853.2  
; FILING DATE: 10-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 9315249.4  
; FILING DATE: 22-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bernhard D. Saxe  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 40283/151/CARA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 90 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "SYNTHETIC"  
US-08-976-183A-49

Query Match 74.5%; Score 38; DB 4; Length 90;  
Best Local Similarity 89.1%; Pred. No. 2.6e-06;  
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 11 TTAGTAGTGGTGGTAGTACACCTACTATTATTAGACAGTGTGAAGG 56

RESULT 15  
US-08-475-000-15  
; Sequence 15, Application US/08475000  
; Patent No. 5811267  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,000  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVEREIDE, PAUL  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0850.007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 357 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..357  
US-08-475-000-15

Query Match 74.5%; Score 38; DB 1; Length 357;  
Best Local Similarity 89.1%; Pred. No. 3.4e-06;  
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 5 ttagtagtggtggtgtagcacctactatttagacactgtgcagg 50  
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DB 152 TTAGTAGTGGTGGTAAACACCTACTATCCAGACAGTGTGAAGG 197

Search completed: August 21, 2002, 10:52:14  
Job time: 9654 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:49:01 ; Search time 2408.76 Seconds  
(without alignments)  
443.072 Million cell updates/sec

Title: US-09-339-922A-103  
Perfect score: 51  
Sequence: 1 aaagttagtagtggtgtgg.....atccagacactgtgcagggc 51

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
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Maximum Match 100%  
Listing first 45 summaries

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- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
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- 17: em\_hum.\*
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- 19: em\_mu.\*
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- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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DEFINITION	AX060882	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
ACCESSION	AX060882	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
VERSION	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
KEYWORDS	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
SOURCE	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
ORGANISM	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
REFERENCE	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
AUTHORS	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
TITLE	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
JOURNAL	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
FEATURES	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
source	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001
CDS	AX060882.1	GI:12406260	51 bp	DNA	linear	PAT 22-JAN-2001

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3	47.8	93.7	87	6	AX060790	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
4	47.8	93.7	351	6	AX060780	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
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6	45.4	89.0	339	10	MMIGH4	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
7	45.4	89.0	375	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
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22	42.8	83.9	363	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
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27	42.8	83.9	363	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
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29	42.8	83.9	363	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
30	42.8	83.9	363	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
31	42.8	83.9	363	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
32	42.8	83.9	363	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
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37	42.8	83.9	363	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
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40	42.8	83.9	363	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
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42	42.8	83.9	363	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
43	42.8	83.9	363	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
44	42.8	83.9	363	10	MMHCVRI5	Sequence 103 from Patent WO0078815.	51 bp	DNA	linear	PAT 22-JAN-2001
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Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAAGTTAGTAGTGGTGGTGTAGCACCCTACTATCCAGACACTGTGCAGGCC 51

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LOCUS      AX060880      51 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 101 from Patent WO0078815.
ACCESSION  AX060880
VERSION     AX060880.1 GI:12406258
KEYWORDS   .
SOURCE      synthetic construct.
ORGANISM    synthetic construct
            artificial sequence.
REFERENCE   1 (bases 1 to 51)
AUTHORS     Huse,W.D. and Wu,H.
TITLE       Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
            encoding same and methods of use
JOURNAL     Patent: WO 0078815-A 101 28-DEC-2000;
            Applied Molecular Evolution (US)
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Best Local Similarity 96.1%; Pred. No. 2.1e-09;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 AAAGTTAGTAGTGGTGGTGTAGCACCCTACTATTTAGACACTGTGCAGGCC 51

RESULT 3
LOCUS      AX060790      87 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 11 from Patent WO0078815.
ACCESSION  AX060790
VERSION     AX060790.1 GI:12406170
KEYWORDS   .
SOURCE      synthetic construct.
ORGANISM    synthetic construct
            artificial sequence.
REFERENCE   1 (bases 1 to 87)
AUTHORS     Huse,W.D. and Wu,H.
TITLE       Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
            encoding same and methods of use
JOURNAL     Patent: WO 0078815-A 11 28-DEC-2000;
            Applied Molecular Evolution (US)
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Query Match      93.7%; Score 47.8; DB 6; Length 87;
Best Local Similarity 96.1%; Pred. No. 2.1e-09;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 10 AAAGTTAGTAGTGGTGGTGTAGCACCCTACTATTTAGACACTGTGCAGGCC 60

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LOCUS      AX060780      351 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 1 from Patent WO0078815.
ACCESSION  AX060780
VERSION     AX060780.1 GI:12406160
KEYWORDS   .
SOURCE      synthetic construct.
ORGANISM    synthetic construct
            artificial sequence.
REFERENCE   1 (bases 1 to 351)
AUTHORS     Huse,W.D. and Wu,H.
TITLE       Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
            encoding same and methods of use
JOURNAL     Patent: WO 0078815-A 1 28-DEC-2000;
            Applied Molecular Evolution (US)
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            /translation="QVQLVSGGSGVQPGKSLRLSCAASGFTFSYDMSWVRQAPGKG
            LEWAKVSSGGSTYYLDTVQGRFTISRDNSKNTLYLQMNSLRAEDTAVYVCARHNYG
            SFAYWGQGTIVTVSS"
BASE COUNT      80 a      82 c      104 g      85 t
ORIGIN

Query Match      93.7%; Score 47.8; DB 6; Length 351;
Best Local Similarity 96.1%; Pred. No. 2.2e-09;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcacctactatccagacactgtgcaggcc 51
|||||
Db 148 AAAGTTAGTAGTGGTGGTGTAGCACCCTACTATTTAGACACTGTGCAGGCC 198

RESULT 5
LOCUS      AX060784      351 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 5 from Patent WO0078815.
ACCESSION  AX060784
VERSION     AX060784.1 GI:12406164
KEYWORDS   .
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 351)
AUTHORS     Huse,W.D. and Wu,H.

```

TITLE Anti-g(a) v2.g(b)3? recombinant human antibodies, nucleic acids  
JOURNAL encoding same and methods of use  
Patent: WO 0078815-A 5 28-DEC-2000;  
Applied Molecular Evolution (US)  
FEATURES Location/Qualifiers  
source 1..351  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
<1..>351  
/note="unnamed protein product"  
/codon\_start=1  
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/db\_xref="GI:12406165"  
/translation="EVQLVESGGGLVPGGSLRLSCAASGFAFSSYDMSWVRQIPKRR  
LEWAKVSSGGSTYPDTVKGRFTISRDNKNTLYLQMSLSKSEDTAMYICARHNYG  
SPAYWGQGLTVTSSA"  
BASE COUNT 83 a 81 c 102 g 85 t  
ORIGIN  
Query Match 93.7%; Score 47.8; DB 6; Length 351;  
Best Local Similarity 96.1%; Pred. No. 2.2e-09;  
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 aaagttagtagtggtgtagcactatccagacactgtgcagggc 51  
|||||  
Db 148 AAAGTTAGTAGTGGTGGTAGCCTACTATTATGACACTGTGCAGGGC 198  
  
RESULT 6  
MMIGH4  
LOCUS M.musculus mRNA (L14-2G9) for IgH heavy chain V region. ROD 12-OCT-1992  
DEFINITION X59107  
ACCESSION  
VERSION X59107.1 GI:51944  
KEYWORDS Ig heavy chain; Ig variable region; immunoglobulin; rearranged.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 339)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kavaler, J.  
TITLE Direct Submission  
JOURNAL Submitted (15-APR-1991) J. Kavaler, Wistar Institute, 3601 Spruce  
Street, Philadelphia PA 19104, USA  
REFERENCE 2 (bases 1 to 339)  
AUTHORS Kavaler, J.  
JOURNAL Unpublished  
FEATURES Location/Qualifiers  
source 1..339  
/organism="Mus musculus"  
/strain="BALB/c"  
/db\_xref="taxon:10090"  
/cell\_line="L14-2G9"  
/cell\_type="B cell"  
/tissue\_type="hybridoma"  
1..339  
/partial  
/codon\_start=1  
/product="IgH heavy chain V region"  
/protein\_id="CAA41833.1"  
/db\_xref="GI:51945"  
/translation="TVSLGSLVPGGSLKLSCAASGFAFSSYDMSWVRQTPKRLKRW  
AVISSGGSTYPDTVKGRFTISRDNKNTLYLQMSLSKSEDTAMYICARHPYGNYYA  
MDYWGQGSVT"  
BASE COUNT 84 a 83 c 92 g 80 t  
ORIGIN  
Query Match 89.0%; Score 45.4; DB 10; Length 339;  
Best Local Similarity 97.9%; Pred. No. 2.3e-08;  
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcactatccagacactgtgcagggc 51  
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Db 140 TTAGTAGTGGTGGTAGCCTACTATCCAGACACTGTGAAGGGC 186  
  
RESULT 7  
MMAHCVR15  
LOCUS M.musculus antibody heavy chain variable region (375bp). ROD 31-AUG-1996  
DEFINITION X90890  
ACCESSION  
VERSION X90890.1 GI:1518290  
KEYWORDS antibody heavy chain; variable region.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 375)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Geiser, M. and Kretzschmar, T.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 375)  
AUTHORS Geiser, M.  
TITLE Direct Submission  
JOURNAL Submitted (17-AUG-1995) M. Geiser, CIBA-GEIGY LTD, CDDT,  
K-681.5.46, CH-4002, Basel, SWITZERLAND  
FEATURES Location/Qualifiers  
source 1..375  
/organism="Mus musculus"  
/strain="Balb/c"  
/db\_xref="taxon:10090"  
/cell\_type="lymphocytes"  
/tissue\_type="spleen"  
/dev\_stage="12 weeks old"  
<1..>375  
/codon\_start=1  
/product="antibody heavy chain variable region"  
/protein\_id="CAA62398.1"  
/db\_xref="GI:1518291"  
/translation="EVKLSEGGGLVPGGSLKLSCAASGFAFSSYDMSWVRQTPKRR  
LEWAVISSGGSTYPDTVKGRFTISRDNKNTLYLQMSLSKSEDTAMYICAROKGF  
YDYLTRNWFVWGAGTLTVSS"  
BASE COUNT 90 a 91 c 107 g 87 t  
ORIGIN  
Query Match 89.0%; Score 45.4; DB 10; Length 375;  
Best Local Similarity 97.9%; Pred. No. 2.3e-08;  
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 ttagtagtggtggtgtagcactatccagacactgtgcagggc 51  
|||||  
Db 152 TTAGTAGTGGTGGTAGCCTACTATCCAGACACTGTGAAGGGC 198  
  
RESULT 8  
MMA229172  
LOCUS Mus musculus rearranged cDNA for VH region of anti arsonate  
DEFINITION antibody (B cell hybridoma A22).  
ACCESSION AJ229172  
VERSION AJ229172.1 GI:3135848  
KEYWORDS anti arsonate antibody; diversity segment; heavy chain;  
immunoglobulin; joining segment; variable segment.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 345)  
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Ismaili, J., Razanajao, D., Van Acker, A., Wuilmart, C., Mancini, I.,  
Heinen, E., Leo, O., Lebecque, S., Urbain, J., and Braйт, M.  
TITLE Molecular and cellular basis of the altered immune response against  
arsonate in irradiated A/J mice autologously reconstituted  
JOURNAL Int. Immunol. 11 (7), 1157-1167 (1999)  
MEDLINE 99315320

```

REFERENCE      2 (bases 1 to 345)
AUTHORS        Urbain J.J.
TITLE          Direct Submission
JOURNAL        Submitted (13-MAY-1998) Urbain J.J., Biologie moleculaire,
                Universite Libre de Bruxelles, 67 rue des chevaux, Rhode-St-Genese,
                1640, BELGIUM
FEATURES       Location/Qualifiers
                source
                1..345
                /organism="Mus musculus"
                /strain="A/J"
                /db_xref="taxon:10090"
                /rearranged
                /cell_line="B cell"
                /cell_type="B cell hybridoma"
                /clone="A22"
                <1..276
                /gene="IGHF"
                /evidence="experimental"
                /product="variable segment of immunoglobulin heavy chain"
                V_segment
                1..276
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                /evidence="experimental"
                /product="variable segment of immunoglobulin heavy chain"
                gene
                1..276
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                /evidence="experimental"
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                277..300
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                /evidence="experimental"
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                J_segment
                301..345
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                /evidence="experimental"
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                1..345
                87.1%; Score 44.4; DB 10; Length 345;
                Query Match      87.1%; Score 44.4; DB 10; Length 345;
                Best Local Similarity 95.7%; Pred. No. 6.1e-08;
                Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5      ttagtagtggtggtgtagcacttaccagacactgtgcaggcc 51
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Db      134      TTAGTAGTGTGTTAGCACCCTACTATCCAGACAGTGTGAGGGC 180
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
A62608/c      A62608      85 bp      DNA      linear      PAT 12-MAR-1998
LOCUS
DEFINITION    Sequence 27 from Patent EP0781847.
ACCESSION     A62608
VERSION       A62608.1 GI:3716515
KEYWORDS      .
SOURCE        unidentified.
              unidentified.
              ORGANISM
              1 (bases 1 to 85)
              Bendig,M.D., Saldana,J.D. and Jones,T.D.
              Humanized monoclonal antibody
              TITLE
              Patent: EP 0781847-A 27 02-JUL-1997;
              MERCK PATENT GMBH (DE)
              COMMENT
              Other publication JP 9183799 19970715.
              Location/Qualifiers
              source
              1..85
              /organism="unidentified"
              /db_xref="taxon:32644"
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              85.9%; Score 43.8; DB 6; Length 85;
              Query Match      85.9%; Score 43.8; DB 6; Length 85;
              Best Local Similarity 95.7%; Pred. No. 1e-07;
              Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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QY      5      ttagtagtggtggtgtagcacttaccagacactgtgcaggcc 51
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      73      TTAGTAGAGGTGGTGTAGCACCCTACTATCCAGACACTGTGAAGGCC 27
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RESULT 10
MUSIGVAAS      345 bp      mRNA      linear      ROD 27-APR-1993
LOCUS
DEFINITION    Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
                sequence.
ACCESSION     L08996
VERSION       L08996.1 GI:197989
KEYWORDS      V-region; immunoglobulin V region; processed gene.
SOURCE        Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
              Mus musculus
              ORGANISM
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
              1 (bases 1 to 345)
              Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
              Pisetky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
              V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
              mice
              J. Immunol. 150, 1591-1610 (1993)
              93163585
              Location/Qualifiers
              source
              1..345
              /organism="Mus musculus"
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              /db_xref="taxon:10090"
              /cell_line="anti-Sm hybridoma 14C10"
              /cell_type="B-cell"
              /tissue_type="spleen"
              /dev_stage="adult"
              BASE COUNT      80 a      85 c      102 g      78 t
              ORIGIN
              85.9%; Score 43.8; DB 10; Length 345;
              Query Match      85.9%; Score 43.8; DB 10; Length 345;
              Best Local Similarity 95.7%; Pred. No. 1.1e-07;
              Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5      ttagtagtggtggtgtagcacttaccagacactgtgcaggcc 51
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      151      TTAGTAGTGTGTTAGCACCCTACTATCCAGACAGTGTGAAGGCC 197
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
MUSIGVAAS      345 bp      mRNA      linear      ROD 27-APR-1993
LOCUS
DEFINITION    Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
                sequence.
ACCESSION     L08996
VERSION       L08996.1 GI:197994
KEYWORDS      V-region; immunoglobulin V region; processed gene.
SOURCE        Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
              Mus musculus
              ORGANISM
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
              1 (bases 1 to 345)
              Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
              Pisetky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
              V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
              mice
              J. Immunol. 150, 1591-1610 (1993)
              93163585
              Location/Qualifiers
              source
              1..345
              /organism="Mus musculus"
              /strain="mrl/mp-lpr/lpr"
              /db_xref="taxon:10090"
              /cell_line="anti-Sm hybridoma 22F6"
              /cell_type="B-cell"

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JOURNAL J. Immunol. 150, 1591-1610 (1993)
MEDLINE 93163585
FEATURES
  source      Location/Qualifiers
  base_count  80 a 86 c 102 g 77 t
  origin      /tissue_type="spleen"
              /dev_stage="adult"

Query Match      85.9%; Score 43.8; DB 10; Length 345;
Best Local Similarity 95.7%; Pred. No. 1.1e-07;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccactatccagacactgtgcagggc 51
    |||||||
Db 152 TTAGTAGTGGTGGTGTAGCACCCTACTATCCAGACACTGTGAAGGC 198

RESULT 12
MUSIGVABB
LOCUS Mus musculus Ig rearranged anti-Sm hybridoma mRNA linear ROD 27-APR-1993
DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
sequence.
ACCESSION L09000
VERSION L09000.1 GI:197998
KEYWORDS V-region; immunoglobulin V region; processed gene.
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 348)
AUTHORS Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
TITLE V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
mice
JOURNAL J. Immunol. 150, 1591-1610 (1993)
MEDLINE 93163585
FEATURES
  source      Location/Qualifiers
  base_count  80 a 87 c 102 g 79 t
  origin      /organism="Mus musculus"
              /strain="mrl/mp-lpr/lpr"
              /db_xref="taxon:10090"
              /cell_line="anti-Sm hybridoma 4D12"
              /cell_type="B-cell"
              /tissue_type="spleen"
              /dev_stage="adult"

Query Match      85.9%; Score 43.8; DB 10; Length 348;
Best Local Similarity 95.7%; Pred. No. 1.1e-07;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccactatccagacactgtgcagggc 51
    |||||||
Db 152 TTAGTAGTGGTGGTGTAGCACCCTACTATCCAGACACTGTGAAGGC 198

RESULT 13
MUSIGVAAV
LOCUS Mus musculus Ig rearranged anti-Sm hybridoma mRNA linear ROD 27-APR-1993
DEFINITION Mus musculus Ig rearranged anti-Sm hybridoma mRNA V-region
sequence.
ACCESSION L08997
VERSION L08997.1 GI:197995
KEYWORDS V-region; immunoglobulin V region; processed gene.
SOURCE Mus musculus (strain mrl/mp-lpr/lpr) adult spleen mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 351)
AUTHORS Bloom,D.D., Davignon,J.-L., Retter,M.W., Shlomchik,M.J.,
Pisetsky,D.S., Cohen,P.L., Eisenberg,R.A. and Clarke,S.H.
TITLE V region gene analysis of anti-sm hybridomas from mrl/mp-lpr/lpr
mice

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JOURNAL J. Immunol. 150, 1591-1610 (1993)
MEDLINE 93163585
FEATURES
  source      Location/Qualifiers
  base_count  82 a 87 c 103 g 79 t
  origin      /organism="Mus musculus"
              /strain="mrl/mp-lpr/lpr"
              /db_xref="taxon:10090"
              /cell_line="anti-Sm hybridoma 2E10"
              /cell_type="B-cell"
              /tissue_type="spleen"
              /dev_stage="adult"

Query Match      85.9%; Score 43.8; DB 10; Length 351;
Best Local Similarity 95.7%; Pred. No. 1.1e-07;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccactatccagacactgtgcagggc 51
    |||||||
Db 152 TTAGTAGTGGTGGTGTAGCACCCTACTATCCAGACACTGTGAAGGC 198

RESULT 14
LOCUS A62623 441 bp DNA linear PAT 12-MAR-1998
DEFINITION Sequence 42 from Patent EP0781847.
ACCESSION A62623
VERSION A62623.1 GI:3716530
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 441)
AUTHORS Bendig,M.D., Saldana,J.D. and Jones,T.D.
TITLE Humanized monoclonal antibody
JOURNAL Patent: EP 0781847-A 42 02-JUL-1997;
MERCK PATENT GMBH (DE)
COMMENT Other publication JP 9183799 19970715.
FEATURES
  source      Location/Qualifiers
  base_count  98 a 99 c 130 g 114 t
  origin      /organism="unidentified"
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              misc_signal 1..11
              sig_peptide 12..68
              CDS 12..>428
              /function="FR'S, CDR'S"
              /codon_start=1
              /product="CHIMERIC MAB 15, HEAVY CHAIN VARIABLE REGION"
              /protein_id="CAA03670.1"
              /db_xref="GI:4530024"
              /translation="MNFGLSLIFLVLTLKGVKCEVQVVESSGGLVKPGSLKLSCAAS
              GFAESDYDMSWVROTPEKRLWVAYLSRGSGSTYPDVKGRFTISRDNAKILFLQM
              TSLKSEDAAMYICARHGEEVPRWEDYWGQGLVTVSA"

Query Match      85.9%; Score 43.8; DB 6; Length 441;
Best Local Similarity 95.7%; Pred. No. 1.1e-07;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ttagtagtggtggtgtagcaccactatccagacactgtgcagggc 51
    |||||||
Db 220 TTAGTAGAGGTGGTGTAGCACCCTACTATCCAGACACTGTGAAGGC 266

RESULT 15
LOCUS A62635 445 bp DNA linear PAT 12-MAR-1998
DEFINITION Sequence 54 from Patent EP0781847.
ACCESSION A62635

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Query Match      85.9%; Score 43.8; DB 6; Length 445;
Best Local Similarity 95.1%; Pred. NO. 1.1e-07;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ttatgtagtggtggttagcacctactatccagacactgtgcagggc 51
Db 224 TTACTAGAGGTGTTGTTAGCACCTACTATCCAGACACTGTGACAGGCC 270

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Search completed: August 21, 2002, 10:49:02  
Job time: 9757 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 09:55:46 ; Search time 6260.2 Seconds  
(without alignments)  
109.956 Million cell updates/sec

Title: US-09-339-922a-103

Perfect score: 51

Sequence: 1 aaagttagtagtggtggtgg.....atccagacactgtgcaggc 51

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hct:*
9: gb_est1:*
10: gb_est2:*
11: gb_hct:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query % Match	Length	DB ID	Description
1	40.6	79.6	861	10	BI455668
2	39	76.5	650	10	BF579001
3	39	76.5	837	10	BG966355
4	38.4	75.3	662	10	BF163874
5	38.4	75.3	883	10	BI151077
6	38.4	75.3	908	10	BF161883
7	38.4	75.3	913	10	BF162056
8	38	74.5	877	10	BF144493
9	37.4	73.3	333	10	BI336517
10	37.4	73.3	424	10	BI337375
11	37.4	73.3	469	9	AI645111
12	37.4	73.3	823	9	AA170256
13	36.4	71.4	342	9	BB869694
14	36.4	71.4	494	10	BG145342
15	36.4	71.4	548	9	AW408295
16	35.8	70.2	758	10	BM083708
17	35.8	70.2	954	10	BG963956

18	35.2	69.0	898	10	BG757960
19	34.8	68.2	404	10	BF452207
20	34.8	68.2	406	9	AW403983
21	34.8	68.2	1559	10	BF138708
22	34.2	67.1	308	10	BF844139
23	34.2	67.1	330	10	F14516
24	34.2	67.1	332	10	BF155433
25	34.2	67.1	367	10	BI305075
26	34.2	67.1	372	9	AA581192
27	34.2	67.1	454	9	AW824857
28	34.2	67.1	648	10	BG340670
29	34.2	67.1	652	10	BG965201
30	34.2	67.1	689	10	BF579926
31	34.2	67.1	718	10	BF138279
32	34.2	67.1	735	10	BG745292
33	34.2	67.1	737	10	BF974929
34	34.2	67.1	862	10	BF143948
35	34.2	67.1	874	10	BF179541
36	34.2	67.1	875	10	BG340548
37	34.2	67.1	966	10	BG745389
38	34.2	67.1	1012	10	BF142302
39	33.4	65.5	672	12	AZ433093
40	33.2	65.1	624	12	BH021317
41	33.2	65.1	677	10	BE286624
42	33.2	65.1	1586	11	BC018461
43	32.6	63.9	294	9	AW606245
44	32.6	63.9	406	9	AW401971
45	32.6	63.9	412	9	AW800162

#### ALIGNMENTS

RESULT	1				
BI455668					
LOCUS	603173862F1	NCI_CGAP_Mam5	Mus musculus	cdna clone	IMAGE:5253279 5',
DEFINITION	mRNA sequence.				
ACCESSION	BI455668				
VERSION	BI455668.1	GI:15246324			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	1 (bases 1 to 861)				
REFERENCE	NIH-MGC	http://mgc.ncl.nih.gov/.			
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)				
TITLE	Unpublished (1999)				
JOURNAL	Contact: Robert Strausberg, Ph.D.				
COMMENT					

FEATURES	Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys			
source	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	http://image.llnl.gov			
	Plate: LLAM11639 row: 1 column: 16			
	High quality sequence stop: 780.			
	Location/Qualifiers			
	1. .861			
	/organism="Mus musculus"			
	/strain="C57/B6"			
	/db_xref="taxon:10090"			
	/clone="IMAGE:5253279"			
	/clone_lib="NCL_CGAP_Mam5"			
	/tissue_type="tumor, gross tissue"			
	/dev_stages="7 months"			
	/lab_host="DH10B"			
	/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;			
	Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.			
	Library constructed by Life Technologies. Investigators			

```

providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
BASE COUNT 205 a 239 c 211 g 206 t
ORIGIN

Query Match 79.6%; Score 40.6; DB 10; Length 861;
Best Local Similarity 91.5%; Pred. No. 0.00021;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtgtagcaccattactatccagacactgtgcaggcc 51
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 279 TTAGTAATGCTGGTGGTAGCACCTATTATCCAGACACTGTGAAGGCC 325

RESULT 2
BF579001
LOCUS
DEFINITION 602096117F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4215844 5',
mRNA sequence.
ACCESSION BF579001
VERSION BF579001.1 GI:11652713
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 650)
/clone_lib="NCI_CGAP_Co24"
/lab_host="NIH-MGC http://mgc.nci.nih.gov/"
/note="Organ: colon; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
High quality sequence stop: 649.
Plate: LLAM9792 row: b column: 05
Location/Qualifiers
1. .650
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4215844"
/clone_lib="NCI_CGAP_Co24"
/lab_host="NIH-MGC http://mgc.nci.nih.gov/"
/note="Organ: colon; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 154 a 177 c 165 g 154 t
ORIGIN

Query Match 76.5%; Score 39; DB 10; Length 650;
Best Local Similarity 89.4%; Pred. No. 0.00071;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ttagtagtggtgtagcaccattactatccagacactgtgcaggcc 51
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 279 TTAATAGTAATGCTGGTAGCACCTACTATCCAGACACTGTGAAGGCC 325

RESULT 3
BG966355
LOCUS
DEFINITION 602832843F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4987379 5',
mRNA sequence.
ACCESSION BG966355

```

```

VERSTON BG966355.1 GI:14353992
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 837)
/clone_lib="NCI_CGAP_Co24"
/lab_host="NIH-MGC http://mgc.nci.nih.gov/"
/note="Organ: colon; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
High quality sequence stop: 692.
Plate: LLAM10998 row: e column: 12
Location/Qualifiers
1. .837
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4987379"
/clone_lib="NCI_CGAP_Co24"
/lab_host="NIH-MGC http://mgc.nci.nih.gov/"
/note="Organ: colon; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 201 a 222 c 218 g 196 t
ORIGIN

Query Match 76.5%; Score 39; DB 10; Length 837;
Best Local Similarity 89.4%; Pred. No. 0.00078;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ttagtagtggtgtagcaccattactatccagacactgtgcaggcc 51
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 286 TTAGTGGTGGTGGTAGCACCTACTATCCAGACAAATGAAGGCC 332

RESULT 4
BF163874
LOCUS
DEFINITION 601772386F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3991460 5',
mRNA sequence.
ACCESSION BF163874
VERSION BF163874.1 GI:11044152
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 662)
/clone_lib="NCI_CGAP_Co24"
/lab_host="NIH-MGC http://mgc.nci.nih.gov/"
/note="Organ: colon; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 154 a 177 c 165 g 154 t
ORIGIN

Query Match 76.5%; Score 39; DB 10; Length 650;
Best Local Similarity 89.4%; Pred. No. 0.00071;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ttagtagtggtgtagcaccattactatccagacactgtgcaggcc 51
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 279 TTAATAGTAATGCTGGTAGCACCTACTATCCAGACACTGTGAAGGCC 325

RESULT 3
BG966355
LOCUS
DEFINITION 602832843F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4987379 5',
mRNA sequence.
ACCESSION BG966355

```

Query Match 75.3%; Score 38.4; DB 10; Length 883;

RESULT	7
BF162056	
LOCUS	913 bp mRNA linear EST 30-OCT-2000
DEFINITION	601768714F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3987986 5', mRNA sequence.
ACCESSION	BF162056
VERSION	BF162056.1 GI:11042257
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus









```

BG145342          494 bp      mRNA      linear      EST 01-FEB-2000
LOCUS              Soares_mouse_MNGB_bcell Mus musculus cDNA clone
DEFINITION IMAGE:3382089 5' similar to SW:HV58_MOUSE P18529 IG HEAVY CHAIN V
REGION 5-76 PRECURSOR. ; mRNA sequence.

ACCESSION BG145342.1 GI:12648749
VERSION     house mouse
KEYWORDS    Mus musculus
SOURCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 494)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TUMOR Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Other_ESTs: uu72g05.xl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1087085
Seq primer: -40RP from Gibco
High quality sequence stop: 471.
Location/Qualifiers
            1..494
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            /clone="IMAGE:3382089"
            /clone_lib="Soares_mouse_MNGB_bcell"
            /lab_host="PHI08 (phage-resistant)"
            /notes="Organ: germinal B-cell; Vector: pT7T3D-Pac
            (Pharmacia) with a modified polylinker; Site_1: Not I;
            Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
            oligo(dT) primer [5'
            TGTTCACCAATCTGAAGGGAGGCGCCCTGGTTTTTTTTTTTTTTTTTTTTTTT
            T 3']; double-stranded cDNA was ligated to Eco RI
            adaptors (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of the modified pT7T3 vector.
            Library is normalized; constructed by Bento Soares and
            M.Fatima Bonaldo."
BASE COUNT  115 a 136 c 131 g 112 t
ORIGIN

Query Match       71.4%; Score 36.4; DB 10; Length 494;
Best Local Similarity 87.0%; Pred. No. 0.0055;
Matches 40; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY  5 ttagtatgttggtggtagcacctactattccagacacctgtgcaggg 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  178 TTAGTAGTGGTAGTTCACCTACTATCCAGACACTGTGAGGG 223

RESULT 15
AW408295          548 bp      mRNA      linear      EST 16-FEB-2000
LOCUS              UI-HP-BK0-abj-d-12-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3056327 5', mRNA sequence.

ACCESSION AW408295
VERSION     human
KEYWORDS    EST.
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE   1 (bases 1 to 548)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov

```

```

Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES             Location/Qualifiers
     source            1..548
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3056327"
                     /clone_lib="NIH_MGC_36"
                     /tissue_type="lymph"
                     /cell_type="germlinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7t3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5Kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT          109 a   148 c   156 g   135 t
ORIGIN

Query Match          71.4%; Score 36.4; DB 9; Length 548;
Best Local Similarity 87.0%; Pred. No. 0.0057;
Matches 40; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatccagacactgtgcaggg 50
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 276 TTAGTTGGGATGGGTGGTGGACCTACTATGCAGACTCTGTGAAGGG 321

Search completed: August 21, 2002, 09:55:47
Job time: 9310 sec

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Search completed: August 21, 2002, 09:55:47  
Job time: 9310 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:27 ; Search time 754.01 Seconds  
(without alignments)  
116.129 Million cell updates/sec

Title: US-09-339-922A-103

Perfect score: 51

Sequence: 1 aaagttagtagtggtgtgg.....atccagacactgtgcagggc 51

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_032802.\*  
1: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA1982.DAT.\*  
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22: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA2001A.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA2001B.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseq-nbml/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	51	22	AAF28235
2	47.8	93.7	51	22	AAF28234
3	47.8	93.7	87	19	AAV49826
4	47.8	93.7	87	22	AAH74629
5	47.8	93.7	87	22	AAF28181
6	47.8	93.7	351	19	AAV49820
7	47.8	93.7	351	19	AAV49822
8	47.8	93.7	351	22	AAH74623
9	47.8	93.7	351	22	AAH74625

10	47.8	93.7	351	22	AAF28175	Vitaxin heavy chai
11	47.8	93.7	351	22	AAF28177	Antibody LM609 hea
12	43.8	85.9	85	18	AAV72258	Mouse Mab 15 heavy
13	43.8	85.9	369	19	AAV07642	anti-CD22 monoclon
14	43.8	85.9	441	18	AAV72269	Chimeric MAB 15 PC
15	43.8	85.9	445	18	AAV72237	Humanised reshaped
16	43.8	85.9	457	18	AAV72267	Mouse Mab 15 heavy
17	43.8	85.9	923	16	AAV51436	Murine MAB SK48-E2
18	42.2	82.7	482	11	AAQ05355	Sequence encoding
19	41.2	80.8	51	20	AAV44992	15D3 antibody heav
20	41.2	80.8	51	20	AAV44994	15D3 VH chain CDR2
21	41.2	80.8	357	19	AAV44997	15D3 antibody heav
22	41.2	80.8	357	20	AAV10957	15D3 VH chain codi
23	41.2	80.8	357	20	AAV08933	Antibody 15D3 heav
24	41.2	80.8	480	13	AAQ20070	MRK16-H chain. Ch
25	40.6	79.6	351	16	AAQ96282	Human IgE receptor
26	40.6	79.6	351	18	AAQ90025	CDNA encoding heav
27	40.6	79.6	357	17	AAV28000	B5 immunoglobulin
28	40.6	79.6	360	17	AAV33445	EGF receptor chime
29	40.6	79.6	363	18	AAV75583	Monoclonal antibod
30	40.6	79.6	363	20	AAV81002	Murine 340 Vh DNA
31	40.6	79.6	363	24	AAV25246	Mouse monoclonal a
32	40.6	79.6	474	18	AAV70808	Mouse anti-idiotyp
33	40.6	79.6	474	18	AAV70810	Mouse anti-idiotyp
34	40.6	79.6	582	18	AAV90020	DNA encoding heav
35	40.6	79.6	761	20	AAV01214	Human antiFc epsll
36	40.6	79.6	770	20	AAV01216	Human antiFc epsll
37	39	76.5	80	24	AAV97073	Humanised TRA-8 he
38	39	76.5	354	14	AAQ48765	Monoclonal antibod
39	39	76.5	422	22	AAV90629	Plasmid gamma1WT-T
40	39	76.5	747	22	AAV30725	Anti-FIX/FIXa anti
41	39	76.5	747	22	AAV30726	Anti-FIX/FIXa anti
42	39	76.5	783	16	AAV08490	Anti-C5 MAB N19/8
43	39	76.5	888	22	AAV87642	Single chain antib
44	38.8	76.1	3223	22	AAV11982	DNA encoding Human
45	38	74.5	125	19	AAV24567	Chimeric antibody

#### ALIGNMENTS

RESULT 1  
AAF28235  
ID AAF28235 standard; DNA; 51 BP.  
XX  
AC AAF28235;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE DNA encoding enhanced 2236-38/ 6H6LH heavy chain CDR2.  
XX  
KW LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis;  
XX inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
XX  
OS Unidentified.  
XX  
PN WO200078815-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 23-JUN-2000; 2000WO-US17454.  
XX  
PR 24-JUN-1999; 99US-0339922.  
XX  
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX  
PI Huse WD, Wu H;  
XX  
DR WPI; 2001-050110/06.  
XX  
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX Clam 14; Page 105; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphaVbeta3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

SQ Sequence 51 BP; 13 A; 10 C; 16 G; 12 T; 0 other;

Query Match 100.0%; Score 51; DB 22; Length 51;

Best Local Similarity 100.0%; Pred. No. 1.7e-10;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaagttagtggtggtgtagcactactatccagacactgtgcaggc 51

Db 1 aaagttagtggtggtgtagcactactatccagacactgtgcaggc 51

RESULT 2

AAF28234

ID AAF28234 standard; DNA; 51 BP.

XX AAF28234;

AC AAF28234;

DT 03-APR-2001 (first entry)

XX

DE DNA encoding enhanced 5H6LH heavy chain CDR2.

XX

XX LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

KW

XX Unidentified.

OS

XX WO200078815-A1.

PN

XX 28-DEC-2000.

PD

XX 23-JUN-2000; 2000WO-US17454.

PF

XX 24-JUN-1999; 99US-0339922.

PR

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

PA

XX Huse WD, Wu H;

PI

XX WPI; 2001-050110/06.

DR

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

XX to alpha(V)beta3(3) integrin, useful in the diagnosis and treatment of

PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

XX

XX Claim 16; Page 105; 132pp; English.

PS

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphaVbeta3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphaVbeta3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and Kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

CC osteoporosis.

XX

SQ Sequence 51 BP; 13 A; 8 C; 16 G; 14 T; 0 other;

Query Match 93.7%; Score 47.8; DB 22; Length 51;

Best Local Similarity 96.1%; Pred. No. 3e-09;

Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtggtggtgtagcactactatccagacactgtgcaggc 51

Db 1 aaagttagtggtggtgtagcactactatccagacactgtgcaggc 51

RESULT 3

AAV49826

ID AAV49826 standard; DNA; 87 BP.

XX AAV49826;

AC AAV49826;

DT 02-NOV-1998 (first entry)

XX

DE LM609 grafted antibody variable region oligonucleotide #3.

XX

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; ss.

XX

OS Synthetic.

OS Mus sp.

XX

PN WO9833919-A2.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US01826.

XX

PR 30-JAN-1997; 97US-0791391.

XX

PA (IXSY-) IXSYS INC.

XX

PI Glaser SM, Huse WD;

XX

DR WPI; 1998-437472/37.

XX

XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

XX

PS Example 2; Page 65; 129pp; English.

XX

CC AAV49824-W49833 are oligonucleotides used in the construction of grafted

CC LM609 monoclonal antibody heavy and light chain variable regions. LM609

CC and the antibody vitaxin bind selectively to integrin alphavbeta3 and

CC can be used to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

CC greater than that of parent the parent antibody.

XX

SQ Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;

Query Match 93.7%; Score 47.8; DB 19; Length 87;

Best Local Similarity 96.1%; Pred. No. 3.3e-09;

Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcactactatccagacactgtgcagggc 51  
 |||||  
 Db 10 aaagttagtagtggtggtgtagcactactattagacactgtgcagggc 60

## RESULT 4

AAH74629  
 ID AAH74629 standard; DNA; 87 BP.

XX AC AAH74629;

XX DT 15-OCT-2001 (first entry)

XX DE PCR primer for heavy chain variable region of LM609 antibody.

XX KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer; PCR primer; ss.

XX OS Mus sp.

XX PN US2001011125-A1.

XX PD 02-AUG-2001.

XX PF 30-JAN-1997; 97US-0790540.

XX PR 30-JAN-1997; 97US-0790540.

XX PA (HUSE/) HUSE W D.

XX PI Huse WD;

XX WPI; 2001-496171/54.

XX PT New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer -

XX PS Example 2; Page 16; 25pp; English.

XX CC PCR primers AAH74627-31 were used to amplify DNA encoding fragments  
 CC of the heavy chain variable region of the monoclonal antibody LM609.  
 CC LM609 is a murine antibody which specifically recognises the integrin  
 CC alphavbeta3, and inhibits its functional activity. The specification  
 CC describes a LM609 grafted antibody which has the complementarity  
 CC determining regions (CDRs) substituted into a non-murine framework.  
 CC Nucleic acids encoding LM609 grafted heavy and light chain polypeptides  
 CC and fragments are useful in diagnostic and therapeutic purposes, such  
 CC as in the production of LM609 grafted antibodies and fragments having  
 CC binding specificity and inhibitory activity against the integrin  
 CC alphavbeta3. The antibody can be used for the diagnosis or treatment  
 CC of alphavbeta3-mediated diseases (e.g. inflammatory disorders, chronic  
 CC articular rheumatism, psoriasis, disorders associated with inappropriate  
 CC or inappropriate invasion of vessels such as diabetic retinopathy,  
 CC neovascular glaucoma and capillary proliferation in atherosclerotic  
 CC plaques, or cancers), and to inhibit binding activity of alphavbeta3  
 CC that are necessary for progression of an alphavbeta3-mediated disease.

XX SQ Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;

Query Match 93.7%; Score 47.8; DB 22; Length 87;  
 Best Local Similarity 96.1%; Pred. No. 3.3e-09;  
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcactactatccagacactgtgcagggc 51  
 |||||  
 Db 10 aaagttagtagtggtggtgtagcactactattagacactgtgcagggc 60

## RESULT 5

AAF28181  
 ID AAF28181 standard; DNA; 87 BP.

XX AC AAF28181;

XX DT 03-APR-2001 (first entry)

XX DE Oligonucleotide #3.

XX KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX OS Unidentified.

XX PN WO200078815-A1.

XX PD 28-DEC-2000.

XX PF 23-JUN-2000; 2000WO-US17454.

XX PR 24-JUN-1999; 99US-0339922.

XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX PI Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -

XX PS Example 2; Page 67; 132pp; English.

XX CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX SQ Sequence 87 BP; 23 A; 18 C; 24 G; 22 T; 0 other;

Query Match 93.7%; Score 47.8; DB 22; Length 87;  
 Best Local Similarity 96.1%; Pred. No. 3.3e-09;  
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcactactatccagacactgtgcagggc 51  
 |||||  
 Db 10 aaagttagtagtggtggtgtagcactactattagacactgtgcagggc 60

## RESULT 6

AAV49820  
 ID AAV49820 standard; DNA; 351 BP.

XX AC AAV49820;

XX DT 02-NOV-1998 (first entry)

XX DE Vitaxin antibody heavy chain variable region DNA.

XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; ss.  
 OS Mus sp.

XX Key Location/Qualifiers  
 FH 1..351  
 FT /\*tag= a  
 FT /product= "vitaxin antibody heavy chain variable region"  
 FT /note= "partial sequence, no start or stop codon given"  
 XX

PN WO9833919-A2.

PD 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

DR P-PSDB; AAW76001.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis

PS Claim 3; Fig 1a; 129pp; English.

XX This sequence encodes the vitaxin antibody variable heavy chain region.  
 CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3  
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
 CC block integrin-mediated signal transduction. This is useful in the  
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
 CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;

Query Match 93.7%; Score 47.8; DB 19; Length 351;  
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;  
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcacctactatccagacactgtgcaggcc 51  
 |||||  
 Db 148 aaagttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 198

RESULT 7

AAV49822

ID AAV49822 standard; DNA; 351 BP.

XX AAV49822;

XX 02-NOV-1998 (first entry)

DE LM609 antibody heavy chain variable region DNA fragment.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; ss.

OS Mus sp.

XX Key Location/Qualifiers  
 FH 1..351  
 FT /\*tag= a  
 FT /product= "LM609 antibody heavy chain variable region"  
 FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis

PS Claim 37; Fig 2a; 129pp; English.

XX This sequence encodes the LM609 antibody variable heavy chain region.  
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3  
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
 CC block integrin-mediated signal transduction. This is useful in the  
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
 CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.

XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;

Query Match 93.7%; Score 47.8; DB 19; Length 351;  
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;  
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtagtggtggtgtagcacctactatccagacactgtgcaggcc 51  
 |||||  
 Db 148 aaagttagtagtggtggtgtagcacctactatttagacactgtgcaggcc 198

RESULT 8

AAH74623

ID AAH74623 standard; DNA; 351 BP.

XX AAH74623;

XX 15-OCT-2001 (first entry)

DE DNA encoding heavy chain variable region of LM609 grafted antibody.

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer; ss.

OS Synthetic.

OS Mus sp.

XX

PN US2001011125-A1.  
 XX 02-AUG-2001.  
 XX 30-JAN-1997; 97US-0790540.  
 XX 30-JAN-1997; 97US-0790540.  
 XX (HUSE/) HUSE W D.  
 XX Huse WD;  
 XX WPI: 2001-496171/54.  
 XX P-PSDB; AAG63587.  
 XX New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer -  
 XX  
 XX Claim 3; Fig 1A; 25pp; English.  
 PS The present sequence encodes the heavy chain variable region of the  
 XX grafted monoclonal antibody LM609. LM609 is a murine antibody which  
 CC specifically recognises the integrin alphavbeta3, and inhibits its  
 CC functional activity. The LM609 grafted antibody has the  
 CC complementarity determining regions (CDRs) substituted into a non-murine  
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain  
 CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis  
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
 CC disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 XX an alphavbeta3-mediated disease.  
 XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;  
 SQ

Query Match 93.7%; Score 47.8; DB 22; Length 351;  
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;  
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcaccctactatccagacactgtgcagggc 51  
 |||||  
 Db 148 aaagttagtagtggtggtgtagcaccctactatttagacactgtgcagggc 198

RESULT 9  
 AAH74625  
 ID AAH74625 standard; DNA; 351 BP.  
 XX  
 AC AAH74625;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX  
 DE DNA encoding heavy chain variable region of LM609 antibody.  
 XX  
 KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN US2001011125-A1.  
 XX  
 PD 02-AUG-2001.  
 XX

PF 30-JAN-1997; 97US-0790540.  
 XX  
 PR 30-JAN-1997; 97US-0790540.  
 XX  
 PA (HUSE/) HUSE W D.  
 XX  
 PI Huse WD;  
 XX  
 DR WPI: 2001-496171/54.  
 DR P-PSDB; AAG63589.  
 XX  
 XX New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer -  
 XX  
 XX Disclosure; Fig 2A; 25pp; English.  
 PS The present sequence encodes the heavy chain variable region of the  
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically  
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.  
 CC The specification describes a LM609 grafted antibody which has the  
 CC complementarity determining regions (CDRs) substituted into a non-murine  
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain  
 CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis  
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
 CC disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 XX an alphavbeta3-mediated disease.  
 XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;  
 SQ

Query Match 93.7%; Score 47.8; DB 22; Length 351;  
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;  
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaagttagtagtggtggtgtagcaccctactatccagacactgtgcagggc 51  
 |||||  
 Db 148 aaagttagtagtggtggtgtagcaccctactatttagacactgtgcagggc 198

RESULT 10  
 AAF28175  
 ID AAF28175 standard; DNA; 351 BP.  
 XX  
 AC AAF28175;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Vitaxin heavy chain variable region DNA.  
 XX  
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 XX 28-DEC-2000.  
 XX  
 XX 23-JUN-2000; 2000WO-US17454.  
 XX  
 XX 24-JUN-1999; 99US-0339922.  
 XX  
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX

PI Huse WD, Wu H;  
 DR WPI; 2001-050110/06.  
 XX  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Fig 1; 132pp; English.  
 XX  
 XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 XX Sequence 351 BP; 80 A; 82 C; 104 G; 85 T; 0 other;  
 SQ

Query Match 93.7%; Score 47.8; DB 22; Length 351;  
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;  
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtggtggtgtagcactactatccagacactgtgcagggc 51  
 |||||  
 DB 148 aaagttagtggtggtgtagcactactatttagacactgtgcagggc 198  
 |||||

RESULT 11  
 AAF28177  
 ID AAF28177 standard; DNA; 351 BP.  
 XX  
 AC AAF28177;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Antibody LM609 heavy chain variable region DNA.  
 XX  
 KW LM609; grafted antibody; alphaVbeta<sub>3</sub> integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200078815-A1.  
 PN  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 XX WPI; 2001-050110/06.  
 DR  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Fig 2; 132pp; English.  
 XX  
 XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or

CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 XX Sequence 351 BP; 83 A; 81 C; 102 G; 85 T; 0 other;  
 SQ

Query Match 93.7%; Score 47.8; DB 22; Length 351;  
 Best Local Similarity 96.1%; Pred. No. 4.5e-09;  
 Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaagttagtggtggtgtagcactactatccagacactgtgcagggc 51  
 |||||  
 DB 148 aaagttagtggtggtgtagcactactatttagacactgtgcagggc 198  
 |||||

RESULT 12  
 AAT72258/C  
 ID AAT72258 standard; DNA; 85 BP.  
 XX  
 AC AAT72258;  
 XX  
 DT 03-JAN-1998 (first entry)  
 XX  
 DE Mouse MAB 15 heavy chain backward PCR primer 4.  
 XX  
 KW Humanised antibody; monoclonal antibody; MAB 15; tumour;  
 KW lung cancer; therapy; polymerase chain reaction; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX EP781847-A1.  
 PN  
 XX  
 PD 02-JUL-1997.  
 XX  
 PF 25-OCT-1996; 96EP-0117154.  
 XX  
 PR 06-NOV-1995; 95EP-0117407.  
 XX  
 XX (MERE ) MERCK PATENT GMBH.  
 PA  
 XX Bendig M, Jones T, Saldana J;  
 PI  
 XX WPI; 1997-334904/31.  
 DR  
 XX Humanised form of murine monoclonal antibody MAB 15 - useful for  
 PT treating lung cancer  
 PT  
 XX Disclosure; Page 27; 71pp; English.  
 PS  
 XX This synthetic oligonucleotide comprises backward PCR primer 4  
 CC that was used with other sense and antisense primers (AAT72255-60)  
 CC to produce a sequence encoding a reshaped humanised monoclonal  
 CC antibody (MAB) 15 heavy chain variable region VH sequence (see  
 CC AAT72237). The full-length product was then amplified with external  
 CC primers (see AAT72261-62) and subcloned into HCMV expression vector  
 CC containing human heavy chain gamma-1 constant region. Humanised  
 CC reshaped MAB 15 is claimed for use in the treatment of human  
 CC tumours, especially lung cancer.  
 XX  
 XX Sequence 85 BP; 19 A; 23 C; 21 G; 22 T; 0 other;  
 SQ

Query Match 85.9%; Score 43.8; DB 18; Length 85;  
 Best Local Similarity 95.7%; Pred. No. 1.2e-07;  
 Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX  
ID HAI/223/ SCANDAU; CDNA; 443 BP.





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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:14 ; Search time 174.26 Seconds  
(without alignments)  
71.889 Million cell updates/sec

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Searched: 383533 seqs, 122816752 residues

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Listing first 45 summaries

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6: /cgn2.6/pdata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43.8	85.9	923	PCT-US94-07659-1	Sequence 1, Appli
2	41.2	80.8	51	US-08-475-000-2	Sequence 2, Appli
3	41.2	80.8	51	US-08-483-199-2	Sequence 2, Appli
4	41.2	80.8	51	US-08-484-508-2	Sequence 2, Appli
5	41.2	80.8	357	US-08-475-000-15	Sequence 15, Appli
6	41.2	80.8	357	US-08-483-199-15	Sequence 15, Appli
7	41.2	80.8	357	US-08-484-508-15	Sequence 15, Appli
8	40.6	79.6	357	US-08-331-398A-21	Sequence 21, Appli
9	40.6	79.6	357	US-08-331-397B-21	Sequence 21, Appli
10	40.6	79.6	357	US-08-759-804A-21	Sequence 21, Appli
11	40.6	79.6	357	US-09-227-693-21	Sequence 21, Appli
12	40.6	79.6	375	US-08-331-398A-59	Sequence 59, Appli
13	40.6	79.6	375	US-08-331-397B-59	Sequence 59, Appli
14	40.6	79.6	375	US-08-759-804A-58	Sequence 58, Appli
15	40.6	79.6	474	US-08-653-402B-5	Sequence 5, Appli
16	40.6	79.6	474	US-08-653-402B-9	Sequence 9, Appli
17	39	76.5	354	US-08-326-362-1	Sequence 1, Appli
18	39	76.5	783	US-08-487-283A-19	Sequence 19, Appli
19	37.4	73.3	357	PCT-US94-07659-5	Sequence 5, Appli
20	37.4	73.3	403	US-08-408-133-4	Sequence 4, Appli
21	37.4	73.3	403	US-08-454-683-4	Sequence 4, Appli
22	37.4	73.3	403	US-08-116-778B-20	Sequence 20, Appli
23	37.4	73.3	403	US-08-454-680-4	Sequence 4, Appli
24	37.4	73.3	403	US-08-438-562-20	Sequence 20, Appli
25	37.4	73.3	403	US-08-483-528B-20	Sequence 20, Appli
26	37.4	73.3	403	US-08-673-799C-20	Sequence 20, Appli
27	37.2	72.9	51	PCT-US93-08435-17	Sequence 17, Appli

c 28 37.2 72.9 102 5 PCT-US93-08435-48 Sequence 48, Appli  
29 37.2 72.9 354 5 PCT-US93-08435-9 Sequence 9, Appli  
30 37.2 72.9 389 5 PCT-US93-08435-11 Sequence 11, Appli  
31 37.2 72.9 389 5 PCT-US93-08435-13 Sequence 13, Appli  
32 37 72.5 405 4 US-08-579-378A-15 Sequence 15, Appli  
33 37 72.5 405 4 US-08-579-378A-19 Sequence 19, Appli  
34 37 72.5 519 1 US-08-339-582-1 Sequence 1, Appli  
35 37 72.5 1329 5 PCT-US96-13152-3 Sequence 3, Appli  
36 36.4 71.4 348 2 US-08-888-366-9 Sequence 9, Appli  
37 36.4 71.4 348 2 US-08-888-366-11 Sequence 11, Appli  
38 36.4 71.4 717 2 US-08-553-497A-17 Sequence 17, Appli  
39 35.8 70.2 413 1 US-08-253-877C-56 Sequence 56, Appli  
40 35.8 70.2 413 2 US-08-452-164A-56 Sequence 56, Appli  
41 35.8 70.2 416 4 US-08-976-183A-30 Sequence 30, Appli  
42 35.8 70.2 717 2 US-07-956-399-3 Sequence 3, Appli  
43 35.8 70.2 721 2 US-08-224-591-15 Sequence 15, Appli  
44 35.8 70.2 721 2 US-08-926-789-15 Sequence 15, Appli  
45 35.8 70.2 733 2 US-08-224-591-17 Sequence 17, Appli

## ALIGNMENTS

RESULT 1  
PCT-US94-07659-1  
: Sequence 1, Application PC/TUS9407659  
: GENERAL INFORMATION:  
: APPLICANT: Young, Peter  
: APPLICANT: Gross, Mitchell  
: APPLICANT: Jonak, Zdenka L.  
: APPLICANT: Theisen, Timothy  
: APPLICANT: Hurle, Mark  
: TITLE OF INVENTION: Recombinant and Humanized IL-1 beta  
: TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory  
: TITLE OF INVENTION: Disorders in Man  
: NUMBER OF SEQUENCES: 21  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: SmithKline Beecham Corporation - Corp.  
: ADDRESSEE: Intellectual Property  
: ADDRESSEE: 709 Swedeland Road  
: CITY: King of Prussia  
: STATE: PA  
: COUNTRY: USA  
: ZIP: 19406-2799  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: PCT/US94/07659  
: FILING DATE:  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/090,534  
: FILING DATE: 09-JUL-1993  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Sutton, Jeffrey A.  
: REGISTRATION NUMBER: 34,028  
: REFERENCE/DOCKET NUMBER: P50171-1  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (610) 270-5024  
: TELEFAX: (610) 270-5090  
: INFORMATION FOR SEQ ID NO: 1:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 923 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: unknown  
: MOLECULE TYPE: DNA (genomic)  
: FEATURE:  
: NAME/KEY: CDS

LOCATION: 169...909  
PCT-US94-07659-1

Query Match 85.9%; Score 43.8; DB 5; Length 923;  
Best Local Similarity 95.7%; Pred. No. 8.9e-09;  
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ttagtgtggtgtagcaccattatccagacactgtgcaggc 51  
|||||  
Db 377 TTAGTAGTGTGTGGTGGCACCTACTATCCAGACACTGTGAAGGC 423

## RESULT 2

US-08-473-000-2

; Sequence 2, Application US/08475000  
; Patent No. 5811267

; GENERAL INFORMATION:

; APPLICANT: RING, DAVID B.

; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY

; NUMBER OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CHIRON CORPORATION

; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097

; CITY: Emeryville

; STATE: CA

; COUNTRY: USA

; ZIP: 94662-8097

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,000

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: SAVERIDE, PAUL

; REGISTRATION NUMBER: 36,914

; REFERENCE/DOCKET NUMBER: 0850.007

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 601-2585

; TELEFAX: (510) 655-3542

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 51 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-473-000-2

## Query Match

Best Local Similarity 80.8%; Score 41.2; DB 1; Length 51;

Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 ttagtgtggtgtagcaccattatccagacactgtgcagg 50  
|||||  
Db 5 TTAGTAGTGTGTGGTGGTAACCTACTATCCAGACACTGTGAAGGG 50

## RESULT 3

US-08-483-199-2

; Sequence 2, Application US/08483199

; Patent No. 5849877

; GENERAL INFORMATION:

; APPLICANT: RING, DAVID B.

; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY

; NUMBER OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
; CITY: Emeryville  
; STATE: CA

; COUNTRY: USA

; ZIP: 94662-8097

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,199

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: SAVERIDE, PAUL

; REGISTRATION NUMBER: 36,914

; REFERENCE/DOCKET NUMBER: 0850.009

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 601-2585

; TELEFAX: (510) 655-3542

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 51 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-483-199-2

## Query Match

Best Local Similarity 80.8%; Score 41.2; DB 2; Length 51;

Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 ttagtgtggtgtagcaccattatccagacactgtgcagg 50  
|||||  
Db 5 TTAGTAGTGTGTGGTGGTAACCTACTATCCAGACACTGTGAAGGG 50

## RESULT 4

US-08-484-508-2

; Sequence 2, Application US/08484508

; Patent No. 5948647

; GENERAL INFORMATION:

; APPLICANT: RING, DAVID B.

; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY

; NUMBER OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CHIRON CORPORATION

; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097

; CITY: Emeryville

; STATE: CA

; COUNTRY: USA

; ZIP: 94662-8097

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,508

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: SAVERIDE, PAUL

; REGISTRATION NUMBER: 36,914

; REFERENCE/DOCKET NUMBER: 0850.008

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 601-585

; TELEFAX: (510) 655-3542

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 51 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-484-508-2

Query Match 80.8%; Score 41.2; DB 2; Length 51;  
Best Local Similarity 93.5%; Pred. No. 4.6e-08;  
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ttactagtgtggtgtagcacctactatccagacactgtgcagg 50  
|||||  
Db 5 TTACTAGTGTGTTGTTAAACCTACTACTATCCAGACAGTGTGAAGGG 50

## RESULT 5

US-08-475-000-15  
; Sequence 15, Application US/08475000  
; Patent No. 5811267  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY R440 - P.O. BOX 8097  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,000  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0850.007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 357 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..357  
; US-08-475-000-15

Query Match 80.8%; Score 41.2; DB 1; Length 357;  
Best Local Similarity 93.5%; Pred. No. 7.7e-08;  
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ttactagtgtggtgtagcacctactatccagacactgtgcagg 50  
|||||  
Db 152 TTACTAGTGTGTTGTTAAACCTACTACTATCCAGACAGTGTGAAGGG 197

## RESULT 6

US-08-483-199-15  
; Sequence 15, Application US/08483199

; Patent No. 5849877  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,199  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAVERIDE, PAUL  
; REGISTRATION NUMBER: 36,914  
; REFERENCE/DOCKET NUMBER: 0850.009  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2585  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 357 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..357  
; US-08-483-199-15

Query Match 80.8%; Score 41.2; DB 2; Length 357;  
Best Local Similarity 93.5%; Pred. No. 7.7e-08;  
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ttactagtgtggtgtagcacctactatccagacactgtgcagg 50  
|||||  
Db 152 TTACTAGTGTGTTGTTAAACCTACTACTATCCAGACAGTGTGAAGGG 197

## RESULT 7

US-08-484-508-15  
; Sequence 15, Application US/08484508  
; Patent No. 5948647  
; GENERAL INFORMATION:  
; APPLICANT: RING, DAVID B.  
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,508

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..357
; OTHER INFORMATION: /note= "B5 Variable Heavy chain (V-H)"
US-08-331-398A-21

Query Match 79.6%; Score 40.6; DB 1; Length 357;
Best Local Similarity 91.5%; Pred. No. 1.3e-07;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ttgtagtggtggtgtagcacctactatccagacactgtgcagggc 51
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 152 TTAGTAATGTTGGTGGTAGCCTATTATCCAGACACTGTAAAGGGC 198

RESULT 9
US-08-331-397B-21
; Sequence 21, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..357
; OTHER INFORMATION: /note= "B5 Variable Heavy chain (V-H)"

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US-08-331-397B-21

Query Match 79.6%; Score 40.6; DB 2; Length 357;  
Best Local Similarity 91.5%; Pred. No. 1.3e-07;  
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatccagacactgtgcagggc 51  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 152 TTAGTAATGGTGGTGTAGCACCTATTATCCAGACACTGTAAAGGC 198

## RESULT 10

US-08-759-804A-21  
; Sequence 21, Application US/08759804A  
; Patent No. 5990296  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Willingham, Mark  
; APPLICANT: Fitzgerald, David J.  
; APPLICANT: Brinkmann, Ulrich  
; APPLICANT: Pai, Lee  
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,  
; FUSION PROTEINS, AND USES THEREOF  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/759,804A  
; FILING DATE: 03-DEC-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/331,398  
; FILING DATE: 28-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen L.  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 015280-126140US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 357 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..357  
; OTHER INFORMATION: /note= "B5 Variable Heavy chain (V-H)"  
US-08-759-804A-21

Query Match 79.6%; Score 40.6; DB 2; Length 357;  
Best Local Similarity 91.5%; Pred. No. 1.3e-07;

Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatccagacactgtgcagggc 51  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 152 TTAGTAATGGTGGTGTAGCACCTATTATCCAGACACTGTAAAGGC 198

## RESULT 11

US-09-227-693-21  
; Sequence 21, Application US/09227693  
; Patent No. 6287562  
; GENERAL INFORMATION:  
; APPLICANT: PASTAN, Ira  
; APPLICANT: BENHAR, Itai  
; APPLICANT: PADLAN, Eduardo A.  
; APPLICANT: JUNG, Sun-Hee  
; APPLICANT: LEE, Byungkook  
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY  
; FRAGMENTS, FUSION PROTEINS, AND USES THEREOF  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/227,693  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/331,396  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/767,331  
; FILING DATE: 30-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/596,289  
; FILING DATE: 12-OCT-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 15280-126-1-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 357 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1..357  
; OTHER INFORMATION: /standard\_name= "B5  
; OTHER INFORMATION: variable heavy chain"  
US-09-227-693-21

Query Match 79.6%; Score 40.6; DB 4; Length 357;  
Best Local Similarity 91.5%; Pred. No. 1.3e-07;  
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttagtagtggtggtgtagcacctactatccagacactgtgcagggc 51  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 152 TTAGTAATGGTGGTGTAGCACCTATTATCCAGACACTGTAAAGGC 198

```

> APPLICANT: Pastan, Ira
> APPLICANT: Benhar, Itai
> TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
> TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
> TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
> TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
> NUMBER OF SEQUENCES: 68
> CORRESPONDENCE ADDRESS:
> ADDRESSEE: Townsend and Townsend and Crew
> STREET: One Market Plaza, Steuart Street Plaza
> CITY: San Francisco
> STATE: California
> COUNTRY: USA
> ZIP: 94105-1492
> COMPUTER READABLE FORM:
> MEDIUM TYPE: Floppy disk
> COMPUTER: IBM PC compatible
> OPERATING SYSTEM: PC-DOS/MS-DOS
> SOFTWARE: PatentIn Release #1.0, Version #1.30
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: US/08/331,397B
> FILING DATE: 28-OCT-1994
> CLASSIFICATION: C35
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 07/767,331
> FILING DATE: 30-SEP-1991
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 07/596,289
> FILING DATE: 12-OCT-1990
> ATTORNEY/AGENT INFORMATION:
> NAME: Hunter, Tom
> REGISTRATION NUMBER: 38,498
> REFERENCE/DOCKET NUMBER: 015280-126120US
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: (415) 543-9600
> TELEFAX: (415) 543-5043
> INFORMATION FOR SEQ ID NO: 59:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 375 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> MOLECULE TYPE: DNA
> FEATURE:
> NAME/KEY: -
> LOCATION: 1..375
> OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
> OTHER INFORMATION: Heavy chain region"
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> US-08-331-397B-59

```

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RESULT 12
US-08-331-398A-59
; Sequence 59, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..375
; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 FV
; OTHER INFORMATION: Heavy chain region"
US-08-331-398A-59

Query Match 79.6%; Score 40.6; DB 1; Length 375;
Best Local Similarity 91.5%; Pred. No. 1.4e-07;
Matches 43; Conservative 0; Mismatches 4; Indels 0

QY 5 ttagtagtggttggtgagcacctactatccagacactgtgcagggc 51
||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 152 TTACTATGGTGGTGTAGCACTATTATCCAGACACTGTAAAGGGC 198

RESULT 13
US-08-331-397B-59
; Sequence 59, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:

```

```

;
; LOCATION: 1..375
;
; OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
; OTHER INFORMATION: Heavy chain region"
;
; US-08-759-804A-58

```

```

Query Match          79.8%; Score 40.6; DB 2; Length 474;
Best Local Similarity 91.5%; Pred. No. 1.4e-07;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 ttatagtgggtggtagcacctactactatccagacactgtgcagggc 51
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 TTAATAGTGGTGGTAGCACCTACTATCCAGACACTGTGAAGGC 255

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:49:02 ; Search time 2408.76 Seconds  
(without alignments)  
208.504 Million cell updates/sec

Title: US-09-339-922A-105

Perfect score: 24

Sequence: 1 catcttcattggcagttttgtctt 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sv.\*

13: gb\_un.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pi.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vl.\*

30: em\_hgt\_hum.\*

31: em\_hgt\_inv.\*

32: em\_hgt\_other.\*

33: em\_hgtgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

RESULT	1	AX060884	Sequence 105 from Patent WO0078815.	24 bp	DNA	linear	PAT 22-JAN-2001
LOCUS	AX060884	Sequence 105 from Patent WO0078815.					
DEFINITION	AX060884	Sequence 105 from Patent WO0078815.					
ACCESSION	AX060884	Sequence 105 from Patent WO0078815.					
VERSION	AX060884.1	GI:12406262					
KEYWORDS		synthetic construct.					
SOURCE		synthetic construct.					
ORGANISM		synthetic construct.					
REFERENCE		1 (bases 1 to 24)					
AUTHORS		Huse, W.D. and Wu, H.					
TITLE		Anti-g(a) v2 g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use					
JOURNAL		Patent: WO 0078815-A 105 28-DEC-2000;					
FEATURES		Applied Molecular Evolution (US)					
		Location/Qualifiers					
		1..24					
		/organism="synthetic construct"					
		/db_xref="taxon:32630"					
		<1..>24					
		/note="Mutated complementarity determining region (CDR)"					
		/codon_start=1					

```

BASE COUNT      3 a      6 c      4 g      11 t
ORIGIN
/transl_table=11
/protein_id="CAC24928.1"
/db_xref="GI:12406263"
/translation="HLGSPFAS"

```

```
Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 24; Conservative 0; Mismatches 0; Indels
```

Qy 1 catcttcattggcagtttttgcttct 24  
|||||  
Db 1 CATCTTCATGGCAGTTTTCCTTCT 24

## RESULT 2

AP003776	152948 bp	linear	HTG 23-JUN-2001
LOCUS	AP003776	DNA	
DEFINITION	Homo sapiens chromosome 11 clone RP11-209L12 map 11q, WORKING DRAFT SEQUENCE, 11 unordered pieces.		

ACCESSION AP003776  
VERSION AP003776.1 GI:14530688  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE Homo sapiens DNA, clone:RP11-209L12.

ORGANISM	REFERENCE
Homo sapiens	1 (bases 1 to 152948)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	

**AUTHORS**  
Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong, Seog, P.,  
Fujiyama, A., Yada, T., Tokoi, Y., Watanabe, H. and Sakaki, Y.

**TITLE**  
Direct Submission

**JOURNAL**  
Submitted (21-JUN-2001) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-2 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
[E-mail: hattori@gsc.riken.go.jp, URL: <http://hgp.gsc.riken.go.jp/>].  
Tel: 81-45-503-9111. Fax: 81-45-503-9170.

**COMMENT**

Center: RIKEN Genomic Sciences Center (GSC)  
Center code: RIKEN  
Web site: <http://hgp.gsc.riken.go.jp/>  
Contact: [hattori@gsc.riken.go.jp](mailto:hattori@gsc.riken.go.jp)

```

----- Project Information
Center project name: HumDraft11
Center clone name: RP11-209L12
----- Summary Statistics

```

Sequencing vector: PCR products  
Chemistry: Dye-terminator ET-amersham; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 148988 bases at least Q40  
Consensus quality: 151056 bases at least Q30  
Consensus quality: 151725 bases at least Q20  
Insert size: 151948; sum-of-contigs  
Quality coverage: 5.98x in Q20 bases; sum-of-contigs

-----  
NOTE: This is a 'working draft' sequence. It currently consists of 11 conigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the conigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

	35942	contig	of	35942	bp	in	length
36043	64596	contig	of	28554	bp	in	length
64637	88056	contig	of	23360	bp	in	length
88157	108127	contig	of	19971	bp	in	length
108228	121652	contig	of	13425	bp	in	length
121753	132902	contig	of	11150	bp	in	length
132033	139176	contig	of	6174	bp	in	length
139027	144517	contig	of	5241	bp	in	length
144618	147983	contig	of	3366	bp	in	length
148084	152287	contig	of	4204	bp	in	length

152388 152948 contig of 561 bp in length.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 11 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

*	35943	35942:	contig of	35942 bp	in length
*	35943	36042:	gap of	100 bp	
*	36043	64596:	contig of	28554 bp	in length
*	64597	64696:	gap of	100 bp	
*	64697	88056:	contig of	23360 bp	in length
*	88057	88156:	gap of	100 bp	
*	88157	108127:	contig of	19971 bp	in length
*	108128	108227:	gap of	100 bp	
*	108228	121652:	contig of	13425 bp	in length
*	121653	121752:	gap of	100 bp	
*	121753	132902:	contig of	11150 bp	in length
*	132903	133002:	gap of	100 bp	
*	133003	139176:	contig of	6174 bp	in length
*	139177	139276:	gap of	100 bp	
*	139277	144517:	contig of	5241 bp	in length
*	144518	144617:	gap of	100 bp	
*	144618	147983:	contig of	3366 bp	in length
*	147984	148083:	gap of	100 bp	
*	148084	152287:	contig of	4204 bp	in length
*	152288	152387:	gap of	100 bp	
*	152388	152948:	contig of	561 bp	in length.

## FEATURES

source

```
/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/chromosome="11"  
/map="11q"  
/clone="RP11-209I12"
```

misc feature

```
misc_feature
/note="assembly_fragment"
36043. .64596
```

```
misc_feature
/note="assembly_fragment"
64697. .88056
```

```
misc_feature      /note="assembly_fragment"
                  88157. 108127
```

```
misc feature
/note="assembly_fragment"
108228.121652
```

```
misc_feature /note="assembly_fragment" 121753. .132902
```

```
misc_feature
/note="assembly_fragment"
133003. .139176
```

```
misc_feature
/note="assembly_fragment
139277.144517
```

```
misc_feature
/note="assembly_fragment"
144618. .147983
```

```
misc_feature
/note="assembly_fragment"
148084.152287
```

```
misc_feature
/note="assembly_fragment"
152388. ,152948
```

	/note="assembly_fragment	
COUNT	42013 a	33863 c 34632 q 41440

# IN

Query Match 87.5%; Score 21; DB 2; Length 152948;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 21; Conservative 0; Mismatches 0; Indels 0

Qy 3 tcttcattggcagttttgcttc 23  
|||||  
Db 134726 TCTTCATGGCAGTTTTCCTTC 134746

## RESULT 3

```

AC015518/c
LOCUS       AC015518
DEFINITION  Homo sapiens clone RP11-22P3, LOW-PASS SEQUENCE SAMPLING.
ACCESSION   AC015518
VERSION     AC015518.3 GI:11345004
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 73992)
AUTHORS    Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 73992)
AUTHORS    Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
             Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
             Brown,A., Castle,A., Collangelo,M., Collins,S., Collymore,A.,
             Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
             Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
             Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
             Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
             Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
             McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
             Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
             Peterson,K., Pollara,V., Riley,K., Roy,A., Santos,R., Severy,P.,
             Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
             Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
             Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
DIRECT SUBMISSION
Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 26, 2000 this sequence version replaced gi:9124480.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-----
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-----
Project Information
Center project name: L4159
Center clone name: 22_P_3
-----
* NOTE: This record contains 92 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1 680: contig of 680 bp in length
* 781 780: gap of 100 bp
* 1450 1449: contig of 669 bp in length
* 1550 2241: contig of 692 bp in length
* 2242 2341: gap of 100 bp
* 2342 3051: contig of 710 bp in length
* 3052 3151: gap of 100 bp
* 3152 3863: contig of 712 bp in length
* 3864 3963: gap of 100 bp
* 3964 4678: contig of 715 bp in length
* 4679 4778: gap of 100 bp
* 4779 5508: contig of 730 bp in length
* 5509 5608: gap of 100 bp
* 5609 6332: contig of 724 bp in length
* 6333 6432: gap of 100 bp
* 6433 7152: contig of 720 bp in length
*
* 7153 7252: gap of 100 bp
* 7253 7933: contig of 681 bp in length
* 7934 8033: gap of 100 bp
* 8034 8713: contig of 680 bp in length
* 8714 8813: gap of 100 bp
* 8814 9508: contig of 695 bp in length
* 9509 9608: gap of 100 bp
* 9609 10316: contig of 708 bp in length
* 10317 10416: gap of 100 bp
* 10417 11114: contig of 698 bp in length
* 11115 11214: gap of 100 bp
* 11215 11924: contig of 710 bp in length
* 11925 12024: gap of 100 bp
* 12025 12730: contig of 706 bp in length
* 12731 12830: gap of 100 bp
* 12831 13540: contig of 710 bp in length
* 13541 13640: gap of 100 bp
* 13641 14353: contig of 713 bp in length
* 14354 14453: gap of 100 bp
* 14454 15168: contig of 715 bp in length
* 15169 15268: gap of 100 bp
* 15269 15977: contig of 709 bp in length
* 15978 16077: gap of 100 bp
* 16078 16801: contig of 724 bp in length
* 16802 16901: gap of 100 bp
* 16902 17590: contig of 689 bp in length
* 17591 17690: gap of 100 bp
* 17691 18374: contig of 684 bp in length
* 18375 18474: gap of 100 bp
* 18475 19166: contig of 692 bp in length
* 19167 19266: gap of 100 bp
* 19267 19980: contig of 714 bp in length
* 19981 20080: gap of 100 bp
* 20081 20764: contig of 684 bp in length
* 20765 20864: gap of 100 bp
* 20865 21550: contig of 686 bp in length
* 21551 21650: gap of 100 bp
* 21651 22359: contig of 709 bp in length
* 22360 22459: gap of 100 bp
* 22460 23193: contig of 734 bp in length
* 23194 23293: gap of 100 bp
* 23294 24016: contig of 723 bp in length
* 24017 24116: gap of 100 bp
* 24117 24823: contig of 707 bp in length
* 24824 24923: gap of 100 bp
* 24924 25640: contig of 717 bp in length
* 25641 25740: gap of 100 bp
* 25741 26460: contig of 720 bp in length
* 26461 26560: gap of 100 bp
* 26561 27245: contig of 685 bp in length
* 27246 27345: gap of 100 bp
* 27346 27980: contig of 635 bp in length
* 27981 28080: gap of 100 bp
* 28081 28764: contig of 684 bp in length
* 28765 28864: gap of 100 bp
* 28865 29574: contig of 710 bp in length
* 29575 29674: gap of 100 bp
* 29675 30372: contig of 698 bp in length
* 30373 30472: gap of 100 bp
* 30473 31177: contig of 705 bp in length
* 31178 31277: gap of 100 bp
* 31278 32026: contig of 749 bp in length
* 32027 32126: gap of 100 bp
* 32127 32848: contig of 722 bp in length
* 32849 32948: gap of 100 bp
* 32949 33667: contig of 719 bp in length
* 33668 33767: gap of 100 bp
* 33768 34468: contig of 701 bp in length
* 34469 34568: gap of 100 bp
* 34569 35293: contig of 725 bp in length
* 35294 35393: gap of 100 bp
* 35394 36079: contig of 686 bp in length
* 36080 36179: gap of 100 bp

```

\* 36180 36879: contig of 700 bp in length  
\* 36880 36979: gap of 100 bp  
\* 36980 37686: contig of 707 bp in length  
\* 37687 37786: gap of 100 bp  
\* 37787 38495: contig of 709 bp in length  
\* 38496 38595: gap of 100 bp  
\* 38596 39302: contig of 707 bp in length  
\* 39303 39402: gap of 100 bp  
\* 39403 40094: contig of 692 bp in length  
\* 40095 40194: gap of 100 bp  
\* 40195 40891: contig of 697 bp in length  
\* 40892 40991: gap of 100 bp  
\* 40992 41697: contig of 706 bp in length  
\* 41698 41797: gap of 100 bp  
\* 41798 42509: contig of 712 bp in length  
\* 42510 42609: gap of 100 bp  
\* 42610 43323: contig of 714 bp in length  
\* 43324 43423: gap of 100 bp  
\* 43424 44141: contig of 718 bp in length  
\* 44142 44241: gap of 100 bp  
\* 44242 44957: contig of 716 bp in length  
\* 44958 45057: gap of 100 bp  
\* 45058 45748: contig of 691 bp in length  
\* 45749 45848: gap of 100 bp  
\* 45849 46554: contig of 706 bp in length  
\* 46555 46654: gap of 100 bp  
\* 46655 47354: contig of 700 bp in length  
\* 47355 47454: gap of 100 bp  
\* 47455 48154: contig of 700 bp in length  
\* 48155 48254: gap of 100 bp  
\* 48255 48958: contig of 704 bp in length  
\* 48959 49058: gap of 100 bp  
\* 49059 49762: contig of 704 bp in length  
\* 49763 49862: gap of 100 bp  
\* 49863 50580: contig of 718 bp in length  
\* 50581 50680: gap of 100 bp  
\* 50681 51403: contig of 723 bp in length  
\* 51404 51503: gap of 100 bp  
\* 51504 52212: contig of 709 bp in length  
\* 52213 52312: gap of 100 bp  
\* 52313 53008: contig of 696 bp in length  
\* 53009 53108: gap of 100 bp  
\* 53109 53795: contig of 687 bp in length  
\* 53796 53895: gap of 100 bp  
\* 53896 54588: contig of 693 bp in length  
\* 54589 54688: gap of 100 bp  
\* 54689 55392: contig of 704 bp in length  
\* 55393 55492: gap of 100 bp  
\* 55493 56201: contig of 709 bp in length  
\* 56202 56301: gap of 100 bp  
\* 56302 57009: contig of 708 bp in length  
\* 57010 57109: gap of 100 bp  
\* 57110 57801: contig of 692 bp in length  
\* 57802 57901: gap of 100 bp  
\* 57902 58603: contig of 702 bp in length

Query Match 82.5%; Score 19.8; DB 2; Length 73992;

Best Local Similarity 91.3%; Pred. No. 72;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcttcattggcaggtttgtctct 24  
|||||  
Db 32608 ATCTTCATGGCAGCTTTCCTCT 32586

## RESULT 4

AC008464

LOCUS

DEFINITION Homo sapiens chromosome 5 clone CTC-353G13, WORKING DRAFT SEQUENCE, HTG 21-JUN-2000

AC008464

ACCESSION 21 unordered pieces.

VERSION AC008464.5 GI:8575879

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

## SOURCE

human.

## ORGANISM

Homo sapiens

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## AUTHORS

1 (bases 1 to 124758)

## TITLE

DOE Joint Genome Institute.

## JOURNAL

Sequencing of Human Chromosome 5

## REFERENCE

Unpublished

## AUTHORS

2 (bases 1 to 124758)

## TITLE

DOE Joint Genome Institute.

## JOURNAL

Direct Submission

## COMMENT

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Jun 21, 2000 this sequence version replaced gi:7708881.

## -----Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: <http://www.jgi.doe.gov>

## -----

## Project Information

Center Project Name: 320887, H318

Center clone name: CIT-HSPC\_353G13

## -----

## Summary Statistics

Consensus quality: 95334 bases at least Q40

Consensus quality: 111998 bases at least Q30

Consensus quality: 116380 bases at least Q20

Estimated insert size: 139000; pulse field gel estimation

Estimated insert size: 129758; sum-of-contigs estimation

Quality coverage: 3.95 in Q20 bases; pulse field gel estimation.

Quality coverage: 4.48 in Q20 bases; sum-of-contigs estimation.

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 21 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1 1255: contig of 1255 bp in length

\* 1256 1355: gap of unknown length

\* 1356 2450: contig of 1095 bp in length

\* 2451 2550: gap of unknown length

\* 2551 3759: contig of 1209 bp in length

\* 3760 3859: gap of unknown length

\* 3860 5053: contig of 1194 bp in length

\* 5054 5153: gap of unknown length

\* 5154 6435: contig of 1282 bp in length

\* 6436 6535: gap of unknown length

\* 6536 8921: contig of 2386 bp in length

\* 8922 9021: gap of unknown length

\* 9022 11789: contig of 2768 bp in length

\* 11790 11889: gap of unknown length

\* 11890 15102: contig of 3213 bp in length

\* 15103 15202: gap of unknown length

\* 15203 18556: contig of 3354 bp in length

\* 18557 18656: gap of unknown length

\* 18657 22919: contig of 4263 bp in length

\* 22920 23019: gap of unknown length

\* 23020 26335: contig of 3316 bp in length

\* 26336 26435: gap of unknown length

\* 26436 33385: contig of 6950 bp in length

\* 33386 33485: gap of unknown length

\* 33486 41028: contig of 7543 bp in length

\* 41029 41128: gap of unknown length

\* 41129 47026: contig of 5898 bp in length

\* 47027 47126: gap of unknown length

\* 47127 53435: contig of 6309 bp in length

\* 53436 53535: gap of unknown length

\* 53536 55887: contig of 2352 bp in length

\* 55888 55987: gap of unknown length

\* 55988 71579: contig of 15592 bp in length

\* 71580 71679: gap of unknown length

\* 71680 75171: contig of 3492 bp in length  
 \* 75172 75271: gap of unknown length  
 \* 75272 82713: contig of 7442 bp in length  
 \* 82714 82813: gap of unknown length  
 \* 82814 103414: contig of 20601 bp in length  
 \* 103415 103514: gap of unknown length  
 \* 103515 124758: contig of 21244 bp in length.

## FEATURES

## source

Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="5"  
 /clone="CPC-353G13"  
 /clone\_lib="Caltech human BAC library C"

BASE COUNT 36048 a 25087 c 25882 g 35713 t 2028 others  
 ORIGIN

Query Match 82.58; Score 19.8; DB 2; Length 124758;

Best Local Similarity 91.3%; Pred. No. 71;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcagtcgagtttgcttct 24

Db 117413 ATGTTTCATGCGAGGTTTGCTTCT 117435

## RESULT 5

## AC013714

LOCUS AC013714 140009 bp DNA linear PRI 03-NOV-2001  
 DEFINITION Homo sapiens chromosome, clone RP11-22P4, complete sequence.

AC013714

AC013714

VERSION AC013714.8 GI:163030479

KEYWORDS HTG.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 140009)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome, clone RP11-22P4

2 (bases 1 to 140009)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
 Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,  
 Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A.,  
 Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,  
 Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,  
 Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,  
 Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,  
 McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,  
 Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,  
 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 140009)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,  
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,  
 Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A.,  
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,  
 Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,  
 Glnde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,  
 Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,  
 Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,  
 MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,  
 McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,

Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,  
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,  
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,  
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R.,  
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,  
 Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

## TITLE

## JOURNAL

## COMMENT

Submitted (03-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA

On Oct 20, 2001 this sequence version replaced gi:16259013.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L4160

Center clone name: 22\_P\_4

## FEATURES

## source

Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="RP11-22P4"  
 /clone\_lib="RPC1-11 Human Male BAC"  
 46. .127

repeat\_region

repeat\_region

repeat\_region

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repeat_region /note="<30 qual SNGL region"
15684..15720 /rpt_family="AT_rich"
repeat_region 16665..16703 /rpt_family="(TG)n"
repeat_region complement(16789..16908)
/rpt_family="L2"
repeat_region 17386..18185 /rpt_family="MER63C"
repeat_region 18846..18980 /rpt_family="MLT1D"
repeat_region 19932..20129 /rpt_family="MIR"
repeat_region complement(20187..20307)
/rpt_family="MIR"
repeat_region 20318..20460 /rpt_family="MER5A"
repeat_region 21019..21144 /rpt_family="MIR"
repeat_region complement(21154..21364)
/rpt_family="MER58A"
repeat_region complement(21723..21982)
/rpt_family="MIR"
repeat_region 22720..22753 /rpt_family="(CA)n"
repeat_region 22843..22869 /rpt_family="(GAAA)n"
repeat_region complement(22910..22958)
/rpt_family="MIR"
repeat_region complement(23319..23697)
/rpt_family="MLT1B"
repeat_region complement(23705..23865)
/rpt_family="MIR"
repeat_region 24597..25037 /rpt_family="L1ME4A"
repeat_region 25227..25269 /rpt_family="AT_rich"
repeat_region complement(26596..26745)
/rpt_family="MER117"
repeat_region 27214..27236 /rpt_family="(GA)n"
repeat_region 27297..27478 /rpt_family="MIR"
repeat_region complement(28096..28255)
/rpt_family="MER5B"
repeat_region complement(29315..29490)
/rpt_family="MER53"
repeat_region 29632..29677 /rpt_family="L2"
repeat_region 30128..30165 /rpt_family="(CA)n"
repeat_region complement(30506..30579)
/rpt_family="MIR"
repeat_region 31588..31677 /rpt_family="MIR"
repeat_region 32021..32177 /rpt_family="MIR"
repeat_region 32178..32538 /rpt_family="THE1B"
repeat_region 32539..32657 /rpt_family="MIR"
repeat_region complement(32663..32809)
/rpt_family="L2"
repeat_region complement(33697..34051)
/rpt_family="THE1B"
repeat_region complement(35133..35383)
/rpt_family="MLT1A1"
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repeat_region 35672..35676 /note="<30 qual SNGL region"
complement(35673..35796)
/rpt_family="MLT1A1"

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repeat_region complement(35812..36064)
/rpt_family="AluY"
repeat_region 36547..36683 /rpt_family="MIR"
repeat_region complement(37757..37841)
/rpt_family="MIR"
repeat_region complement(37864..37923)
/rpt_family="MIR3"
repeat_region complement(38144..38429)
/rpt_family="AluSx"

Query Match      82.5%; Score 19.8; DB 9; Length 140009;
Best Local Similarity 91.3%; Pred No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcttcattggcagttttgtctct 24
|||||
Db 26629 ATCTTCATGGCACATTTTCCTTCT 26651

RESULT 6
AC008705/c
LOCUS AC008705 159709 bp DNA linear PRI 18-DEC-2001
DEFINITION Homo sapiens chromosome 5 clone CTB-77H17, complete sequence.
ACCESSION AC008705
VERSION AC008705.6 GI:17921194
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 159709)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 159709)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 159709)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 159709)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Dec 18, 2001 this sequence version replaced gi:15799574.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.

FEATURES             source
1..159709
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTB-77H17"

BASE COUNT 46361 a 34053 c 32796 g 46499 t
ORIGIN

Query Match      82.5%; Score 19.8; DB 9; Length 159709;
Best Local Similarity 91.3%; Pred No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcttcattggcagttttgtctct 24
|||||

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Db 151639 ATGTTTCAGCGAGTTTGCTTCT 151617

## RESULT 7

AC026321

LOCUS

DEFINITION

AC026321 163283 bp DNA linear HTG 05-OCT-2001  
Homo sapiens chromosome 3 clone RP11-26K1, WORKING DRAFT SEQUENCE,  
12 unordered pieces.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 163283)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Banks,T., Barbaria,J.,

Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,

Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,

Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,

Cartier,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,

Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,

Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,

Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,

Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,

Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,

Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,

Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,

Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,

Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,

Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,

Hollins,B., Honsli,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,

Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,

Joudah,S., Kratison,E., Kelly,S., Khan,U., King,L., Korvah,J.,

Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,

Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,

Louisege,H., Lozadro,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,

Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,

Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,

Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,

Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,

Nguyen,A., Nguyen,S., Nguyen,N., Nickerson,E., Nwokkwo,S.,

Ogih,M., Okuwonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,

Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,

Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,

Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N.,

Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,

Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,

Tang,H., Tansey,J., Taylor,C., Taylor,P., Telford,B., Thomas,N.,

Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,

Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,

Watlington,S., Williams,G., Williamson,A., Wleczkyk,R., Wooden,S.,

Worley,K., Wu,C., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,

Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 163283)

Worley,K.C.

Direct Submission

Submitted (22-MAR-2000) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Sep 25, 2001 this sequence version replaced gi:9966567.

## COMMENT

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- project information

Center project name: HAPR

Center clone name: RP11-26K1

----- Summary Statistics

Sequencing vector: M13: L08821  
Chemistry: Dye-terminator Big Dye: 83% of reads  
Assembly program: Phrap: version 0.990329  
Consensus quality: 145707 bases at least Q40  
Consensus quality: 155746 bases at least Q30  
Consensus quality: 159150 bases at least Q20  
Estimated insert size: 160720; sum-of-contrigs estimation  
Quality coverage: 0x in Q20 bases; agarose-fp estimation  
Quality coverage: 4.2x in Q20 bases; sum-of-contrigs estimation  
-----

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 12 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence.  
\* as soon as it is available and the accession number will  
\* be preserved.

	1	35745:	contig of 35745 bp in length
	35746	35845:	gap of unknown length
	35846	61648:	contig of 25803 bp in length
	61649	61748:	gap of unknown length
	61749	88812:	contig of 27064 bp in length
	88813	88912:	gap of unknown length
	88913	103528:	contig of 14616 bp in length
	103529	103628:	gap of unknown length
	103629	118839:	contig of 15211 bp in length
	118840	118939:	gap of unknown length
	118940	130598:	contig of 11659 bp in length
	130599	130698:	gap of unknown length
	130699	141004:	contig of 10306 bp in length
	141005	141104:	gap of unknown length
	141105	147790:	contig of 6686 bp in length
	147791	147890:	gap of unknown length
	147891	152770:	contig of 4780 bp in length
	152771	152770:	gap of unknown length
	152771	157138:	contig of 4368 bp in length
	157139	157238:	gap of unknown length
	157239	160268:	contig of 3030 bp in length
	160269	160368:	gap of unknown length
	160369	163283:	contig of 2915 bp in length.

## FEATURES

Location/Qualifiers  
1..163283  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"

BASE COUNT 50282 a 31786 c 32976 g 47106 t 1133 others  
ORIGIN

Query Match 82.5%; Score 19.8; DB 2; Length 163283;  
Best Local Similarity 91.3%; Pred. No. 70;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catcttcagtcgagtttgccttc 23  
||||| ||||||| ||||||| |||||||

Db 75829 CATCATCGGCAGTTTCGCTTC 75851

## RESULT 8

AC008134

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AC008134 175132 bp DNA linear PRI 01-DEC-2001  
Homo sapiens 3q26.2-27 BAC RPC11-263C16 (Roswell Park Cancer  
Institute Human BAC Library) complete sequence.

AC008134

AC008134.3 GI:5801655

HTG.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 175132)  
 Muzny,D.M., Adams,C., Aronson,A., Bailey,M., Barbara,J., Buhay,C., Blankenburg,K., Bodota,B., Bouck,J., Bowie,S., Brooks,A., Chacko,J., Chen,Z., Bunac,C., Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C., David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N., Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Frantz,P., Ganesh,R., Garcia,D.K., Gorrell,J.H., Gorrell,L.L., Guevara,W., Harris,K., He,X., Hernandez,J., Hodgson,A., Hoques,M., Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M., Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z., Lichtarge,O., Liu,J., Liu,W., Logan,O., Lu,J., Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Meli,G., Moore,S., Moorish,T., Morgan,M., Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S., Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L., Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S., Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sugang,R., Tabot,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wabwah,M., Watlington,S., Weinstein,G., Weinstein,I.R., Williamson,A., Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Naylor,S.L. and Gibbs,R.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 175132)  
 Worley,K.C.  
 Direct Submission  
 Submitted (25-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 175132)  
 Worley,K.C.  
 Direct Submission  
 Submitted (28-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 4 (bases 1 to 175132)  
 Worley,K.C.  
 Direct Submission  
 Submitted (01-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 5 (bases 1 to 175132)  
 Worley,K.C.  
 Direct Submission  
 Submitted (01-DEC-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On Aug 28, 1999 this sequence version replaced gi:5764701.  
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email [gc-help@bcm.tmc.edu](mailto:gc-help@bcm.tmc.edu)

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

#### ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

#### QUALSTAT-REPORT-----

----- Summary Statistics -----  
 Contig length: 175132  
 Phrap values in estimate: 172880  
 Average error rate (BCM-Phrap estimate): 0.000229977  
 Fraction of Phrap values less than 40 : 0.0260585  
 Number of consensus changing edits: 15  
 Number of N's in consensus : 0

----- Consensus changing edits -----  

Position	Original+Context	Edited+Context
43389	gtctaattga(n)actttgtacc	gtctaattga(a)actttgtacc
47062	gactgcgcg(n)ctcgcccttc	gactgcgcg(c)ctcgcccttc
64597	atctcgttac(a)aatgcaaccc	atctcgttac(c)aatgcaaccc
64700	tcctgtacaaa(t)gcacccctgt	tcctgtacaaa(a)gcacccctgt
76432	tcataattat(n)atttttaag	tcataattat(t)atttttaag
89673	aatgtctatt(n)tcataaagcc	aatgtctatt(t)tcataaagcc
89706	gggtgtttat(n)taagatgcaa	gggtgtttat(t)taagatgcaa
96986	ttagacctt(n)atacctgttt	ttagacctt(t)atacctgttt
119902	taaaaaaaa(n)aaaaaaggaa	taaaaaaaa(a)aaaaaaggaa
141888	aaagaataaa(n)aagaacaaca	aaagaataaa(a)aagaacaaca
149374	aattacta(n)attggctgct	aattacta(c)attggctgct
151541	gttcaactc(n)ttttttttt	gttcaactc(a)ttttttttt
152439	tcagttctt(c)ccatttaagta	tcagttctt(a)ccatttaagta
153782	aaaaaaaaa(n)gatncaacta	aaaaaaaaa(a)gatncaacta
153786	aaaaaangat(n)cacttacata	aaaaaangat(a)cacttacata

#### ----- Distribution of Quality < 40 Bases -----

# bases	5	10	15	20	25	30	35	40
10001	*	*	*	*	*	*	*	*
9001	*	*	*	*	*	*	*	*
8001	*	*	*	*	*	*	*	*
7001	*	*	*	*	*	*	*	*
6001	*	*	*	*	*	*	*	*
5001	*	*	*	*	*	*	*	*
4001	*	*	*	*	*	*	*	*
3001	*	*	*	*	*	*	*	*
2001	*	*	*	*	*	*	*	*
1001	*	*	*	*	*	*	*	*
01	*	*	*	*	*	*	*	*

Phrap Value Range

Version: 1.01 qxfo.

Location/Qualifiers

1. .175132

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="3q26.2-27"

/clone="RPC11-263C16"

complement(1..2014)

/note="overlaps bases 1..2014 of clone AC092919"

/function="clone overlap"

#### FEATURES

source

misc\_feature



```

repeat_region complement(187..492)
repeat_region /rpt_family="AluJo"
665..829
/rpt_family="MIR"
repeat_region /rpt_family="L1MB4"
1042..1189
complement(1190..1475)
/rpt_family="AluJb"
1476..1547
/rpt_family="L1MB4"
1769..1817
/rpt_family="(TA)n"
complement(2108..2753)
/rpt_family="L2"
complement(2820..3551)
/rpt_family="L2"
3626..3650
/rpt_family="AT-rich"
3874..4094
/rpt_family="L1MC4"
4111..4245
/rpt_family="MER20"
4250..4616
/rpt_family="MSTA"
4624..4710
complement(5062..5109)
/rpt_family="MIR"
complement(5187..5498)
/rpt_family="AluSp"
complement(5530..5663)
/rpt_family="L2"
complement(5972..6147)
/rpt_family="MER5A"
6997..7133
/rpt_family="FLAM_C"
7463..7500
/rpt_family="(TCTA)n"
complement(9036..9342)
/rpt_family="AluSp"
complement(9464..9695)
/rpt_family="MIR"
complement(11255..11314)
/rpt_family="MER5B"
11653..11682
/rpt_family="(TA)n"

Query Match 82.5% Score 19.8; DB 9; Length 175132;
Best Local Similarity 91.3%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catcttcagtcgagtttgcctc 23
|||||
Db 111192 CATCATCATGGCAGTTTCGCTTC 111214

RESULT 9
AC019265 178328 bp DNA linear HTG 03-NOV-2000
LOCUS Homo sapiens clone RP11-6N20, WORKING DRAFT SEQUENCE, 2 ordered
pieces
ACCESSION AC019265
VERSION AC019265.4 GI:11079354
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 178328)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-6N20
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 178328)

AUTHORS
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,
DeArelano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Menes,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.

Direct Submission
Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141 USA
On Nov 3, 2000 this sequence version replaced gi:7239535.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRK
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2911
Center clone name: 6_N_20
----- Summary Statistics
Sequencing vector: M13; M7815; 45% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 177609 bases at least Q40
Consensus quality: 177915 bases at least Q30
Consensus quality: 178053 bases at least Q20
Insert size: 165000; agarose-fp
Insert size: 178228; sum-of-contigs
Quality coverage: 11.2 in Q20 bases; agarose-fp
Quality coverage: 10.4 in Q20 b.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 96718: contig of 96718 bp in length
* 96719 96818: gap of 100 bp
* 96819 178328: contig of 81510 bp in length.
FEATURES
source
1..178328
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-6N20"
/clone_lib="RPCI-11 Human Male BAC"
1..96718
/note="assembly_fragment
clone_end:SP6
vector_side:left"
96819..178328
/note="assembly_fragment
clone_end:T7
vector_side:right"
misc_feature
54890 a 35740 c 33735 g 53863 t 100 others
BASE COUNT
ORIGIN

```

```

Query Match      82.5%; Score 19.8; DB 2; Length 178328;
Best Local Similarity 91.3%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catcttcaggcaggtttgtcttc 23
||||| ||||||| ||||||| |||||||
Db 55871 CATCATCGGCAGTTCGCTTC 55893

RESULT 10
AC092971 179375 bp DNA linear HTG 09-AUG-2001
LOCUS Homo sapiens chromosome 3q clone RP11-6N20, WORKING DRAFT SEQUENCE,
3 unordered pieces.
AC092971.1 GI:15136598
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 179375)
Munoz,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsdrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
Benton,J., Blinage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowles,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Ieal,B., Lewis,L.C.,
Lewis,B., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louisgied,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,
Ogih,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,
Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shoostari,N.,
Sison,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 179375)
Worley,K.C.
Direct Submission
Submitted (09-AUG-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM

Query Match      82.5%; Score 19.8; DB 2; Length 179375;
Best Local Similarity 91.3%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 catcttcaggcaggtttgtcttc 23
||||| ||||||| ||||||| |||||||
Db 108605 CATCATCGGCAGTTCGCTTC 108627

RESULT 11
AL589696 207415 bp DNA linear HTG 18-JAN-2002
LOCUS Mus musculus chromosome 15 clone RP23-454M13, *** SEQUENCING IN
DEFINITION PROGRESS ***, in ordered pieces.
ACCESSION AL589696
VERSION AL589696.8 GI:18375812
KEYWORDS HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
Dunn,M.
Direct Submission
Submitted (17-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 25, 2002 this sequence version replaced gi:16944949.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information

```

Center project name: bm454m13  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: Plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 99% of reads  
Chemistry: Dye-primer Big Dye; 0% of reads  
Consensus quality: 207161 bases at least Q40  
Consensus quality: 207332 bases at least Q30  
Consensus quality: 207385 bases at least Q20  
Insert size: 207415; sum-of-contigs  
Insert size: 201201; 5.9% error; agarose-fp  
Quality coverage: 12.54% in Q20 bases; sum-of-contigs Quality  
coverage: 12.99% in Q20 bases; agarose-fp  
-----  
\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
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Location/Qualifiers  
1..207415  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/chromosome="15"  
/clone="RP23-454M13"  
/clone\_lib="RPCI-23"  
misc\_feature 1..207415  
/note="assembly\_fragment:04323  
clone\_end:SP6  
vector\_side:right  
clone\_end:T7  
vector\_side:left"  
BASE COUNT 65722 a 42071 c 39838 g 59784 t  
ORIGIN  
  
Query Match 82.5%; Score 19.8; DB 2; Length 207415;  
Best Local Similarity 91.3%; Pred. No. 69;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 atcttcagtcagcttttgccttc 24  
||||| ||||||| |||||  
Db 106803 ATCTTCATGTCAGCTTTTCCCTTCT 106825  
  
RESULT 12  
AC109337  
LOCUS  
DEFINITION Homo sapiens chromosome 15 clone RP11-62303 map 15, LOW-PASS HTG 03-FEB-2002  
AC109337  
SEQUENCE SAMPLING.  
AC109337  
VERSION AC109337.1 GI:18482270  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 64742)  
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
TITLE Homo sapiens chromosome 15, clone RP11-62303  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 64742)  
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,  
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,  
Chospel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,  
Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,  
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,  
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R.,  
Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,  
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,  
McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T.,

Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,  
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,  
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,  
Reta.R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,  
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,  
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,  
Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L24566  
Center clone name: 623\_O\_3  
-----  
\* NOTE: This record contains 81 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
\* 1 703: contig of 703 bp in length  
\* 704 803: gap of 100 bp  
\* 804 1511: contig of 708 bp in length  
\* 1512 1611: gap of 100 bp  
\* 1612 2320: contig of 709 bp in length  
\* 2321 2420: gap of 100 bp  
\* 2421 3113: contig of 693 bp in length  
\* 3114 3213: gap of 100 bp  
\* 3214 3991: contig of 778 bp in length  
\* 3992 4091: gap of 100 bp  
\* 4092 4811: contig of 720 bp in length  
\* 4812 4911: gap of 100 bp  
\* 4912 5609: contig of 698 bp in length  
\* 5610 5709: gap of 100 bp  
\* 5710 6395: contig of 686 bp in length  
\* 6396 6495: gap of 100 bp  
\* 6496 7198: contig of 703 bp in length  
\* 7199 7298: gap of 100 bp  
\* 7299 8006: contig of 708 bp in length  
\* 8007 8106: gap of 100 bp  
\* 8107 8799: contig of 693 bp in length  
\* 8800 8899: gap of 100 bp  
\* 8900 9606: contig of 707 bp in length  
\* 9607 9706: gap of 100 bp  
\* 9707 10407: contig of 701 bp in length  
\* 10408 10507: gap of 100 bp  
\* 10508 11207: contig of 700 bp in length  
\* 11208 11307: gap of 100 bp  
\* 11308 12001: contig of 694 bp in length  
\* 12002 12101: gap of 100 bp  
\* 12102 12789: contig of 688 bp in length  
\* 12790 12889: gap of 100 bp  
\* 12890 13594: contig of 705 bp in length  
\* 13595 13694: gap of 100 bp  
\* 13695 14372: contig of 678 bp in length  
\* 14373 14472: gap of 100 bp  
\* 14473 15167: contig of 695 bp in length

```
* 15168 15267: gap of 100 bp
* 15268 15954: contig of 687 bp in length
* 15955 16054: gap of 100 bp
* 16055 16736: contig of 682 bp in length
* 16737 16836: gap of 100 bp
* 16837 17534: contig of 698 bp in length
* 17535 17634: gap of 100 bp
* 17635 18342: contig of 708 bp in length
* 18343 18442: gap of 100 bp
* 18443 19148: contig of 706 bp in length
* 19149 19248: gap of 100 bp
* 19249 19958: contig of 710 bp in length
* 19959 20058: gap of 100 bp
* 20059 20796: contig of 738 bp in length
* 20797 20896: gap of 100 bp
* 20897 21594: contig of 698 bp in length
* 21595 21694: gap of 100 bp
* 21695 22406: contig of 712 bp in length
* 22407 22506: gap of 100 bp
* 22507 23207: contig of 701 bp in length
* 23208 23307: gap of 100 bp
* 23308 24003: contig of 696 bp in length
* 24004 24103: gap of 100 bp
* 24104 24814: contig of 711 bp in length
* 24815 24914: gap of 100 bp
* 24915 25614: contig of 700 bp in length
* 25615 25714: gap of 100 bp
* 25715 26426: contig of 712 bp in length
* 26427 26526: gap of 100 bp
* 26527 27230: contig of 704 bp in length
* 27231 27330: gap of 100 bp
* 27331 28027: contig of 697 bp in length
* 28028 28127: gap of 100 bp
* 28128 28819: contig of 692 bp in length
* 28820 28919: gap of 100 bp
* 28920 29614: contig of 695 bp in length
* 29615 29714: gap of 100 bp
* 29715 30403: contig of 689 bp in length
* 30404 30503: gap of 100 bp
* 30504 31201: contig of 698 bp in length
* 31202 31301: gap of 100 bp
* 31302 31983: contig of 682 bp in length
* 31984 32083: gap of 100 bp
* 32084 32772: contig of 689 bp in length
* 32773 32872: gap of 100 bp
* 32873 33575: contig of 703 bp in length
* 33576 33675: gap of 100 bp
* 33676 34394: contig of 719 bp in length
* 34395 34494: gap of 100 bp
* 34495 35200: contig of 706 bp in length
* 35201 35300: gap of 100 bp
* 35301 36015: contig of 715 bp in length
* 36016 36115: gap of 100 bp
* 36116 36819: contig of 704 bp in length
* 36820 36919: gap of 100 bp
* 36920 37544: contig of 625 bp in length
* 37545 37644: gap of 100 bp
* 37645 38295: contig of 651 bp in length
* 38296 38395: gap of 100 bp
* 38396 39095: contig of 700 bp in length
* 39096 39195: gap of 100 bp
* 39196 39964: contig of 769 bp in length
* 39965 40064: gap of 100 bp
* 40065 40766: contig of 702 bp in length
* 40767 40866: gap of 100 bp
* 40867 41570: contig of 704 bp in length
* 41571 41670: gap of 100 bp
* 41671 42376: contig of 706 bp in length
* 42377 42476: gap of 100 bp
* 42477 43184: contig of 708 bp in length
* 43185 43284: gap of 100 bp
* 43285 43992: contig of 708 bp in length
* 43993 44092: gap of 100 bp
```

```
* 44093 44797: contig of 705 bp in length
* 44798 44897: gap of 100 bp
* 44898 45604: contig of 707 bp in length
* 45605 45704: gap of 100 bp
* 45705 46384: contig of 680 bp in length
* 46385 46484: gap of 100 bp
* 46485 47193: contig of 709 bp in length
* 47194 47293: gap of 100 bp
* 47294 47950: contig of 657 bp in length
* 47951 48050: gap of 100 bp
* 48051 48759: contig of 709 bp in length
* 48760 48859: gap of 100 bp
* 48860 49544: contig of 685 bp in length
* 49545 49644: gap of 100 bp
* 49645 50348: contig of 704 bp in length
* 50349 50448: gap of 100 bp
* 50449 51140: contig of 692 bp in length
* 51141 51240: gap of 100 bp
* 51241 51943: contig of 703 bp in length
* 51944 52043: gap of 100 bp
* 52044 52726: contig of 683 bp in length
* 52727 52826: gap of 100 bp
* 52827 53534: contig of 708 bp in length
* 53535 53634: gap of 100 bp
* 53635 54347: contig of 713 bp in length
* 54348 54447: gap of 100 bp
* 54448 55156: contig of 709 bp in length
```

```
Query Match      80.8%  Score 19.4;  DB 2;  Length 64742;
Best Local Similarity 95.2%  Pred. No. 1.1e+02;
Matches 20;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
```

```
Qy 3 tcttcattggcagtttgcctc 23
   |||||||
Db 30754 TCATCATGGCAGTTTGCTTC 30774
```

```
RESULT 13
AC092306
```

```
LOCUS          AC092306               72628 bp    DNA    linear    HTG 03-JUL-2001
DEFINITION     Homo sapiens chromosome 19 clone LLNLR-231D4, WORKING DRAFT
SEQUENCE, 29 unordered pieces.
```

```
ACCESSION      AC092306
VERSION        AC092306.1  GI:14589495
KEYWORDS       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE         human.
```

```
ORGANISM       Homo sapiens
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
AUTHORS        DOE Joint Genome Institute.
TITLE          Sequencing of Human Chromosome 19
```

```
JOURNAL        Unpublished
```

```
REFERENCE      2 (bases 1 to 72628)
```

```
AUTHORS        DOE Joint Genome Institute.
```

```
TITLE          Direct Submission
```

```
JOURNAL        Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
```

```
COMMENT
```

```
-----Genome Center
```

```
Center: Joint Genome Institute
```

```
Center Code: JGI
```

```
Web site: http://www.jgi.doe.gov
```

```
-----
```

```
Project Information
```

```
Center Project Name: 22390, R27120
```

```
Center clone name: LLNL-R_231D4
```

```
-----
```

```
Summary Statistics
```

```
Consensus quality: 50309 bases at least Q40
```

```
Consensus quality: 61253 bases at least Q30
```

```
Consensus quality: 63234 bases at least Q20
```

```
Estimated insert size: 40040; agarose-fp estimation
```

```
Estimated insert size: 69828; sum-of-contigs estimation
```

Quality coverage: 6.43 in Q20 bases; agarose-fp estimation  
 Quality coverage: 3.69 in Q20 bases; sum-of-contigs estimation.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 29 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

```

1 1169: contig of 1169 bp in length
* 1170 1269: gap of unknown length
* 1270 2596: contig of 1327 bp in length
* 2597 2696: gap of unknown length
* 2697 3972: contig of 1275 bp in length
* 3972 4071: gap of unknown length
* 4071 5072: contig of 1001 bp in length
* 5072 5173: gap of unknown length
* 5173 6557: contig of 1385 bp in length
* 6558 6657: gap of unknown length
* 6658 8182: contig of 1525 bp in length
* 8183 8282: gap of unknown length
* 8283 9470: contig of 1187 bp in length
* 9470 9569: gap of unknown length
* 9570 10792: contig of 1223 bp in length
* 10793 10893: contig of unknown length
* 10893 12259: contig of 1366 bp in length
* 12259 14063: contig of 1705 bp in length
* 14064 14163: gap of unknown length
* 14164 15780: contig of 1617 bp in length
* 15781 15880: gap of unknown length
* 15881 17150: contig of 1270 bp in length
* 17151 17250: gap of unknown length
* 17251 18725: contig of 1475 bp in length
* 18726 18825: gap of unknown length
* 18826 20171: contig of 1345 bp in length
* 20172 20271: gap of unknown length
* 20272 22116: contig of 1845 bp in length
* 22117 22216: gap of unknown length
* 22217 23300: contig of 1084 bp in length
* 23301 23400: gap of unknown length
* 23401 25414: contig of 2014 bp in length
* 25415 25514: gap of unknown length
* 25515 27380: contig of 1866 bp in length
* 27381 27480: gap of unknown length
* 27481 29137: contig of 1657 bp in length
* 29138 29237: gap of unknown length
* 29238 31083: contig of 1845 bp in length
* 31084 31183: gap of unknown length
* 31184 32661: contig of 1478 bp in length
* 32662 32761: gap of unknown length
* 32762 34307: contig of 1546 bp in length
* 34308 34407: gap of unknown length
* 34408 35843: contig of 1436 bp in length
* 35844 35943: gap of unknown length
* 35944 37241: contig of 1298 bp in length
* 37242 40168: contig of 2827 bp in length
* 40169 40268: gap of unknown length
* 40269 44545: contig of 4277 bp in length
* 44546 44645: gap of unknown length
* 44646 50390: contig of 5745 bp in length
* 50391 50490: gap of unknown length
* 50491 57556: contig of 7066 bp in length
* 57557 57656: gap of unknown length
* 57657 72628: contig of 14972 bp in length.

```

# FEATURES

```

Location/Qualifiers
1. .72628
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="LLNLR-231D4"

```

```

BASE COUNT 18774 a 16108 c 16603 g 18339 t 2804 others
ORIGIN

```

```

Query Match 80.8%; Score 19.4; DB 2; Length 72628;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 3 ttttcagtcgagttttgtctc 23
|| |||||
Db 21310 TCATCATGCGAGTTTGTCTC 21330

```

```

RESULT 14
HS692C8
LOCUS

```

```

DEFINITION HS692C8 125698 bp DNA linear PRI 15-MAR-2001
Human DNA sequence from clone RP4-692C8 on chromosome
20p11.22-12.2. Contains GSSs and STSs, complete sequence.

```

```

ACCESSION AL034561
VERSION AL034561.5 GI:12545143
KEYWORDS HTG.
SOURCE human.

```

## ORGANISM

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE 1 (bases 1 to 125698)
AUTHORS Matthews,L.
TITLE Direct Submission
JOURNAL

```

## COMMENT

Submitted (23-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequests@sanger.ac.uk  
 On Jan 26, 2001 this sequence version replaced gi:4464247.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence has been finished according to sequence map criteria  
 as follows. An attempt is made to resolve all sequencing problems,  
 such as compressions and repeats, but not necessarily within known  
 annotated repeat sequence elements. Where the sequence is  
 ambiguous, there is an annotation using the 'unsure' feature key.  
 The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information  
 on the WORMPEP database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 20, constructed by the Sanger Centre Chromosome 20  
 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr20  
 RP4-692C8 is from the library RPCI-4 constructed by the group of  
 Pieter de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm  
 VECTOR: pCYPAC2  
 This sequence is the entire insert of clone RP4-692C8.

## FEATURES

### source

```

1. 125698
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/map="p11.22-12.2"
/clone="RP4-692C8"
/clone.lib="RPCI-4"

```

```

repeat_region 1..1233
/note="LI repeat: matches 3336. .4554 of consensus"
repeat_region 1230..3674
/note="LI repeat: matches 2527. .5039 of consensus"
repeat_region 3675..4015
/note="LI MAL repeat: matches 5962. .6304 of consensus"
repeat_region 4034..6971

```

repeat\_region /note="L1M1 repeat: matches 1389. .1590 of consensus"  
repeat\_region /note="L1M1 repeat: matches 1868. .2541 of consensus"  
repeat\_region 7653. .7937  
repeat\_region /note="L1PA4 repeat: matches 5862. .6146 of consensus"  
repeat\_region 7938. .9168  
repeat\_region /note="L1M1 repeat: matches 958. .1869 of consensus"  
misc\_feature 10285. .10802  
misc\_feature /note="match: GSS: Em:AQ767211"  
misc\_feature complement(12619. .13196)  
misc\_feature /note="match: GSS: Em:B69623"  
misc\_feature complement(12739. .13190)  
misc\_feature /note="match: GSS: Em:AQ270964"  
misc\_feature complement(13127. .13629)  
misc\_feature /note="match: GSS: Em:AQ187800"  
misc\_feature 13635. .14372  
misc\_feature /note="match: GSS: Em:AQ420261"  
misc\_feature 13637. .14075  
misc\_feature /note="match: GSS: Em:AQ407983"  
misc\_feature 13652. .14060  
misc\_feature /note="match: GSS: Em:AQ403809"  
misc\_feature complement(15664. .16024)  
misc\_feature /note="match: GSS: Em:AQ043704"  
misc\_feature complement(16006. .16524)  
misc\_feature /note="match: GSS: Em:AQ695438"  
misc\_feature complement(16090. .16493)  
misc\_feature /note="match: GSS: Em:AQ776673"  
repeat\_region 16833. .17237  
repeat\_region /note="L1MD2 repeat: matches 5555. .5934 of consensus"  
repeat\_region 17546. .19508  
misc\_feature /note="L1MD2 repeat: matches 3547. .5555 of consensus"  
misc\_feature complement(19331. .19799)  
repeat\_region /note="match: GSS: Em:AQ695800"  
repeat\_region 19680. .19934  
repeat\_region /note="L1MC5 repeat: matches 7273. .7523 of consensus"  
repeat\_region 19935. .20246  
repeat\_region /note="AluA5 repeat: matches 1. .309 of consensus"  
repeat\_region 20247. .20623  
repeat\_region /note="L1MC5 repeat: matches 7523. .7913 of consensus"  
repeat\_region 20638. .20804  
misc\_feature /note="FRAM repeat: matches 1. .162 of consensus"  
misc\_feature complement(21615. .22036)  
misc\_feature /note="match: GSS: Em:AQ423530"  
misc\_feature 22090. .22639  
misc\_feature /note="match: GSS: Em:AQ382070"  
repeat\_region 22099. .22507  
repeat\_region /note="match: GSS: Em:AQ412213"  
repeat\_region 22201. .22288  
repeat\_region /note="44 copies 2 mer aa 63% conserved"  
repeat\_region 22616. .24206  
repeat\_region /note="L1PA7 repeat: matches 4544. .6145 of consensus"  
repeat\_region 24383. .24695  
repeat\_region /note="L1ME repeat: matches 5174. .5480 of consensus"  
repeat\_region 24701. .24738  
repeat\_region /note="19 copies 2 mer tg 100% conserved"  
repeat\_region 24796. .24958  
misc\_feature /note="MER63 repeat: matches 1. .789 of consensus"  
misc\_feature 26026. .26451  
misc\_feature /note="match: GSS: Em:AQ312975"  
misc\_feature 26047. .26517  
repeat\_region /note="match: GSS: Em:AQ428497"  
repeat\_region 30300. .30347  
repeat\_region /note="CRNA-ASP-GAC repeat: matches 1. .46 of consensus"  
repeat\_region 30723. .30815  
repeat\_region /note="MER89 repeat: matches 5. .98 of consensus"  
repeat\_region 31055. .31155  
repeat\_region /note="MER89 repeat: matches 388. .490 of consensus"  
repeat\_region 31716. .31791  
misc\_feature /note="MER89 repeat: matches 474. .559 of consensus"  
misc\_feature complement(34341. .34846)  
repeat\_region /note="match: GSS: Em:AQ423311"  
repeat\_region 35950. .35985  
repeat\_region /note="18 copies 2 mer tc 94% conserved"

repeat\_region 37953. .39151  
repeat\_region /note="L1MC3 repeat: matches 6507. .7735 of consensus"  
repeat\_region 41925. .42085  
repeat\_region /note="L1PA16 repeat: matches 5999. .6157 of consensus"  
repeat\_region 42390. .42516  
repeat\_region /note="L1PA16 repeat: matches 5872. .5999 of consensus"  
repeat\_region 42534. .42713  
misc\_feature /note="Alusg/x repeat: matches 123. .302 of consensus"  
misc\_feature 43671. .44128  
misc\_feature /note="match: GSS: Em:AQ005776"  
misc\_feature 43703. .43840  
repeat\_region /note="match: GSS: Em:B34641"  
repeat\_region 43938. .44717  
repeat\_region /note="L1PA2 repeat: matches 2. .776 of consensus"  
repeat\_region 44713. .44953  
repeat\_region /note="L1PA2 repeat: matches 900. .6146 of consensus"  
repeat\_region 50213. .50462  
repeat\_region /note="MSTA repeat: matches 192. .426 of consensus"  
repeat\_region 50769. .50955  
repeat\_region /note="MSTA repeat: matches 1. .192 of consensus"  
repeat\_region 51555. .51626  
repeat\_region /note="MSTB repeat: matches 355. .426 of consensus"  
repeat\_region 52001. .52354  
repeat\_region /note="MSTB repeat: matches 1. .370 of consensus"  
repeat\_region 53067. .53239  
repeat\_region /note="MER5B repeat: matches 1. .178 of consensus"  
repeat\_region 54514. .54736  
repeat\_region /note="L1R16C repeat: matches 166. .387 of consensus"  
repeat\_region 56342. .56429  
misc\_feature /note="MLT1J repeat: matches 46. .182 of consensus"  
repeat\_region 57523. .57994  
repeat\_region /note="match: GSS: Em:AQ560111"  
repeat\_region 59147. .59180  
repeat\_region /note="17 copies 2 mer aa 94% conserved"  
repeat\_region 59847. .60120  
repeat\_region /note="match: GSS: Em:AQ040668"  
repeat\_region 60897. .61171  
repeat\_region /note="match: STS: Em:HSPF11E9"  
repeat\_region 61139. .61336  
repeat\_region /note="L1PB3 repeat: matches 5949. .6146 of consensus"  
repeat\_region 61856. .62275  
repeat\_region /note="L1ME repeat: matches 5317. .5752 of consensus"  
repeat\_region 62742. .63019  
repeat\_region /note="L1ME repeat: matches 5532. .5818 of consensus"  
misc\_feature complement(62900. .63417)  
repeat\_region /note="match: GSS: Em:AQ167031"  
repeat\_region 63136. .63432  
repeat\_region /note="L1ME repeat: matches 5072. .5380 of consensus"  
repeat\_region 64545. .64712  
repeat\_region /note="84 copies 2 mer ta 58% conserved"  
repeat\_region complement(65036. .65356)  
repeat\_region /note="match: STS: Em:G08057"  
repeat\_region 65145. .65196  
repeat\_region /note="26 copies 2 mer ag 75% conserved"  
repeat\_region 65200. .65411  
repeat\_region /note="MLT2D repeat: matches 295. .514 of consensus"  
repeat\_region 65421. .65475  
repeat\_region /note="MERVL repeat: matches 3416. .3471 of consensus"  
repeat\_region 65461. .67498  
repeat\_region /note="HERVL repeat: matches 1375. .3438 of consensus"  
repeat\_region 68860. .68997  
repeat\_region /note="69 copies 2 mer tt 59% conserved"  
repeat\_region complement(69498. .69643)  
repeat\_region /note="match: GSS: Em:AQ678423"  
repeat\_region 70239. .70400  
repeat\_region /note="L1R16C repeat: matches 70. .235 of consensus"  
repeat\_region 70439. .70577  
repeat\_region /note="L1MB8 repeat: matches 6030. .6171 of consensus"  
repeat\_region 71763. .71936  
repeat\_region /note="MER5B repeat: matches 13. .177 of consensus"

Query Match 80.8%; Score 19.4; DB 9; Length 125698;  
Best Local Similarity 95.2%; Pred. No. 1.1e+02;

Matches' 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ttttcattggcagtttgccttc 23  
|||  
Db 84877 TCATCATGGCAGTTTGTCTTC 84897

RESULT 15

AC024600 147876 bp DNA linear PRI 24-AUG-2000  
LOCUS Homo sapiens chromosome 10 clone RP11-179K3, complete sequence.  
DEFINITION AC024600  
ACCESSION AC024600  
VERSION AC024600.4 GI:9887597  
KEYWORDS HTG.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 147876)  
AUTHORS Smith,D.R.

TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome  
Sequence Data  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 147876)  
AUTHORS Smith,D.R.

TITLE Direct Submission  
JOURNAL Submitted (01-MAR-2000) Genome Therapeutics Corporation, 100 Beaver  
Street, Waltham, MA 02453, USA  
REFERENCE 3 (bases 1 to 147876)  
AUTHORS Smith,D.R.

TITLE Direct Submission  
JOURNAL Submitted (24-AUG-2000) Genome Therapeutics Corporation, 100 Beaver  
Street, Waltham, MA 02453, USA  
COMMENT On Aug 24, 2000 this sequence version replaced gi:8569065.

FEATURES  
source  
1. 147876  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="10"  
/clone="RP11-179K3"  
/clone\_lib="RPCI-11"  
BASE COUNT 46967 a 25749 c 26005 g 49155 t  
ORIGIN

Query Match 80.8%; Score 19.4; DB 9; Length 147876;  
Best Local Similarity 95.2%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ttttcattggcagtttgccttc 23  
|||  
Db 71619 TCATCATGGCAGTTTGTCTTC 71639

Search completed: August 21, 2002, 10:49:56  
Job time: 9811 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 09:55:47 ; Search time 6260.2 Seconds  
(without alignments) updates/sec  
51.744 Million cell

Title: US-09-339-922A-105

Perfect score: 24

Sequence: 1 catcttcagtcagtttgcttct 24

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estl:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.4	85.0	855	12	CNS02E0S
2	19.8	82.5	313	9	AW256968
3	19.8	82.5	471	10	C84597
4	19.8	82.5	582	9	BE154166
5	19.8	82.5	597	9	AW686308
6	19.8	82.5	617	9	BE204884
7	19.8	82.5	626	10	BE999842
8	19.8	82.5	633	9	AW559550
9	19.8	82.5	645	10	BF642179
10	19.8	82.5	656	9	AW695027
11	19.8	82.5	663	9	AW692889
12	19.8	82.5	682	10	BG452255
13	19.2	80.0	241	10	BF378810
14	19.2	80.0	491	9	AW786151
15	19.2	80.0	536	10	BF191434
16	19.2	80.0	538	10	BF193498
17	19.2	80.0	610	12	AQ744319

18 19.2 80.0 653 12 AG073249  
c 19 19.2 80.0 776 10 BG747830  
c 20 19.2 80.0 1037 10 BM478125  
c 21 18.8 78.3 452 10 BI820101  
c 22 18.8 78.3 568 9 AW850973  
c 23 18.8 78.3 587 12 AQ944218  
c 24 18.8 78.3 600 12 AQ660116  
c 25 18.8 78.3 716 12 A2213382  
c 26 18.8 78.3 722 12 AQ645036  
c 27 18.8 78.3 724 10 BG426971  
c 28 18.8 78.3 764 9 AL554662  
c 29 18.8 78.3 813 10 BG707577  
c 30 18.4 76.7 770 12 AG167827  
c 31 18.2 75.8 153 12 A2986091  
c 32 18.2 75.8 198 10 BG508089  
c 33 18.2 75.8 221 10 BF963803  
c 34 18.2 75.8 407 12 AQ989925  
c 35 18.2 75.8 442 10 BI797255  
c 36 18.2 75.8 459 9 AU162173  
c 37 18.2 75.8 465 10 BF425397  
c 38 18.2 75.8 475 12 AQ246544  
c 39 18.2 75.8 501 10 BF598453  
c 40 18.2 75.8 517 12 BH340494  
c 41 18.2 75.8 524 12 AQ322747  
c 42 18.2 75.8 524 12 AQ348649  
c 43 18.2 75.8 536 10 BI893110  
c 44 18.2 75.8 536 10 BM178753  
c 45 18.2 75.8 548 10 BM086100

#### ALIGNMENTS

RESULT 1

CNS02E0S

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

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/db_xref="taxon:99883"
/clone="261K20"
/clone_lib="G"
/notes="Genoscope sequence ID : COAG261BF10SP1-end :
PUC-ori"
BASE COUNT      185 a   200 c   213 g   253 t   4 others
ORIGIN

Query Match
Best Local Similarity 85.0%; Score 20.4; DB 12; Length 855;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 tcttcattgcagtttgccttct 24
||||| ||||| ||||| ||||| |||||
Db 784 TCTTCATGCGAGTTTGCCTTT 805

RESULT 2
AW256968
LOCUS      AW256968      313 bp      mRNA      linear      EST 20-DEC-1999
DEFINITION EST305105 KV2 Medicago truncatula cDNA clone KV2-6B17, mRNA
sequence.
ACCESSION AW256968
VERSION   AW256968.1 GI:6605225
KEYWORDS  EST.
SOURCE    barrel medic.
ORGANISM  Medicago truncatula
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
           Medicago.
REFERENCE 1 (bases 1 to 313)
AUTHORS   VandenBosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H., Ellis,L.,
           Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
           Fraser,C.M.
           ESTs from roots of Medicago truncatula after Rhizobium inoculation
           Unpublished (1999)
           Contact: VandenBosch K
           Department of Biology
           Texas A&M University
           College Station, TX 77843-3258, USA
           Tel: 409 845 7707
           Fax: 409 845 2891
           Email: kate@mail.bio.tamu.edu
           Texas A&M EST name: T115673e
           TIGR sequence name: M7AAK09TK
           More information is available at: . (and for clone ordering info)
           http://chrystie.tamu.edu/medicago
           Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
           Location/Qualifiers
             1..313
               /organism="Medicago truncatula"
               /cultivar="genotype A17"
               /db_xref="taxon:3880"
               /clone_lib="KV2"
               /tissue_type="Seedling roots"
               /dev_stage="2 days post-inoculation with Sinorhizobium
               meliloti"
               /lab_host="E. coli strain SOLR"
               /note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
               XhoI; cDNA was prepared from polyA+ enriched RNA. The
               cDNA was directionally ligated into the Unizap XR vector
               from Stratagene and packaged using Gigapack III Gold
               packaging extracts. Plasmids containing cDNA inserts
               were excised from the recombinant lambda-zap phage using
               Ex-assist helper phage and propagated in SOLR cells."
BASE COUNT      88 a   62 c   70 g   93 t
ORIGIN

Query Match
Best Local Similarity 82.5%; Score 19.8; DB 9; Length 313;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Best Local Similarity 91.3%; Pred. No. 2.5e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcttcattgcagtttgccttct 24
||||| ||||| ||||| ||||| |||||
Db 139 ATCTTCATGCGTGTGTTGCTTCT 161

RESULT 3
C84597/c
LOCUS      C84597      471 bp      mRNA      linear      EST 26-MAR-1999
DEFINITION C84597 osteoclast subtracted library Oryctolagus cuniculus cDNA,
mRNA sequence.
ACCESSION C84597
VERSION   C84597.1 GI:4527857
KEYWORDS  EST.
SOURCE    rabbit.
ORGANISM  Oryctolagus cuniculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 471)
AUTHORS   Kobori,M., Ikeda,Y., Nara,H., Kato,M., Kumegawa,M., Nojima,H. and
           Kawashima,H.
           Large scale isolation of osteoclast-specific genes by an improved
           method involving the preparation of a subtracted cDNA library
           Genes Cells 3 (7), 459-475 (1998)
           98424349
           Contact: Kobori M
           Molecular Medicine Laboratories
           Institute for Drug Discovery Research,Yamanouchi Pharmaceutica
           21, Miyukigaoka, Tsukuba, Ibaraki 305, Japan
           Email: kobori@yamanouchi.co.jp
           PROJECT = 'OSG'.
           Location/Qualifiers
             1..471
               /organism="Oryctolagus cuniculus"
               /db_xref="taxon:9986"
               /clone_lib="osteoclast subtracted library"
               /tissue_type="long bone"
               /cell_type="osteoclast"
               /cell_line="primary"
               /dev_stage="5 day-old"
BASE COUNT      73 a   141 c   140 g   108 t   9 others
ORIGIN

Query Match
Best Local Similarity 82.5%; Score 19.8; DB 10; Length 471;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 catcttcattgcagtttgccttc 23
||||| ||||| ||||| ||||| |||||
Db 200 CTCTTCATGCGAGCTTTGCTTC 178

RESULT 4
BE154166
LOCUS      BE154166      582 bp      mRNA      linear      EST 21-JUN-2000
DEFINITION PM1-H70340-201299-004-h02 HT0340 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE154166
VERSION   BE154166.1 GI:8616887
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
           Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
           Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
           Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
           M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
           Simpson,A.J.

```



Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."

BASE COUNT 187 a 144 c 125 g 161 t  
ORIGIN

Query Match 82.5%; Score 19.8; DB 9; Length 617;  
Best Local Similarity 91.3%; Pred. No. 3e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcagcgagctttgcttct 24  
||||||| || |||||||||  
Db 417 ATCTTCATCGCTGTTTGTCTCT 439

RESULT 7  
BE999842  
LOCUS BE999842 626 bp mRNA linear EST 06-OCT-2000  
DEFINITION EST431565 GVSN Medicago truncatula cDNA clone pgVSN-24B2, mRNA  
sequence.  
ACCESSION BE999842  
VERSION BE999842.1 GI:10700118  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.

REFERENCE 1 (bases 1 to 626)  
AUTHORS Fedorova,M., Pierson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P., Town  
,C.D., Bowman,C.L., Craven,M.B., Cho,J. and Fraser,C.M.  
ESTs from senescent nodules of Medicago truncatula  
Unpublished (2000)  
TITLE Department of Agronomy and Plant Genetics  
JOURNAL University of Minnesota  
COMMENT 411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA  
Tel: 612 625 5715  
Fax: 651-649-5058

Email: vance004@maroon.tc.umn.edu  
University of Minnesota name: M273820e TIGR sequence name:  
MTKBJ01TK More information is available at:  
http://chrysie.tamu.edu/medicago  
Seq primer: Skmod (CTA gAA CTA gTg gAT CC).

Location/Qualifiers

FEATURES source

1. .626  
/organism="Medicago truncatula"  
/cultivar="genotype A17"  
/db\_xref="taxon:3880"  
/clone="pgVSN-24B2"  
/clone\_lib="GVSN"  
/tissue\_type="senescent root nodules"  
/dev\_stage="mixture of effective nodules from 40 day old  
plants harvested 36 hours post shoot removal and nodules  
collected from 2 month old plants at mid-pod stage"  
/lab\_host="E. coli strain SOLR"  
/note="Vector: pBluescript SK +/-; Site\_1: EcoRI; Site\_2:  
XhoI; cDNA was prepared from polyA+ enriched RNA from the  
mixture of effective nodules of 40 day old plants  
harvested 36 hours post shoot removal and nodules  
collected from 2 month old plants at mid-pod stage. The  
cDNA was directionally ligated into the Uni-ZAP XR vector  
from Stratagene and packaged using Gigapack III Gold  
packaging extracts. Plasmids containing cDNA inserts were  
excised from the recombinant lambda-ZAP phage using  
Ex-Assist helper phage and propagated in SOLR cells."

BASE COUNT 183 a 153 c 122 g 168 t  
ORIGIN

Query Match 82.5%; Score 19.8; DB 10; Length 626;  
Best Local Similarity 91.3%; Pred. No. 3e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcagcgagctttgcttct 24  
||||||| || |||||||||  
Db 455 ATCTTCATCGCTGTTTGTCTCT 477

RESULT 8  
AW559550  
LOCUS AW559550 633 bp mRNA linear EST 07-SEP-2000  
DEFINITION EST314598 DSIR Medicago truncatula cDNA clone pDSIR-24A9, mRNA  
sequence.  
ACCESSION AW559550  
VERSION AW559550.1 GI:7204976  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.

REFERENCE 1 (bases 1 to 633)  
AUTHORS Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,J.S., Peng  
,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,  
Holt,I.E. and Fraser,C.M.  
ESTs from roots of Medicago truncatula after inoculation with  
Phytophthora medicaginis  
Unpublished (1999)  
TITLE Department of Agronomy and Plant Genetics  
JOURNAL University of Minnesota  
COMMENT 411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA  
Tel: 612 625 5715  
Fax: 651-649-5058

Email: vance004@maroon.tc.umn.edu  
Minnesota EST name:M250836e ; TIGR sequence name:MTBAM05TK ; More  
information, including clone ordering, is available at:  
'http://chrysie.tamu.edu/medicago'  
Seq primer: Skmod (CTA gAA CTA gTg gAT CC).

Location/Qualifiers

FEATURES source

1. .633  
/organism="Medicago truncatula"  
/cultivar="genotype A17"  
/db\_xref="taxon:3880"  
/clone="pDSIR-24A9"  
/clone\_lib="DSIR"  
/tissue\_type="roots infected with Phytophthora  
medicaginis"  
/dev\_stage="roots harvested at 10 days post inoculation  
with Phytophthora medicaginis"  
/lab\_host="E. coli strain XL0LR"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
XhoI; cDNA was prepared from polyA+ enriched RNA from  
roots harvested at 10 days post inoculation with  
Phytophthora medicaginis. The cDNA was directionally  
ligated into the Uni-ZAP XR vector from Stratagene and  
packaged using Gigapack III Gold packaging extracts.  
Plasmids containing cDNA inserts were excised from the  
recombinant lambda-ZAP phage using Ex-Assist helper phage  
and propagated in XL0LR cells. Note: EST may be of fungal  
origin."

BASE COUNT 183 a 142 c 140 g 168 t  
ORIGIN

Query Match 82.5%; Score 19.8; DB 9; Length 633;  
Best Local Similarity 91.3%; Pred. No. 3e+02;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcagcgagctttgcttct 24  
||||||| || |||||||||

Db 342 ATCTTCATCGCTGTTTGCTTCT 364

# RESULT 9

BF642179 645 bp mRNA linear EST 19-DEC-2000  
 LOCUS NF061E08IN1F1066 Insect herbivory Medicago truncatula cDNA clone  
 DEFINITION NF061E08IN 5', mRNA sequence.  
 ACCESSION BF642179  
 VERSION BF642179.1 GI:11906337  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.

REFERENCE 1 (bases 1 to 645)  
 AUTHORS Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores  
 H.R., Inman,J.T., Weller,J.W. and May,G.D.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 JOURNAL Medicago truncatula insect herbivory library  
 COMMENT Unpublished (2000)  
 Contact: Korth K  
 Dept. of Plant Pathology  
 University of Arkansas  
 217 Plant Science Building, Fayetteville, AR 72701, USA  
 Tel: 501 575 5191  
 Fax: 501 575 7601  
 Email: korth@comp.uark.edu  
 Insert Length: 645 Std Error: 0.00  
 Plate: 061 row: E column: 08  
 Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES  
 source  
 1..645  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF061E08IN"  
 /clone\_lib="Insect herbivory"  
 /tissue\_type="local and systemic leaves"  
 /dev\_stage="mature"  
 /note="Vector: Lambda Zap; Library was produced from fully  
 expanded M. truncatula leaves of plants fed upon by  
 Spodoptera exigua (beet armyworm) for 24 hours. Systemic  
 (undamaged leaves from injured plants) and wounded leaves  
 were harvested and pooled."  
 BASE COUNT 194 a 146 c 136 g 169 t  
 ORIGIN

Query Match 82.5%; Score 19.8; DB 10; Length 645;  
 Best Local Similarity 91.3%; Pred. No. 3e+02;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcaggcagttttgcttct 24  
 ||||| || ||||| |||||

Db 405 ATCTTCATCGCTGTTTGCTTCT 427

# RESULT 10

AW695027 656 bp mRNA linear EST 15-JUN-2000  
 LOCUS NF082F07ST1F1062 Developing stem Medicago truncatula cDNA clone  
 DEFINITION NF082F07ST 5', mRNA sequence.

ACCESSION AW695027  
 VERSION AW695027.1 GI:7569789  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.

# REFERENCE AUTHORS

1 (bases 1 to 656)  
 He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell  
 C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon  
 R.A.

# TITLE JOURNAL COMMENT

Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula stem library  
 Unpublished (2000)  
 Contact: Dixon RA  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7302  
 Fax: 580 221 7380  
 Email: radixon@noble.org  
 Insert Length: 656 Std Error: 0.00  
 Plate: 082 row: F column: 07  
 Seq primer: TCACACAGGAACAGCTATGAC.

# FEATURES source

1..656  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF082F07St"  
 /clone\_lib="Developing stem"  
 /tissue\_type="stem"  
 /dev\_stage="Pooled developmental"  
 /note="Vector: Lambda Zap; Contains a mixture of  
 internodal stem segments"  
 BASE COUNT 192 a 159 c 125 g 180 t  
 ORIGIN

Query Match 82.5%; Score 19.8; DB 9; Length 656;  
 Best Local Similarity 91.3%; Pred. No. 3e+02;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcttcaggcagttttgcttct 24  
 ||||| || ||||| |||||

Db 459 ATCTTCATCGCTGTTTGCTTCT 481

# RESULT 11

AW692889 663 bp mRNA linear EST 15-JUN-2000  
 LOCUS NF056G09ST1F1000 Developing stem Medicago truncatula cDNA clone  
 DEFINITION NF056G09ST 5', mRNA sequence.

ACCESSION AW692889  
 VERSION AW692889.1 GI:7567625  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.

# REFERENCE AUTHORS

1 (bases 1 to 663)  
 He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell  
 C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon  
 R.A.

# TITLE JOURNAL COMMENT

Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula stem library  
 Unpublished (2000)  
 Contact: Dixon RA  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7302  
 Fax: 580 221 7380  
 Email: radixon@noble.org  
 Insert Length: 663 Std Error: 0.00  
 Plate: 056 row: G column: 09  
 Seq primer: TCACACAGGAACAGCTATGAC.

# FEATURES source

1..663  
 Location/Qualifiers



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REFERENCE 1 (bases 1 to 491)
AUTHORS   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
          Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
          and Keele, J.W.
TITLE     Design and use of two pooled tissue normalized cDNA libraries for
          EST discovery in swine
JOURNAL   Unpublished (2000)
COMMENT   Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called and alt_trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -minscore 18
          and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGAGTCAGCAGC
Plate: 41 row: P column: 10
Seq primer: ATTAGTGACACTATAG.
FEATURES
  source
    Location/Qualifiers
      1..491
        /organism="Sus scrofa"
        /db_xref="taxon:9823"
        /clone_lib="MARC 1Pig"
        /tissue_type="pooled"
        /lab_host="DH10B"
        /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
        Library made from pooled tissue from day 11, 13, 15, 20,
        and 30 embryos."
BASE COUNT 135 a 120 c 117 g 119 t
ORIGIN
Query Match      80.0%; Score 19.2; DB 9; Length 491;
Best Local Similarity 87.5%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catcttcaggcagttgtctct 24
||||||| || ||||| |||||
Db 393 CATCTTCAAGGAAGTTTCTCT 370

RESULT 15
BF191434/c
LOCUS      536 bp mRNA linear EST 02-NOV-2000
DEFINITION 239021 MARC 2Pig Sus scrofa cDNA 5', mRNA sequence.
ACCESSION  BF191434
VERSION     BF191434.1 GI:11074803
KEYWORDS   EST.
SOURCE     pig.
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 536)
AUTHORS   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
          Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
          and Keele, J.W.
TITLE     Design and use of two pooled tissue normalized cDNA libraries for
          EST discovery in swine
JOURNAL   Unpublished (2000)
COMMENT   Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called and alt_trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -minscore 18
          and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGAGTCAGCAGC
Plate: 72 row: N column: 23
Seq primer: ATTAGTGACACTATAG.
FEATURES
  source
    Location/Qualifiers
      1..536
        /organism="Sus scrofa"
        /db_xref="taxon:9823"
        /clone_lib="MARC 2Pig"
        /tissue_type="pooled"
        /lab_host="DH10B"
        /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
        Library made from pooled tissue from testis, ovary,
        endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 129 a 118 c 136 g 153 t
ORIGIN
Query Match      80.0%; Score 19.2; DB 10; Length 536;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catcttcaggcagttgtctct 24
||||||| || ||||| |||||
Db 128 CATCTTCAAGGAAGTTTCTCT 105

Search completed: August 21, 2002, 09:55:54
Job time: 9317 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:28 ; Search time 754.01 Seconds  
(without alignments)  
54.849 Million cell updates/sec

Title: US-09-339-922A-105

Perfect score: 24

Sequence: 1 catcttcattgcagttttgtcttct 24

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_032802.\*

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24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	22	AAF28236
2	19.2	80.0	30	19	AAV49874
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C 4	17.6	73.3	5681	22	AAK68974
C 5	17.6	73.3	7576	22	AAK36813
C 6	17.6	73.3	11626	21	AAK70607
C 7	17.6	73.3	27048	22	AAK202354
C 8	17.6	73.3	269223	22	AAF28554
C 9	17.4	72.5	1698	22	AAK503895

10	17.2	71.7	30	19	AAV49857
11	17.2	71.7	30	22	AAF28213
C 12	17.2	71.7	259	21	AAC32907
C 13	17.2	71.7	301	21	AAC50555
C 14	17.2	71.7	885	17	AAAT18832
15	17.2	71.7	2312	22	AAK70886
16	17.2	71.7	6742	22	AAK66424
17	17.2	71.7	8033	23	ABL19178
18	17.2	71.7	10772	22	AAK66425
19	17.2	71.7	12788	23	ABL10968
C 20	17.2	71.7	31169	22	AAS41761
C 21	17.2	71.7	31169	22	AAK75191
C 22	16.8	70.0	359	22	AAK10607
C 23	16.8	70.0	483	22	ABA55876
24	16.8	70.0	483	22	AAK40494
25	16.8	70.0	483	22	AAK29575
26	16.8	70.0	483	22	AAI14150
27	16.8	70.0	483	22	AAI03997
C 28	16.8	70.0	1584	16	AAO86997
C 29	16.8	70.0	1770	21	AAI14243
C 30	16.8	70.0	3170	21	AAA4244
C 31	16.8	70.0	12595	22	AAS42100
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C 34	16.6	69.2	386	22	AAK65659
C 35	16.6	69.2	386	22	AAK79606
C 36	16.6	69.2	386	22	AAK79607
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39	16.6	69.2	500	21	AAC36178
40	16.6	69.2	637	22	AAH19204
C 41	16.6	69.2	700	22	AAH92715
C 42	16.6	69.2	1008	21	AAC35990
C 43	16.6	69.2	1305	22	AAK54639
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#### ALIGNMENTS

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XX AAF28236;  
XX AC  
XX AC  
DT 03-APR-2001 (first entry)  
XX  
DE DNA encoding enhanced 5H6LH heavy chain CDR3.  
XX  
KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
XX  
OS Unidentified.  
XX  
FN WO200078815-A1.  
XX  
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XX  
PF 23-JUN-2000; 2000WO-US17454.  
XX  
PR 24-JUN-1999; 99US-0339922.  
XX  
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX  
XX Huse WD, Wu H;  
XX  
DR WPI; 2001-050110/06.  
XX  
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -

PS Claim 14; Page 105; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta\_3 integrin or

CC their functional fragments. The antibodies or their functional

CC fragments can be used in the diagnosis and treatment of

CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory

CC diseases (such as psoriasis and chronic articular rheumatism),

CC disorders associated with inappropriate or inopportune invasion of

CC vessels (such as diabetic retinopathy, neovascular glaucoma and

CC cancer disorders such as tumours and kaposi's sarcoma), retinal

CC diseases (such as macular degeneration), restenosis and

XX osteoporosis.

XX Sequence 24 BP; 3 A; 6 C; 4 G; 11 T; 0 other;

Query Match 100.0%; Score 24; DB 22; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.094;

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RESULT 2

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ID AAV49874 standard; DNA; 30 BP.

XX AAV49874;

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-H region CDR3 DNA fragment #13.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

XX LM609; inhibitor; integrin-mediated signal transduction; treatment;

XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

XX macular degeneration; osteoporosis; primer; V-H region; CDR;

XX complementarity determining region; ss.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX P-PSDB; AAW76037.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

XX integrin - and related grafted antibodies based on murine monoclonal

XX LM609, also related nucleic acid, used to treat, prevent or diagnose

XX angiogenesis or restenosis

XX Disclosure; Page 43; 129pp; English.

XX AAV49844-V49877 are nucleotide fragments of the grafted monoclonal

XX antibody LM609 heavy and light chain variable region. LM609 and the

XX antibody vitaxin bind selectively to integrin alphavbeta3 and can be used

XX to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,

CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The

CC antibodies contain non-murine framework regions so are suitable for use

CC in humans. Enhanced types of LM609 have affinity more than 90 times

XX greater than that of parent the parent antibody.

XX Sequence 30 BP; 8 A; 7 C; 6 G; 9 T; 0 other;

Query Match 80.0%; Score 19.2; DB 19; Length 30;

Best Local Similarity 87.5%; Pred. No. 15;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 catcttcagtcgcagtttgcctct 24

DB 7 cataaccatggcagtttgcctct 30

RESULT 3

AAF28230

ID AAF28230 standard; DNA; 30 BP.

XX AAF28230;

XX 03-APR-2001 (first entry)

XX DNA encoding multiple mutant VH CDR3 #1.

XX LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;

XX inflammatory; cancer; retina; restenosis; osteoporosis; ss.

XX Unidentified.

XX WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX Huse WD, Wu H;

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity

XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of

XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

XX osteoporosis -

XX Disclosure; Page 43; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies

XX exhibiting selective binding affinity to alphavbeta\_3 integrin or

XX their functional fragments. The antibodies or their functional

XX fragments can be used in the diagnosis and treatment of

XX alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory

XX diseases (such as psoriasis and chronic articular rheumatism),

XX disorders associated with inappropriate or inopportune invasion of

XX vessels (such as diabetic retinopathy, neovascular glaucoma and

XX cancer disorders such as tumours and kaposi's sarcoma), retinal

XX diseases (such as macular degeneration), restenosis and

XX osteoporosis.

XX Sequence 30 BP; 8 A; 7 C; 6 G; 9 T; 0 other;

Query Match 80.0%; Score 19.2; DB 22; Length 30;



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AC	AAK68974;		
DT	06-NOV-2001 (first entry)		
DE	Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:23786.		
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		
KW	cytostatic; gene therapy; vaccine; metastasis; ds.		
OS	Homo sapiens.		
PN	WO200157182-A2.		
XX	09-AUG-2001.		
XX	17-JAN-2001; 2001WO-US01354.		
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PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251889.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-451930/48.  
XX  
XX New cardiovascular system related polynucleotides and polypeptides,  
XX useful for diagnosing, treating and/or preventing disorders of the  
XX cardiovascular system -  
XX  
XX Claim 1; SEQ ID No 2313; 674pp; English.  
XX  
XX Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode  
XX the cardiovascular system antigen polypeptides of the invention.  
XX Cardiovascular system antigens and their associated polynucleotides are  
XX useful in the diagnosis, treatment and prevention of various types of  
XX disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
XX chickens or sheep. A pathological condition can be determined by  
XX detecting the presence or absence of a mutation in a cardiovascular  
XX system antigen polynucleotide. The treatable disorders include autoimmune  
XX diseases such as rheumatoid arthritis, hyperproliferative disorders such  
XX as neoplasms of the breast or liver, cardiovascular disorders such as  
XX cardiac arrest, cerebrovascular disorders such as cerebral ischaemia,  
XX nervous system disorders such as Alzheimer's disease, infections caused  
XX by bacteria, viruses and fungi, ocular disorders such as corneal  
XX infection, endocrine disorders such as premature labour and infertility,  
XX gastrointestinal disorders such as Crohn's disease, renal disorders such  
XX as glomerulonephritis and respiratory disorders such as asthma and  
XX pleurisy. The polypeptides can also be used to aid wound healing, to  
XX prevent skin aging due to sunburn, to maintain organs before  
XX transplantation, to regenerate tissues and in chemotaxis.  
XX Note: The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.

Query Match 73.3%; Score 17.6; DB 22; Length 7576;  
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ID AAA70607 standard; cDNA; 11626 BP.

XX AAAT70607;

XX DT 06-DEC-2000 (first entry)

XX Sindh-like virus strain XJ-160 complete genome sequence.

XX Genome; Sindh-like virus strain XJ-160; primer: RT-PCR; vaccine;  
XX epidemic; Sindh encephalitis; evolution; epidemiology; ds.

XX Sindh-like virus strain XJ-160.

XX CNU252444-A.

PD 10-MAY-2000.

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XX 27-OCT-1998; 98CN-0120692.
XX 27-OCT-1998; 98CN-0120692.
XX (VIRO-) INST VIROLOGY CHINESE ACAD PREVENTIVE ME.
XX Liang G, Li L, Zhou G;
XX WPI; 2000-443225/39.
XX Whole genome sequence of Sindbis virus strain and its cloning method -
XX Claim 1; Page 2-5; 17pp; Chinese.
XX This sequence represents the complete genome of the Sindbis-like virus
XX strain XJ-160. The genome was cloned as 15 fragments using the PCR
XX primers AAA70608-A70635 into the plasmid pGEM-T. The invention relates
XX to the isolation and method of cloning the complete genome for the
XX Sindbis-like virus strain XJ-160 by a RT-PCR process. The XJ-160
XX strain virus appears to be the optimal candidate for a vaccine to
XX prevent epidemics of Sindbis encephalitis. The sequence of this
XX strain's genome shows the difference between this viral strain and
XX other epidemic Sindbis virus strains at the molecular level and is
XX useful for understanding the source, evolution and molecular
XX epidemiology of Sindbis viruses.
XX Sequence 11626 BP; 3283 A; 2770 C; 2850 G; 2723 T; 0 other;

Query Match 73.3%; Score 17.6; DB 21; Length 11626;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 catcttcacggcagtttgcctct 24
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Db 2331 CAATTTCACGGCAGTTTCCTCT 2308

RESULT 7
ID AAS02354
AC AAS02354 standard; DNA; 27048 BP.
AC AAS02354;
DT 12-SEP-2001 (first entry)
DE Porcine Gal alpha(1,3) galactosyl transferase gene introns 3-8.
XX Pig; Gal alpha(1,3) galactosyl transferase; intron 3-8; gene targeting;
KW transgenic animal; transplant rejection; immunomodulation;
KW systemic lupus erythematosus; immune-haemolytic anaemia;
KW rheumatoid arthritis; ds.
XX Sus scrofa.
OS
XX Key Location/Qualifiers
FH Intron 1..4851
FT /*tag= a
FT /*number= 3
FT primer_bind 10..23
FT /*tag= b
FT primer_bind complement (3998..4020)
FT /*tag= c
FT exon 4852..4937
FT /*tag= d
FT /*number= 4
FT /*note= "The exon sequence is represented by dashes
FT in the sequence presented in figure 1 in the
FT specification and have been replaced with N's to
FT maintain the sequence numbering"
FT 4938..11715
FT intron
FT /*tag= d

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FT /*number= 4
FT /*note= "This sequence is specifically claimed in
FT claim 14"
FT 11521..11537
FT /*tag= e
FT primer_bind complement (11688..11716)
FT /*tag= f
FT exon 11716..11752
FT /*tag= g
FT /*number= 5
FT /*note= "The exon sequence is represented by dashes
FT in the sequence presented in figure 1 in the
FT specification and have been replaced with N's to
FT maintain the sequence numbering"
FT 11753..13747
FT /*tag= h
FT exon 13748..13810
FT /*tag= i
FT /*number= 6
FT /*note= "The exon sequence is represented by dashes
FT in the sequence presented in figure 1 in the
FT specification and have been replaced with N's to
FT maintain the sequence numbering"
FT 13811..14358
FT /*tag= j
FT exon 14359..14463
FT /*tag= k
FT /*number= 7
FT /*note= "The exon sequence is represented by dashes
FT in the sequence presented in figure 1 in the
FT specification and have been replaced with N's to
FT maintain the sequence numbering"
FT 14464..21627
FT /*tag= l
FT exon 21628..21705
FT /*tag= m
FT /*number= 8
FT /*note= "The exon sequence is represented by dashes
FT in the sequence presented in figure 1 in the
FT specification and have been replaced with N's to
FT maintain the sequence numbering"
FT 21766..27048
FT /*tag= n
FT /*number= 8
FT /*note= "This sequence is specifically claimed in
FT claim 42"
FT WO200123541-A2.
XX 05-APR-2001.
XX 02-OCT-2000; 2000WO-US27065.
XX 30-SEP-1999; 99US-0156953.
XX (ALEX-) ALEXION PHARM INC.
XX Fodor WL, Ramsoondar JJ;
XX WPI; 2001-266147/27.
XX Modulating the expression of a eukaryotic gene in a cell, involves
XX transfecting the cell with a nucleic acid construct that disrupts at
XX least a portion of the DNA sequence of the gene to be modulated -
XX Example 1; Fig 1; 86pp; English.
XX The sequence represents Porcine Gal alpha(1,3) galactosyl transferase
CC

```

CC infection and life-threatening, systemic diseases including endocarditis  
CC and meningitis.  
XX  
SQ Sequence 269223 BP; 77067 A; 56596 C; 57380 G; 78180 T; 0 other;

Query Match 73.3%; Score 17.6; DB 22; Length 269223;  
Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 catcttcatgacagtttgccttct 24  
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Db 267189 CATCTTTGGCAGTTTGGTGT 267166

RESULT 9  
AAS03895/c  
ID AAS03895 standard; cDNA; 1698 BP.  
XX AC  
XX AAS03895;  
XX AC  
XX XX  
DT 29-AUG-2001 (first entry)  
XX DE  
DE Human secreted protein gene #14.  
XX  
KW Human secreted protein; autoimmune disorder; hyperproliferative disorder;  
KW cardiovascular disorder; cerebrovascular disorder; angiogenesis;  
KW nervous system disorder; bacterial infection; viral infection; ss;  
KW fungal infection; ocular disorder; wound healing; tissue regeneration;  
KW epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.  
XX OS  
OS Homo sapiens.  
XX  
XX WO200123598-A1.  
XX PN  
XX  
PD 05-APR-2001.  
XX  
XX 26-SEP-2000; 2000WO-US26324.  
XX PF  
XX 27-SEP-1999; 99US-0155807.  
XX PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX PA  
XX  
XX Komatsoulis G, Ruben SM, Rosen CA;  
XX PT  
XX  
XX WPI: 2001-281684/29.  
XX DR  
XX P-PSDB; AAU01939.  
XX DR  
XX  
XX PT  
XX  
XX Forty one nucleic acid molecules encoding human secreted proteins, useful  
XX in the prevention, treatment and diagnosis of cancer, immune disorders,  
XX cardiovascular disorders and neurological diseases -  
XX  
XX Disclosure; Page 454; 518pp; English.  
XX

Sequences AAS03873-AAS03922 represent isolated nucleic acid molecules and  
PCR primers of the invention. acid of the invention. Secreted proteins  
and their related nucleic acids can be used in the diagnosis of or  
susceptibility to a pathological condition by determining the presence or  
absence of a mutation in a nucleic acid or the presence or amount of  
expression of a secreted protein. The sequences are used to prevent,  
treat or ameliorate a medical condition in e.g. humans, mice, rabbits,  
goats, horses, cats, dogs, chickens or sheep. The antibodies to the  
polypeptides can also be used in alleviating symptoms associated with  
disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme  
linked immunosorbent assays (ELISA). The disorders include autoimmune  
diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.  
neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac  
arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,  
nervous system disorders e.g. Alzheimer's disease, infections caused by  
bacteria, viruses and fungi and ocular disorders e.g. corneal infection.  
The peptides can also be used to aid wound healing and epithelial cell  
proliferation, to help prevent skin ageing due to sunburn, to maintain  
organs before transplantation, to regenerate tissues, in chemotaxis and

Query Match 71.7%; Score 17.2; DB 19; Length 30;  
Best Local Similarity 86.4%; Pred. No. 1.3e+02;

AAC 22907:



XX Melki J, Munnich A;  
PI WPI; 1996-232098/24.  
DR P-PSDB; AAR94966.  
XX  
XX Human survival motor neuron gene T-BCD541, variant C-BCD541 and  
PT murine equiv. - useful to develop primers and probes for in vitro  
PT detection of motor neuron diseases e.g. spinal muscular atrophy  
XX  
XX Claim 11; Fig 12; 47pp; English.  
XX  
XX A cDNA clone (AAT18832) was identified as the mouse homologue of  
CC the human survival motor neuron (SMN) gene, T-BCD541 (AAT18868).  
CC It was isolated by screening a mouse foetal cDNA library using  
CC human SMN cDNA (AAT18828) as a probe. The encoded protein (AAR94966)  
CC shows 83% homology to the human SMN protein (AAR94963). A transgenic  
CC mouse model is presented that hyperexpresses all or part of the SMN  
CC gene, and a transgenic mouse that by homologous recombination  
CC with a mutated mouse SMN gene produces abnormalities in the  
CC SMN gene.  
XX  
XX Sequence 885 BP; 257 A; 235 C; 207 G; 186 T; 0 other;  
SQ

Query Match 71.7%; Score 17.2; DB 17; Length 885;  
Best Local Similarity 86.4%; Pred. No. 2.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tcttcattggcaggtttgtctct 24  
||||| ||||| ||| |||||  
DB 240 TCTTCTGGCAGGTTTCTTCT 219

RESULT 15  
AAK70886  
ID AAK70886 standard; DNA; 2312 BP.  
XX  
AC AAK70886;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25698.  
XX  
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200157182-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01354.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216847.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR

PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226688.  
PR 23-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
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PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
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PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 01-NOV-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR



PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
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PR 17-NOV-2000; 2000US-0249207.  
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PR 17-NOV-2000; 2000US-0249217.  
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PR 17-NOV-2000; 2000US-0249244.  
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PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/haematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 25698; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic

CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention.  
XX  
SQ Sequence 2312 BP; 643 A; 482 C; 564 G; 623 T; 0 other;

Query Match 71.7%; Score 17.2; DB 22; Length 2312;  
Best Local Similarity 86.4%; Pred. No. 2.6e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ttttcattggcagttttgcttct 24  
||||| ||| |||||||||  
Db 1216 tttttgttagttttgctttt 1237

Search completed: August 21, 2002, 10:08:39  
Job time: 10057 sec

GenCore version 4.5  
Copyright (C) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:14 ; Search time 174.26 Seconds  
(without alignments)  
33.830 Million cell updates/sec

Title: US-09-339-922A-105  
Perfect score: 24  
Sequence: 1 catcttcagtcagtttgccttct 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.2	71.7	885	3	Sequence 20, Appl
C 2	16.6	69.2	2622	4	Sequence 170, App
C 3	16.2	67.5	72928	3	Sequence 1, Appli
C 4	16	66.7	671	1	Sequence 18, Appl
C 5	16	66.7	671	2	Sequence 18, Appl
C 6	16	66.7	2037	1	Sequence 4, Appli
C 7	16	66.7	2037	1	Sequence 4, Appli
C 8	16	66.7	2037	1	Sequence 4, Appli
C 9	16	66.7	2037	1	Sequence 4, Appli
C 10	16	66.7	2037	1	Sequence 4, Appli
C 11	16	66.7	2037	1	Sequence 4, Appli
C 12	16	66.7	2811	4	Sequence 3, Appli
C 13	16	66.7	2813	2	Sequence 99, Appl
C 14	16	66.7	2813	4	Sequence 99, Appl
C 15	16	66.7	3080	4	Sequence 4, Appli
C 16	16	66.7	3258	2	Sequence 2, Appli
C 17	16	66.7	5141	1	Sequence 9, Appli
C 18	16	66.7	5141	2	Sequence 9, Appli
C 19	16	66.7	5141	2	Sequence 9, Appli
C 20	16	66.7	5141	4	Sequence 9, Appli
C 21	16	66.7	5639	3	Sequence 1, Appli
C 22	16	66.7	6285	1	Sequence 49, Appl
C 23	16	66.7	6285	1	Sequence 49, Appl
C 24	16	66.7	6285	1	Sequence 49, Appl
C 25	16	66.7	6285	1	Sequence 49, Appl
C 26	16	66.7	6285	3	Sequence 49, Appl
C 27	16	66.7	6285	5	Sequence 49, Appl

C 28	16	66.7	6306	5	PCT-US94-00658-1	Sequence 1, Appli
C 29	16	66.7	6367	1	US-08-470-299-1	Sequence 1, Appli
C 30	16	66.7	6367	3	US-08-776-511-3	Sequence 3, Appli
C 31	16	66.7	6557	1	US-08-286-740-3	Sequence 3, Appli
C 32	16	66.7	6557	5	PCT-US95-09576-3	Sequence 3, Appli
C 33	16	66.7	6889	1	US-08-286-740-2	Sequence 2, Appli
C 34	16	66.7	6889	5	PCT-US95-09576-2	Sequence 2, Appli
C 35	16	66.7	6926	1	US-08-470-299-2	Sequence 2, Appli
C 36	16	66.7	7360	1	US-08-286-740-1	Sequence 1, Appli
C 37	16	66.7	7360	5	PCT-US95-09576-1	Sequence 1, Appli
C 38	16	66.7	7892	2	US-07-916-098A-40	Sequence 68, Appl
C 39	16	66.7	8120	3	US-09-027-449-68	Sequence 68, Appl
C 40	16	66.7	8120	3	US-09-026-985-68	Sequence 2, Appli
C 41	16	66.7	8540	1	US-08-149-099C-2	Sequence 2, Appli
C 42	16	66.7	8540	2	US-08-478-967A-2	Sequence 1, Appli
C 43	16	66.7	8541	1	US-08-476-275-1	Sequence 5, Appli
C 44	16	66.7	8614	4	US-09-247-352-5	Sequence 6, Appli
C 45	16	66.7	8858	4	US-09-247-352-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-08-545-196B-20/C  
; Sequence 20, Application US/08545196B  
; Patent No. 6080577  
; GENERAL INFORMATION:  
; APPLICANT: MELKI, JUDITH  
; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE  
; TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/545,196B  
; FILING DATE: 19-OCT-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FARACI, C. J.  
; REGISTRATION NUMBER: 32,350  
; REFERENCE/DOCKET NUMBER: 2121-110P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 885 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 18..881  
; US-08-545-196B-20

Query Match 71.7%; Score 17.2; DB 3; Length 885;  
Best Local Similarity 86.4%; Pred. No. 32;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 tcttcattgagcagttttgtctct 24  
Db 240 TCTCTTGGCAGGTTTCTTCT 219

## RESULT 2

US-09-130-616-170  
; Sequence 170, Application US/09130616C  
; Patent No. 6221850  
; GENERAL INFORMATION:  
; APPLICANT: McKay, Robert A.  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett  
; APPLICANT: Nero, Pam  
; APPLICANT: Gaarde, William A.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS  
; FILE REFERENCE: ISPH-0318  
; CURRENT APPLICATION NUMBER: US/09/130,616C  
; CURRENT FILING DATE: 1998-08-07  
; EARLIER APPLICATION NUMBER: 08/910,629  
; EARLIER FILING DATE: 1997-08-03  
; NUMBER OF SEQ ID NOS: 178  
; SEQ ID NO 170  
; LENGTH: 2622  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-09-130-616-170

Query Match 69.2%; Score 16.6; DB 4; Length 2622;  
Best Local Similarity 82.6%; Pred. No. 69;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 attcttcagtcagttttgtctct 24  
Db 1676 attcttcagtcagttttgtctct 1698

## RESULT 3

US-09-009-913-1  
; Sequence 1, Application US/09009913  
; Patent No. 6087485  
; GENERAL INFORMATION:  
; APPLICANT: Axys Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Asthma Related Genes  
; NUMBER OF SEQUENCES: 339  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bozicevic & Reed, LLP  
; STREET: 285 Hamilton Ave, Suite 200  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,913  
; FILING DATE: 21-JAN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sherwood, Pamela J  
; REGISTRATION NUMBER: 36,677  
; REFERENCE/DOCKET NUMBER: SEQ-4P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-327-3231  
; TELEFAX: 650-327-3231

TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 72928 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
US-09-009-913-1

Query Match 67.5%; Score 16.2; DB 3; Length 72928;  
Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 catcttcagtcagttttgtctct 21  
Db 27567 CCTCTTCATGACAGTTTCTCT 27587

## RESULT 4

US-08-644-664B-18/c  
; Sequence 18, Application US/08644664B  
; Patent No. 5776746  
; GENERAL INFORMATION:  
; APPLICANT: Denney Jr., Dan W.  
; TITLE OF INVENTION: Gene Amplification Methods  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/644,664B  
; FILING DATE: 01-MAY-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ingolia, Diane E.  
; REGISTRATION NUMBER: 40,027  
; REFERENCE/DOCKET NUMBER: GENITOPE-00912  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 671 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..573  
US-08-644-664B-18

Query Match 66.7%; Score 16; DB 1; Length 671;  
Best Local Similarity 79.2%; Pred. No. 1.1e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catcttcagtcagttttgtctct 24  
Db 586 CATCTTCTGTAGTCTTCTTCT 563

```
RESULT 5
US-08-761-277A-18/c
; Sequence 18, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
; TITLE OF INVENTION: Leukemia
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESS: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761.277A
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/644,664
; FILING DATE: 01-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: GENITOPE-02406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 671 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 13..573
; US-08-761-277A-18

Query Match 66.7%; Score 16; DB 2; Length 671;
Best Local Similarity 79.2%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 catcttcagcgagctttgtctct 24
||||||| || |||||
Db 586 CATCTTCTGTTAGCTTTCTTCT 563

RESULT 6
US-08-143-497-4/c
; Sequence 4, Application US/08143497
; Patent No. 5585237
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: DORAI, HAIMANTI
; APPLICANT: KAPLAN, PAUL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM RECOMBINANT DNA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
```

```
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/143,497
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..2037
; OTHER INFORMATION: /note= "adeval"
; US-08-143-497-4

Query Match 66.7%; Score 16; DB 1; Length 2037;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 catcttcagcgagctttgtctct 24
||||||| || |||||
Db 1962 CATCTTCTGTTAGCTTTCTTCT 1939

RESULT 7
US-08-461-666-4/c
; Sequence 4, Application US/08461666
; Patent No. 5614385
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: DORAI, HAIMANTI
; APPLICANT: KAPLAN, PAUL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM RECOMBINANT DNA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,666
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,497
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D.
```

```

/ INFORMATION FOR SEQ ID NO: 4:
/     LENGTH: 2037 base pairs
/     TYPE: nucleic acid
/     STRANDEDNESS: single
/     TOPOLOGY: linear
/     MOLECULE TYPE: cDNA
/     FEATURE:
/     NAME/KEY: misc.feature

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Qy 1 catcttcatggcagttttgcttct 24  
||||| || ||| ||| ||| |||  
Db 162 CATCTTCCCTGTTAGTCTTCTTCT 1939

```
RESULT 10
US-08-757-300-4/C
; Sequence 4, Application US/08757300
; Patent No. 5712119
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: DORAI, HAIMANTI
; APPLICANT: KAPLAN, PAUL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM RECOMBINANT DNA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08757,300
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/143,497
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; LENGTH: 2037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2037
; OTHER INFORMATION: /note= "adeval"
US-08-757-300-4

Query Match 66.7%; Score 16; DB 1; Length 2037;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catcttcaggcagttgtctct 24
||||| || ||| ||| |||
Db 1962 CATCTTCCTGTTAGTCTTCTTCT 1939

RESULT 11
US-08-464-589-4/C
; Sequence 4, Application US/08464589
; Patent No. 5733782
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: DORAI, HAIMANTI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
```

```
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/464,589
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,498
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2037
; OTHER INFORMATION: /note= "adeval"
US-08-464-589-4

Query Match 66.7%; Score 16; DB 1; Length 2037;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catcttcaggcagttgtctct 24
||||| || ||| ||| |||
Db 1962 CATCTTCCTGTTAGTCTTCTTCT 1939

RESULT 12
US-08-482-073-3/C
; Sequence 3, Application US/08482073
; Patent No. 6307025
; GENERAL INFORMATION:
; APPLICANT: Hession, Catherine A.
; APPLICANT: Lobb, Roy R.
; APPLICANT: Goelz, Susan E.
; APPLICANT: Osborn, Laurelee
; APPLICANT: Benjamin, Christopher D.
; APPLICANT: Rosa, Margaret D.
; TITLE OF INVENTION: ENDOTHELIAL CELL-LEUKOCYTE ADHESION
; TITLE OF INVENTION: MOLECULES (ELAMS) AND MOLECULES INVOLVED IN LEUKOCYTE
; TITLE OF INVENTION: ADHESION (MILAS)
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,073
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,336
; FILING DATE:
; APPLICATION NUMBER: US 07/608298
; FILING DATE: 31-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 90/02357
; FILING DATE: 27-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/452675
; FILING DATE: 18-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/359516
; FILING DATE: 01-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/354151
; FILING DATE: 28-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B124CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2811 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-482-073-3
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Query Match 66.7%; Score 16; DB 4; Length 2811;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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```
Oy 1 catcttcagtcagcttttgcttct 24
||||| ||||||| |||
Db 2259 CATCTTGATGCGACTTACTGTCT 2236
```

```
RESULT 13
US-08-344-155C-99/c
; Sequence 99, Application US/08344155C
; Patent No. 5883082
; GENERAL INFORMATION:
; APPLICANT: Bennett and Stepkowski
; TITLE OF INVENTION: Compositions and Methods for Preventing
; TITLE OF INVENTION: and Treating Allograft Rejection
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodland Falls Corporate Park
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,155C
; FILING DATE: No. 5883082ember 23, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 939,855
; FILING DATE: September 2, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05209
; FILING DATE: July 23, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/063,167
; FILING DATE: 5/17/93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/007,997
; FILING DATE: 1/21/93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,855
; FILING DATE: 9/2/92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,286
; FILING DATE: 8/14/90
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0098
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2813
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
;
US-08-344-155C-99
```

```
Query Match 66.7%; Score 16; DB 2; Length 2813;
Best Local Similarity 79.2%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Oy 1 catcttcagtcagcttttgcttct 24
||||| ||||||| |||
Db 2259 CATCTTGATGCGACTTACTGTCT 2236
```

```
RESULT 14
US-08-009-490A-90/c
; Sequence 90, Application US/09009490A
; Patent No. 6300491
; GENERAL INFORMATION:
; APPLICANT: Bennett and Mirabelli
; TITLE OF INVENTION: Oligonucleotide Modulation
; TITLE OF INVENTION: of Cell Adhesion
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,490A
; FILING DATE: January 20, 1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,740
; FILING DATE: May 12, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 063,167
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; FILING DATE: May 17, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 969,151  
; FILING DATE: February 10, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 007,997  
; FILING DATE: January 20, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 939,855  
; FILING DATE: September 2, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 567,286  
; FILING DATE: August 14, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane Massey Licata  
; REGISTRATION NUMBER: 32,257  
; REFERENCE/DOCKET NUMBER: ISPH-0268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (609) 810-1515  
; TELEFAX: (609) 810-1454  
; INFORMATION FOR SEQ ID NO: 90:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2813  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: NO  
US-09-009-490A-90

Query Match 66.7%; Score 16; DB 4; Length 2813;  
Best Local Similarity 79.2%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 catcttcattggcagtttgcctct 24  
||||| ||||| ||||| |||||  
Db 2259 CATCTTGATGGCAGTTACTGTCT 2236

## RESULT 15

US-08-482-073-4/c  
; Sequence 4, Application US/08482073  
; Patent No. 6307025  
; GENERAL INFORMATION:  
; APPLICANT: Hession, Catherine A.  
; APPLICANT: Lobb, Roy R.  
; APPLICANT: Goelz, Susan E.  
; APPLICANT: Osborn, Laurelee  
; APPLICANT: Benjamin, Christopher D.  
; APPLICANT: Rosa, Margaret D.  
; TITLE OF INVENTION: ENDOTHELIAL CELL-LEUKOCYTE ADHESION  
; TITLE OF INVENTION: MOLECULES (ELAMS) AND MOLECULES INVOLVED IN LEUKOCYTE  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,073  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,336  
; FILING DATE:

; APPLICATION NUMBER: US 07/608298  
; FILING DATE: 31-OCT-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US 90/02357  
; FILING DATE: 27-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/452675  
; FILING DATE: 18-DEC-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/359516  
; FILING DATE: 01-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/354151  
; FILING DATE: 28-APR-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B124CIP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3080 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-482-073-4

Query Match 66.7%; Score 16; DB 4; Length 3080;  
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Db 2528 CATCTTGATGGCAGTTACTGTCT 2505

Search completed: August 21, 2002, 10:52:19  
Job time: 9659 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: August 21, 2002, 10:49:56 ; Search time 2408.76 Seconds  
(without alignments)  
286.693 Million cell updates/sec

Title: US-09-339-922A-107  
Perfect score: 33  
Sequence: 1 caggccagccaaagtattagcaaccactacac 33

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues 3595312  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.:

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- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
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- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	33	100.0	39	6	AX060820	Sequence	
3	33	100.0	321	6	AX060782	Sequence	
4	33	100.0	321	6	AX060786	Sequence	
5	33	100.0	321	6	AX060810	Sequence	
C	6	30	90.9	72	6	AX060794	Sequence
	7	30	90.9	75	6	AX060803	Sequence
C	8	29.8	90.3	33	6	AX060888	Sequence
	9	29.4	89.1	128	6	AX060867	Sequence
C	10	29.4	89.1	128	6	AX060867	Sequence
C	11	29.4	89.1	128	6	AX060867	Sequence
C	12	29.4	89.1	128	6	AX060867	Sequence
	13	29.4	89.1	243	10	AX060830	Sequence
14	29.4	89.1	285	10	AX060842	Sequence	
15	29.4	89.1	286	10	AX060843	Sequence	
16	29.4	89.1	297	10	AX0607617	Sequence	
17	29.4	89.1	300	10	AX0608ABJ	Sequence	
18	29.4	89.1	303	10	AX060864	Sequence	
19	29.4	89.1	306	10	AX0608L91	Sequence	
20	29.4	89.1	317	10	AX0608L1K13	Sequence	
21	29.4	89.1	317	10	AX0608L1K14	Sequence	
22	29.4	89.1	318	10	AX0608KVR4	Sequence	
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37	29.4	89.1	370	10	AX0608U5IGKXD	Sequence	
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ALIGNMENTS

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REFERENCE	AX060886.1	GI:12406264	33 bp	DNA	linear	PAT 22-JAN-2001	
AUTHORS	AX060886.1	GI:12406264	33 bp	DNA	linear	PAT 22-JAN-2001	
TITLE	AX060886.1	GI:12406264	33 bp	DNA	linear	PAT 22-JAN-2001	
JOURNAL	AX060886.1	GI:12406264	33 bp	DNA	linear	PAT 22-JAN-2001	
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Db 1 CAGCCAGCCAAAGTATTAGCAACCACCTACAC 33

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DEFINITION Sequence 41 from Patent WO0078815.
ACCESSION  AX060820
VERSION     AX060820.1 GI:12406198
KEYWORDS   .
SOURCE      house mouse.
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 39)
AUTHORS     Huse, W.D. and Wu, H.
TITLE       Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
            encoding same and methods of use
JOURNAL     Patent: WO 0078815-A 41 28-DEC-2000;
            Applied Molecular Evolution (US)
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ACCESSION  AX060782
VERSION     AX060782.1 GI:12406162
KEYWORDS   .
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
            artificial sequence.
REFERENCE   1 (bases 1 to 321)
AUTHORS     Huse, W.D. and Wu, H.
TITLE       Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
            encoding same and methods of use
JOURNAL     Patent: WO 0078815-A 3 28-DEC-2000;
            Applied Molecular Evolution (US)

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Location/Qualifiers
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DEFINITION Sequence 7 from Patent WO0078815.
ACCESSION  AX060786
VERSION     AX060786.1 GI:12406166
KEYWORDS   .
SOURCE      house mouse.
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 321)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE       Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
            encoding same and methods of use
JOURNAL     Patent: WO 0078815-A 7 28-DEC-2000;
            Applied Molecular Evolution (US)
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DEFINITION Sequence 31 from Patent WO0078815.
ACCESSION  AX060810

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VERSION AX060810.1 GI:12406189  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequence.  
REFERENCE 1 (bases 1 to 321)  
AUTHORS Huse, W.D. and Wu, H.  
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
JOURNAL Patent: WO 0078815-A 31 28-DEC-2000;  
Applied Molecular Evolution (US)  
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AX060794/c  
LOCUS AX060794 72 bp DNA linear PAT 22-JAN-2001  
DEFINITION Sequence 15 from Patent WO0078815.  
ACCESSION AX060794  
VERSION AX060794.1 GI:12406174  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
artificial sequence.  
REFERENCE 1 (bases 1 to 72)  
AUTHORS Huse, W.D. and Wu, H.  
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
JOURNAL Patent: WO 0078815-A 15 28-DEC-2000;  
Applied Molecular Evolution (US)  
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LOCUS AX060803 75 bp DNA linear PAT 22-JAN-2001  
DEFINITION Sequence 24 from Patent WO0078815.  
ACCESSION AX060803  
VERSION AX060803.1 GI:12406183  
KEYWORDS  
SOURCE synthetic construct.

ORGANISM synthetic construct  
artificial sequence.  
REFERENCE 1 (bases 1 to 75)  
AUTHORS Huse, W.D. and Wu, H.  
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
JOURNAL Patent: WO 0078815-A 24 28-DEC-2000;  
Applied Molecular Evolution (US)  
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VERSION AX060888.1 GI:12406266  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
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REFERENCE 1 (bases 1 to 33)  
AUTHORS Huse, W.D. and Wu, H.  
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
JOURNAL Patent: WO 0078815-A 109 28-DEC-2000;  
Applied Molecular Evolution (US)  
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LOCUS AR126867 128 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 91 from patent US 6180370.  
ACCESSION AR126867  
VERSION AR126867.1 GI:14113460  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 128)  
AUTHORS Queen,C.L., and Selick,H.E.  
TITLE Humanized immunoglobulins and methods of making the same  
JOURNAL Patent: US 6180370-A 91 30-JAN-2001;  
FEATURES Location/Qualifiers  
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VERSION I31962.1 GI:1822753  
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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 128)  
AUTHORS Queen,C.L., and Selick,H.E.  
TITLE Humanized immunoglobulins  
JOURNAL Patent: US 5585089-A 91 17-DEC-1996;  
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LOCUS I78574 128 bp DNA linear PAT 03-APR-1998  
DEFINITION Sequence 91 from patent US 5693761.  
ACCESSION I78574  
VERSION I78574.1 GI:3014728  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 128)  
AUTHORS Queen,C.L., Schneider,W.P. and Selick,H.E.  
TITLE Polynucleotides encoding improved humanized immunoglobulins  
JOURNAL Patent: US 5693761-A 91 02-DEC-1997;  
FEATURES Location/Qualifiers  
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VERSION I78629.1 GI:3014783  
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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 128)  
AUTHORS Queen,C.L., Co,M.Sung., Schneider,W.P., Landolfi,N.F., Coelingh,K.L. and Selick,H.E.  
TITLE Humanized immunoglobulins  
JOURNAL Patent: US 5693762-A 91 02-DEC-1997;  
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LOCUS MMU19309 243 bp mRNA linear ROD 21-JUN-1995  
DEFINITION Mus musculus immunoglobulin kappa light chain variable region mRNA,  
clone MRL1-17, partial cds.  
ACCESSION U19309  
VERSION U19309.1 GI:619954  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 243)  
AUTHORS Roark,J.H., Kuntz,C.L., Nguyen,K.A., Caton,A.J. and Erikson,J.  
TITLE Breakdown of B cell tolerance in a mouse model of systemic lupus erythematosus  
JOURNAL J Exp. Med. 181 (3), 1157-1167 (1995)  
MEDLINE 95173583  
REFERENCE 2 (bases 1 to 243)  
AUTHORS Roark,J.H.  
TITLE Direct Submission  
JOURNAL Submitted (02-JAN-1995) Jessica H. Roark, Wistar Institute, 3601 Spruce St., Philadelphia, PA 19104, USA  
FEATURES Location/Qualifiers  
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Search completed: August 21, 2002, 10:49:57  
Job time: 9812 sec

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5	29.4	89.1	833	10	BG965682	BG965682 602834412
6	29.4	89.1	835	10	BI083006	BI083006 602874524
7	29.4	89.1	949	10	BF579007	BF579007 602096124
8	23	69.7	849	10	BF583521	BF583521 602101553
9	22.2	67.3	517	12	AZ928596	AZ928596 479.d11f1
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	21.6	65.5	239	10	BF756995	BF756995 MR0-CT045
14	21.6	65.5	290	10	BG058466	BG058466 nah17g07.
15	21.6	65.5	740	10	BG397970	BG397970 602439490
16	21.4	64.8	414	10	BG225085	BG225085 kp64a02.y
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the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized; constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 53 a 61 c 45 g 43 t  
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Query Match 89.1%; Score 29.4; DB 10; Length 202;  
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Matches 30; Conservative 0; Mismatches 1;

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RESULT 2  
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LOCUS 2M0146D17R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
DEFINITION clone UUGC2M0146D17 R, DNA sequence.

ACCESSION AZ846516  
VERSION AZ846516.1 GI:13016424

KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 517)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0146 row: D column: 17  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 517.  
Location/Qualifiers

FEATURES  
source 1..517  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0146D17"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 159 a 99 c 118 g 141 t  
ORIGIN

Query Match 89.1%; Score 29.4; DB 12; Length 517;  
Best Local Similarity 96.8%; Pred. No. 0.14; Indels 0; Gaps 0;  
Matches 30; Conservative 0; Mismatches 1;

QY 3 ggcagcgcaaaagtattagcaaccacctacac 33  
|||||  
Db 370 GCCCAGCCCAAGTATTAGCAACACCTACAC 340

RESULT 3  
BF582153 738 bp mRNA linear EST 12-DEC-2000  
LOCUS 602099743F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4219402 5',  
DEFINITION mRNA sequence.

ACCESSION BF582153  
VERSION BF582153.1 GI:11655865

KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 738)  
AUTHORS NTH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LLAM9801 row: f column: 11  
High quality sequence stop: 714.  
Location/Qualifiers

FEATURES  
source 1..738  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4219402"  
/clone\_lib="NCI\_CGAP\_Co24"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 210 a 189 c 172 g 167 t  
ORIGIN

Query Match 89.1%; Score 29.4; DB 10; Length 738;  
Best Local Similarity 96.8%; Pred. No. 0.15; Indels 0; Gaps 0;  
Matches 30; Conservative 0; Mismatches 1;

QY 3 ggcagcgcaaaagtattagcaaccacctacac 33  
|||||  
Db 144 GCCCAGCCCAAGTATTAGCAACACCTACAC 174

RESULT 4  
BI105452 772 bp mRNA linear EST 26-JUN-2001  
LOCUS 602891971F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:5037137 5',  
DEFINITION



```

mRNA sequence.
ACCESSION BI105452
VERSION BI105452.1 GI:14556345
SOURCE EST.
ORGANISM house mouse.
Mammalia; Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 772)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1102 row: n column: 18
High quality sequence stop: 771.
Location/Qualifiers
1..772
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/Note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
214 a 208 c 173 g 177 t
BASE COUNT
ORIGIN

Query Match 89.1%; Score 29.4; DB 10; Length 772;
Best Local Similarity 96.8%; Pred. No. 0.16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ggccagccaaagtattagcaaccactacac 33
|||||
Db 136 GGCCAGCCAAAGTATTAGCAACTACCTACAC 166

RESULT 5
LOCUS BG966582
DEFINITION 602834412F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988955 5',
mRNA sequence.
ACCESSION BI083006
VERSION BI083006.1 GI:14501336
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 833)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11047 row: p column: 06
High quality sequence stop: 769.
Location/Qualifiers
1..833
/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
225 a 229 c 186 g 195 t
BASE COUNT
ORIGIN

mRNA sequence.
ACCESSION BG966582
VERSION BG966582.1 GI:14354219
SOURCE EST.
ORGANISM house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 833)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11002 row: g column: 04
High quality sequence stop: 830.
Location/Qualifiers
1..833
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/Note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Salt; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
227 a 227 c 186 g 193 t
BASE COUNT
ORIGIN

Query Match 89.1%; Score 29.4; DB 10; Length 833;
Best Local Similarity 96.8%; Pred. No. 0.16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ggccagccaaagtattagcaaccactacac 33
|||||
Db 136 GGCCAGCCAAAGTATTAGCAACTACCTACAC 166

RESULT 6
LOCUS BI083006
DEFINITION 60287452F2 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5006453 5',
mRNA sequence.
ACCESSION BI083006
VERSION BI083006.1 GI:14501336
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 835)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11047 row: p column: 06
High quality sequence stop: 769.
Location/Qualifiers
1..835
/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
225 a 229 c 186 g 195 t
BASE COUNT
ORIGIN

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```

Query Match      89.1%; Score 29.4; DB 10; Length 835;
Best Local Similarity 96.8%; Pred. No. 0.16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gccagccaaagtattagcaaccactacac 33
|||||
Db 150 GCCAGCCAAAGTATTAGCAACACCTACAC 180

RESULT 7
BF579007 949 bp mRNA linear EST 12-DEC-2000
LOCUS 602096124F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4216180 5',
DEFINITION mRNA sequence.
ACCESSION BF579007
VERSION BF579007.1 GI:11652719
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 278 a 241 c 210 g 220 t
ORIGIN

FEATURES
source
1..949
Location/Qualifiers
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match      89.1%; Score 29.4; DB 10; Length 949;
Best Local Similarity 96.8%; Pred. No. 0.16;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 gccagccaaagtattagcaaccactacac 33
|||||
Db 149 GCCAGCCAAAGTATTAGCAACACCTACAC 179

RESULT 8
BF583521 849 bp mRNA linear EST 12-DEC-2000
LOCUS 60210153F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224853 5',
DEFINITION mRNA sequence.
ACCESSION BF583521
VERSION BF583521.1 GI:11657239
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 278 a 241 c 210 g 220 t
ORIGIN

FEATURES
source
1..949
Location/Qualifiers
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match      89.1%; Score 23; DB 10; Length 849;
Best Local Similarity 83.9%; Pred. No. 54;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 gccagccaaagtattagcaaccactacac 33
|||||
Db 146 GCCAGCCAGAGTATTAGCAACATTACAC 176

RESULT 9
AZ928596 517 bp DNA linear GSS 01-APR-2001
LOCUS 479.dif11h11.s1 Saccharomyces kluyveri Saccharomyces kluyveri
DEFINITION genomic clone 479.dif11h11.s1, DNA sequence.
ACCESSION AZ928596
VERSION AZ928596.1 GI:13499502
KEYWORDS GSS.
SOURCE Saccharomyces kluyveri.
ORGANISM Saccharomyces kluyveri
/organism="Saccharomyces kluyveri"
/strain="NRRL Y-12651 (CBS 3082)"
/db_xref="taxon:4934"

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```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 849)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9815 row: 1 column: 14
High quality sequence stop: 627.
Location/Qualifiers
1..849
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 274 a 215 c 183 g 177 t
ORIGIN

FEATURES
source
1..849
Location/Qualifiers
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match      69.7%; Score 23; DB 10; Length 849;
Best Local Similarity 83.9%; Pred. No. 54;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 gccagccaaagtattagcaaccactacac 33
|||||
Db 146 GCCAGCCAGAGTATTAGCAACATTACAC 176

RESULT 9
AZ928596 517 bp DNA linear GSS 01-APR-2001
LOCUS 479.dif11h11.s1 Saccharomyces kluyveri Saccharomyces kluyveri
DEFINITION genomic clone 479.dif11h11.s1, DNA sequence.
ACCESSION AZ928596
VERSION AZ928596.1 GI:13499502
KEYWORDS GSS.
SOURCE Saccharomyces kluyveri.
ORGANISM Saccharomyces kluyveri
/organism="Saccharomyces kluyveri"
/strain="NRRL Y-12651 (CBS 3082)"
/db_xref="taxon:4934"

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/clone="479.dif1h11.s1"  
 /clone\_lib="Saccharomyces kluyveri"  
 /note="Random genomic sequence"  
 138 a 171 c 105 g 100 t 3 others

BASE COUNT  
 ORIGIN

Query Match 67.3%; Score 22.2; DB 12; Length 517;  
 Best Local Similarity 88.9%; Pred. No. 99;  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaaccac 27  
 ||| ||||| ||||| ||||| ||||| |||||  
 Db 368 CAGTCCAGCCACAGTATTAGCATCCAC 394

RESULT 10  
 AZ653355/c  
 LOCUS 569 bp DNA linear GSS 14-DEC-2000  
 DEFINITION 1M0527C04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0527C04 F, DNA sequence.

ACCESSION AZ653355  
 VERSION  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 569)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A.  
 and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0527 row: C column: 04

Seq primer: CGTTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 569.

FEATURES  
 source

1..569  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0527C04"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: pWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi14732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 132 a 113 c 131 g 193 t  
 ORIGIN

Query Match 66.1%; Score 21.8; DB 12; Length 569;  
 Best Local Similarity 78.8%; Pred. No. 1.5e+02;  
 Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaaccacctacac 33  
 ||| ||||| ||| ||| ||| ||| ||| |||  
 Db 68 CAGGCCAGCCACACTTTTATCAACAGCTACAC 36

RESULT 11

BE251590 60110617F1 NIH\_MGC\_16 Homo sapiens cdna clone IMAGE:3351076 5',  
 LOCUS mRNA sequence.  
 DEFINITION BE251590  
 ACCESSION BE251590.1 GI:9121719  
 VERSION  
 KEYWORDS EST.  
 SOURCE human.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 619)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-re@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLC148 row: b column: 05

High quality sequence start: 4

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

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High quality sequence stop: 618.

High quality sequence stop: 618.

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High quality sequence stop: 618.

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High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

High quality sequence stop: 618.

```

RESULT 12
BF786148/c
LOCUS
DEFINITION
602110427f1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4238599
5', mRNA sequence.
ACCESSION
BF786148
VERSION
BF786148.1 GI:12091184
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus.
REFERENCE
1 (bases 1 to 878)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAN9850 row: f column: 08
High quality sequence start: 267
High quality sequence stop: 747.
Location/Qualifiers
1. .878
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/strain="FVB/N"
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/clone="IMAGE:4238599"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
BASE COUNT 192 a 209 c 260 g 217 t
ORIGIN

Query Match 66.1%; Score 21.8; DB 10; Length 878;
Best Local Similarity 78.8%; Pred. No. 1.6e+02;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 caggccagccaaagtattagcaaccactaac 33
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DB 680 CAGGACATCCACAGCATCAGCACGCCCTACTC 648

RESULT 13
BF756995
LOCUS
DEFINITION
MR0-CT0451-021100-017-h04 CT0451 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF756995
VERSION
BF756995.1 GI:12104895
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 239)
AUTHORS
Dias Neco, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
MEDLINE
COMMENT
PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-CT0451-
021100-017-h04&t3=2000-11-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 239.
Location/Qualifiers
1. 239
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0451"
/dev_stages="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 59 a 79 c 50 g 51 t
ORIGIN

Query Match 65.5%; Score 21.6; DB 10; Length 239;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaaccacta 30
||||| ||||| ||||| ||||| |||||
DB 173 GGCCAGTCAGAGTATTAGCAACTACTTA 200

RESULT 14
BG058466
LOCUS
DEFINITION
nah17q07.y1 NCI_CGAP_HN21 Homo sapiens cDNA clone IMAGE:4231477 5',
similar to SW:KV3H_HUMAN P04207 IG KAPPA CHAIN V-III REGION CLL
PRECURSOR ;, mRNA sequence.
ACCESSION
BG058466
VERSION
BG058466.1 GI:12524992
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 290)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. 290
/organism="Homo sapiens"

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Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 157 GGCAGTCAGAGTATTAGCAACTACTTA 184

Search completed: August 21, 2002, 09:56:01
Job time: 9324 sec

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PT osteoporosis -  
 PS Claim 16; Page 107; 132pp; English.  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX Sequence 33 BP; 12 A; 12 C; 5 G; 4 T; 0 other;  
 SQ  
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 Best Local Similarity 100.0%; Pred. NO. 8.8e-05;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 caggccagccaaagtatttagcaaccactacac 33  
 Db 1 caggccagccaaagtatttagcaaccactacac 33  
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 ID AAV49848 standard; DNA; 39 BP.  
 XX  
 AC AAV49848;  
 XX  
 DT 02-NOV-1998 (first entry)  
 XX  
 DE LM609 grafted antibody V-L region CDR1 DNA fragment #1.  
 XX  
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;  
 KW complementarity determining region; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9833919-A2.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 30-JAN-1998; 98WO-US01826.  
 XX  
 PR 30-JAN-1997; 97US-0791391.  
 XX  
 PA (IXSY-) IXSYS INC.  
 XX  
 PI Glaser SM, Huse WD;  
 XX  
 DR WPI; 1998-437472/37.  
 DR P-PSDB; AAW76011.  
 XX  
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX  
 PS Disclosure; Page 40; 129pp; English.  
 XX  
 CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal  
 CC antibody LM609 heavy and light chain variable region. LM609 and the  
 CC antibody Vitaxin bind selectively to integrin alphavbeta3 and can be used  
 CC to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,  
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically  
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
 CC antibodies contain non-murine framework regions so are suitable for use  
 CC in humans. Enhanced types of LM609 have affinity more than 90 times  
 XX greater than that of parent the parent antibody.  
 SQ Sequence 39 BP; 13 A; 12 C; 7 G; 7 T; 0 other;  
 Query Match 100.0%; Score 33; DB 19; Length 39;  
 Best Local Similarity 100.0%; Pred. NO. 9e-05;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caggccagccaaagtatttagcaaccactacac 33  
 Db 1 caggccagccaaagtatttagcaaccactacac 33

RESULT 3  
 AAF28204  
 ID AAF28204 standard; DNA; 39 BP.  
 XX  
 AC AAF28204;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE DNA encoding LM609 VL CDR1 peptide.  
 XX  
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 DR WPI; 2001-050110/06.  
 XX  
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Page 40; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 39 BP; 13 A; 12 C; 7 G; 7 T; 0 other;

Query Match 100.0%; Score 33; DB 22; Length 39;

Best Local Similarity 100.0%; Pred. NO. 9e-05;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagccgacccaaagtattagcaaccacctacac 33  
|||||  
Db 1 cagccgacccaaagtattagcaaccacctacac 33

RESULT 4  
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ID AAV49843 standard; DNA; 321 BP.  
XX AAV49843:  
AC AC  
XX DT  
XX 02-NOV-1998 (first entry)  
XX LM609 antibody light chain variable region DNA grafted fragment.  
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis; ss.  
XX OS  
XX Mus sp.  
XX OS  
XX Location/Qualifiers  
FH 1. 321  
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FT /product= "LM609 grafted antibody light chain variable  
FT region"  
FT /note= "partial sequence, no start or stop codon given"  
XX WO9833919-A2.  
XX  
XX 06-AUG-1998.  
XX  
XX 30-JAN-1998; 98WO-US01826.  
XX  
XX 30-JAN-1997; 97US-0791391.  
XX  
XX (IXSY-) IXSYS INC.  
XX  
XX Glaser SM, Huse WD;  
XX  
XX  
XX WPI: 1998-437472/37.  
XX P-PSDB; AAW76006.  
XX  
XX Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3  
XX integrin - and related grafted antibodies based on murine monoclonal  
XX LM609, also related nucleic acid, used to treat, prevent or diagnose  
XX angiogenesis or restenosis  
XX  
XX Claim 24; Fig 7; 129pp; English.  
XX  
XX This sequence encodes a LM609 grafted antibody variable light chain  
XX region. LM609 and the antibody vitaxin bind selectively to integrin  
XX alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a ligand  
XX and thus block integrin-mediated signal transduction. This is useful in  
XX the treatment, prevention and diagnosis of alphaVbeta3-mediated disease,  
XX specifically angiogenesis and restenosis (but also e.g. (non-)immune  
XX inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
XX psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
XX etc.). The antibodies contain non-murine framework regions so are  
XX suitable for use in humans. Enhanced types of LM609 have affinity more  
XX than 90 times greater than that of parent the parent antibody.  
XX  
XX Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match  
Best Local Similarity 100.0%; Score 33; DB 19; Length 321;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	70	caggccgccaagattattagcaaccacctacac	102
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ID	AAV49821	standard; DNA; 321 BP.	
XX	AC	AC	
XX	AAV49821;		
XX	02-NOV-1998	(first entry)	
DT			
XX	Vitaxin antibody light chain variable region DNA.		
DE			
XX	Vitaxin; antibody; variable region; heavy chain; light chain; integrin;		
XX	LM609; inhibitor; integrin-mediated signal transduction; treatment;		
KW	LM609; angiogenesis; restenosis; inflammation; diabetic retinopathy;		
KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;		
KW	macular degeneration; osteoporosis; ss.		
XX			
OS	Mus sp.		
XX			
XX	Key	Location/Qualifiers	
FH	CDS	1..321	
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FT		/product= "vitaxin antibody light chain variable region"	
FT		/note= "partial sequence, no start or stop codon given"	
XX			
XX	WO9833919-A2.		
XX			
XX	06-AUG-1998.		
XX			
PF	30-JAN-1998;	98WO-US01826.	
XX			
XX	30-JAN-1997;	97US-0791391.	
PR			
XX	(IXSY-) IXSYS INC.		
PA			
XX	Glaser SM, Huse WD;		
PI			
XX	WPI; 1998-437472/37.		
DR	P-PSDB; AAW76002.		
DR			
XX			
PT	Humanised antibody, Vitaxin, that binds selectively to alphavbeta3		
PT	integrin - and related grafted antibodies based on murine monoclonal		
PT	LM609, also related nucleic acid, used to treat, prevent or diagnose		
PT	angiogenesis or restenosis		
XX			
XX	Claim 6; Fig 1b; 129pp; English.		
PS			
XX			
CC	This sequence encodes the vitaxin antibody variable light chain region.		
CC	Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3		
CC	and can be used to inhibit binding of alphavbeta3 to a ligand and thus		
CC	block integrin-mediated signal transduction. This is useful in the		
CC	treatment, prevention and diagnosis of alphavbeta3-mediated disease,		
CC	specifically angiogenesis and restenosis (but also e.g. (non-)immune		
CC	inflammation, diabetic retinopathy, neovascular glaucoma, cancer,		
CC	psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis		
CC	etc.). The antibodies contain non-murine framework regions so are		
CC	suitable for use in humans. Enhanced types of LM609 have affinity more		
CC	than 90 times greater than that of parent the parent antibody.		
XX			
SQ	Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;		

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Query Match      100.0%; Score 33; DB 19; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```



```

Db      70 caggccagccaaagtattagcaaccacctacac 102

RESULT      6
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ID      AAV49823 standard; DNA; 321 BP.
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XX
AC      AAV49823;
DT      02-NOV-1998 (first entry)
XX
XX      LM609 antibody light chain variable region DNA fragment.
DE
DE      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; ss.
XX
OS      Mus sp.
XX
FH      Key
FT      CDS
FT      Location/Qualifiers
FT      1..321
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FT      /transl_except= "(pos: 145..147, aa: Xaa)"
FT      /note= "Xaa is unspecified"
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PN      W09833919-A2.
XX
XX      06-AUG-1998.
XX
XX      30-JAN-1998; 98W0-US01826.
XX
XX      30-JAN-1997; 97US-0791391.
XX
XX      (IXSY-) IXSYS INC.
XX
XX      Glaser SM, Huse WD;
XX
XX      WPI; 1998-437472/37.
XX      P-PSDB; AAW75004.
XX
XX      Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT      integrin - and related grafted antibodies based on murine monoclonal
PT      LM609, also related nucleic acid, used to treat, prevent or diagnose
PT      angiogenesis or restenosis
XX
PS      Claim 40; Fig 2b; 129pp; English.
XX
XX      This sequence encodes the LM609 antibody variable light chain region.
CC      LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC      and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC      block integrin-mediated signal transduction. This is useful in the
CC      treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC      specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC      inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC      psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC      etc.). The antibodies contain non-murine framework regions so are
CC      suitable for use in humans. Enhanced types of LM609 have affinity more
CC      than 90 times greater than that of parent the parent antibody.
XX
XX      Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;
SQ

Query Match      100.0%; Score 33; DB 19; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 caggccagccaaagtattagcaaccacctacac 33
      |||||||
Db      70 caggccagccaaagtattagcaaccacctacac 102

RESULT      7
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ID      AAH74624 standard; DNA; 321 BP.
XX
XX
AC      AAH74624;
DT      15-OCT-2001 (first entry)
XX
XX      DNA encoding light chain variable region of LM609 grafted antibody.
DE
DE      Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW      chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW      neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW      cancer; ss.
XX
OS      Synthetic.
OS      Mus sp.
XX
FH      Key
FT      CDS
FT      Location/Qualifiers
FT      1..321
FT      /*tag= a
FT      /transl_except= "(pos: 145..147, aa: Xaa)"
FT      /note= "Xaa is unspecified"
XX
PN      US2001011125-A1.
XX
XX      02-AUG-2001.
XX
XX      30-JAN-1997; 97US-0790540.
XX
XX      30-JAN-1997; 97US-0790540.
XX
XX      (HUSE/) HUSE W D.
XX
XX      Huse WD;
XX
XX      WPI; 2001-496171/54.
XX      P-PSDB; AAG63588.
XX
XX      New LM609 grafted antibody exhibiting selective binding affinity to
PT      alphavbeta3, comprising at least one LM609 grafted heavy and light
PT      chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT      disorders or cancer -
XX
PS      Claim 6; Fig 1B; 25pp; English.
XX
XX      The present sequence encodes the light chain variable region of the
CC      grafted monoclonal antibody LM609. LM609 is a murine antibody which
CC      specifically recognises the integrin alphavbeta3, and inhibits its
CC      functional activity. The LM609 grafted antibody has the
CC      complementarity determining regions (CDRs) substituted into a non-murine
CC      framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC      polypeptides and fragments are useful in diagnostic and therapeutic
CC      purposes, such as in the production of LM609 grafted antibodies and
CC      fragments having binding specificity and inhibitory activity against
CC      the integrin alphavbeta3. The antibody can be used for the diagnosis
CC      or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC      disorders, chronic articular rheumatism, psoriasis, disorders
CC      associated with inappropriate or inopportune invasion of vessels such
CC      as diabetic retinopathy, neovascular glaucoma and capillary
CC      proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC      binding activity of alphavbeta3 that are necessary for progression of
CC      an alphavbeta3-mediated disease.
XX
XX      Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;
SQ

Query Match      100.0%; Score 33; DB 22; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 caggccagccaaagtattagcaaccacctacac 33
      |||||||

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AAAF28176 standard; DNA; 321 BP.

AAAF28176; 03-APR-2001 (first entry)

Vitaxin light chain variable region DNA.

LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis; inflammatory; cancer; retina; restenosis; osteoporosis; ds.

Unidentified.

WO200078815-A1.

28-DEC-2000.

23-JUN-2000; 2000WO-US17454.

24-JUN-1999; 99US-0339922.

(MOLE-) APPLIED MOLECULAR EVOLUTION.

Huse WD, Wu H;

WPI; 2001-050110/06.

Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -

Disclosure; Fig 1; 132pp; English.

The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphaVbeta\_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphaVbeta\_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and osteoporosis.

Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;

Query Match 100.0%; Score 33; DB 22; Length 321;

Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps

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|||||

Db 70 cagggccgcaaaagtattagcaaccacctacac 102

RESULT 10

AAAF28178

AAAF28178 standard; DNA; 321 BP.

AAAF28178;

03-APR-2001 (first entry)

Antibody LM609 light chain variable region DNA.

LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis; inflammatory; cancer; retina; restenosis; osteoporosis; ds.

Unidentified.

XX PN WO200078815-A1.  
 XX XX 28-DEC-2000.  
 XX XX 23-JUN-2000; 2000WO-US17454.  
 XX XX 24-JUN-1999; 99US-0339922.  
 XX XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX PI Huse WD, Wu H;  
 XX XX WPI; 2001-050110/06.  
 XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX XX Disclosure; Fig 2; 132pp; English.  
 XX XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX XX Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;  
 SQ

Query Match 100.0%; Score 33; DB 22; Length 321;  
 Best Local Similarity 100.0%; Pred. No. 0.00012;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caggccagcacaagattattagcaaccacccacac 33  
 |||||  
 Db 70 caggccagcacaagattattagcaaccacccacac 102  
 |||||

RESULT 11  
 AAF28199  
 ID AAF28199 standard; DNA; 321 BP.  
 XX AC AAF28199;  
 XX XX 03-APR-2001 (first entry)  
 XX DE DNA encoding light chain variable region of LM609.  
 XX XX LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.  
 XX OS Unidentified.  
 XX XX WO200078815-A1.  
 XX PN 28-DEC-2000.  
 XX XX 23-JUN-2000; 2000WO-US17454.  
 XX XX 24-JUN-1999; 99US-0339922.  
 XX XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX PI Huse WD, Wu H;

DR WPI; 2001-050110/06.  
 XX XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX XX Disclosure; Fig 7; 132pp; English.  
 XX XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX XX Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;  
 SQ

Query Match 100.0%; Score 33; DB 22; Length 321;  
 Best Local Similarity 100.0%; Pred. No. 0.00012;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caggccagcacaagattattagcaaccacccacac 33  
 |||||  
 Db 70 caggccagcacaagattattagcaaccacccacac 102  
 |||||

RESULT 12  
 AAV71825/c  
 ID AAV71825 standard; DNA; 101 BP.  
 XX AC AAV71825;  
 XX XX 15-MAR-1999 (first entry)  
 XX DE Alpha-v beta-3 Mab D12HZLCREI VL oligonucleotide SBA3167.  
 KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;  
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
 KW angiogenesis; diabetic retinopathy; inflammation;  
 KW macular degeneration; osteoporosis; Paget's disease;  
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;  
 KW D12HZLCREI; ss.  
 XX OS Mus sp.  
 OS Synthetic.  
 XX XX WO9840488-A1.  
 XX PN 17-SEP-1998.  
 XX XX 12-MAR-1998; 98WO-US04987.  
 XX XX 12-MAR-1997; 97US-0039609.  
 XX XX (SMK ) SMITHKLINE BEECHAM CORP.  
 XX XX Johanson KO, Jonak ZL, Taylor AH;  
 XX WPI; 1999-034590/03.  
 XX XX New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
 PT osteoporosis  
 XX XX

PS Example 14; Page 51; 97pp; English.

XX SBA3167 is one of 4 overlapping oligonucleotides (see AAV71824-27);  
 CC used to construct DNA (see AAV71805) encoding a region of the murine  
 CC D12 monoclonal antibody light chain variable region (VL) that is  
 CC modified in humanised D12 VL D12HZLCREI. The synthetic D12 VL  
 CC gene was utilised in the construction of an expression vector for  
 CC the humanised D12 VL (see AAW87455). D12 is a murine anti-human  
 CC alpha-v beta-3 vitronectin receptor monoclonal antibody. Humanised  
 CC D12 antibodies of the invention can be used for passive  
 CC immunotherapy of disorders mediated by the alpha-v beta-3  
 CC vitronectin receptor, e.g. restenosis and angiogenic-related  
 CC disorders.

XX Sequence 101 BP; 21 A; 20 C; 31 G; 29 T; 0 other;

Query Match 93.9%; Score 31; DB 20; Length 101;

Best Local Similarity 100.0%; Pred. No. 0.00074;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaaccactacac 33

Db 99 GGCACGCAAAAGTATTAGCAACCACCTACAC 69

RESULT 13

AAV71816

ID AAV71816 standard; DNA; 108 BP.

XX AC AAV71816;

XX DT 15-MAR-1999 (first entry)

XX XX

DE Alpha-v beta-3 MAB D12HZHC 1-0 VL oligonucleotide SBA1327.

XX KW

Humanised antibody; monoclonal antibody; MAB; antibody engineering;

XX KW

mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

XX KW

cancer; metastasis; rheumatoid arthritis; atherosclerosis;

XX KW

angiogenesis; diabetic retinopathy; inflammation;

XX KW

macular degeneration; osteoporosis; Paget's disease;

XX KW

hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;

XX KW

D12HZHC 1-0; ss.

XX OS

Mus sp.

XX OS

Synthetic.

XX PN

WO9840488-A1.

XX PN

17-SEP-1998.

XX PF

12-MAR-1998; 98WO-US04987.

XX PF

12-MAR-1997; 97US-0039609.

XX PR

(SMIK ) SMITHKLINE BEECHAM CORP.

XX PI

Johanson KO, Jonak ZL, Taylor AH;

XX PI

WPI; 1999-034590/03.

XX DR

New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for

XX PT

immunotherapeutic treatment of e.g. diabetic retinopathy,

XX PT

inflammatory disorders, atherosclerosis, restenosis, cancers or

XX PT

osteoporosis

XX XX

Example 13; Page 47; 97pp; English.

XX XX

SBA1327 is one of 4 overlapping oligonucleotides (see AAV71816-19)  
 CC used to construct DNA (see AAV71802) encoding a region of the murine  
 CC D12 monoclonal antibody light chain variable region (VL) that is  
 CC modified in humanised D12 VL D12HZHC 1-0. The synthetic D12 VL  
 CC gene was utilised in the construction of an expression vector for

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

CC the humanised D12 VL (see AAV71800). D12 is a murine anti-human  
 CC alpha-v beta-3 vitronectin receptor monoclonal antibody. Humanised  
 CC D12 antibodies of the invention can be used for passive  
 CC immunotherapy of disorders mediated by the alpha-v beta-3  
 CC vitronectin receptor, e.g. restenosis and angiogenic-related  
 CC disorders.

XX SQ Sequence 108 BP; 28 A; 34 C; 22 G; 24 T; 0 other;

Query Match 93.9%; Score 31; DB 20; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.00074;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaaccactacac 33

Db 72 ggcacgcaaaagtattagcaaccactacac 102

RESULT 14

AAV71803

ID AAV71803 standard; cDNA; 315 BP.

XX AC AAV71803;

XX DT 15-MAR-1999 (first entry)

XX XX

DE Jk gene segment.

XX KW

Humanised antibody; monoclonal antibody; MAB; antibody engineering;

XX KW

mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

XX KW

cancer; metastasis; rheumatoid arthritis; atherosclerosis;

XX KW

angiogenesis; diabetic retinopathy; inflammation;

XX KW

macular degeneration; osteoporosis; Paget's disease;

XX KW

hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;

XX KW

D12HZREI; Jk gene; ds.

XX OS

Mus sp.

XX OS

Synthetic.

XX PN

WO9840488-A1.

XX PN

17-SEP-1998.

XX PF

12-MAR-1998; 98WO-US04987.

XX PF

12-MAR-1997; 97US-0039609.

XX PR

(SMIK ) SMITHKLINE BEECHAM CORP.

XX PI

Johanson KO, Jonak ZL, Taylor AH;

XX PI

WPI; 1999-034590/03.

XX DR

P-PSDB; AAW87456.

XX DR

New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
 immunotherapeutic treatment of e.g. diabetic retinopathy,  
 inflammatory disorders, atherosclerosis, restenosis, cancers or  
 osteoporosis

XX XX

Example 14; Page 66; 97pp; English.

XX PS

This DNA sequence comprises a segment of the Jk gene. It was  
 prepared from 4 overlapping synthetic oligonucleotides (see  
 AAV71824-27) and used in the construction of an expression vector  
 for D12HZREI humanised light chain variable region (see AAW87458)  
 comprising a human REI framework and complementarity determining  
 regions from the anti-human alpha-v beta-3 vitronectin receptor  
 monoclonal antibody D12. Humanised D12 antibodies can be used for  
 passive immunotherapy of disorders mediated by the alpha-v beta-3  
 vitronectin receptor, e.g. restenosis and angiogenic associated  
 diseases.

XX CC

SQ Sequence 315 BP; 81 A; 88 C; 70 G; 76 T; 0 other;

Query Match 93.9%; Score 31; DB 20; Length 315;  
Best Local Similarity 100.0%; Pred. No. 0.00087;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaaccacctacac 33  
|||||  
Db 72 ggcagccaaagtattagcaaccacctacac 102

## RESULT 15

AAV71805

ID AAV71805 standard; cDNA; 315 BP.

XX

AC AAV71805;

XX

DT 15-MAR-1999 (first entry)

XX

XX Humanised anti-alpha-v beta-3 MAb D12H2LCREI VL CDNA.

DE

XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;  
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;  
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;  
KW angiogenesis; diabetic retinopathy; inflammation;  
KW macular degeneration; osteoporosis; Paget's disease;  
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;  
KW D12H2LCREI; ds.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO9840488-A1.

XX

PD 17-SEP-1998.

XX

PF 12-MAR-1998; 98WO-US04987.

XX

PR 12-MAR-1997; 97US-0039609.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Johanson KO, Jonak ZL, Taylor AH;

XX

DR WPI: 1999-034590/03.

DR P-PSDB; AAW87458.

XX

PT New anti alpha\_v beta\_3 vitronectin receptor antibodies - used for  
PT immunotherapeutic treatment of e.g. diabetic retinopathy,  
PT inflammatory disorders, atherosclerosis, restenosis, cancers or  
PT osteoporosis

XX

PS Example 14; Page 68-69; 97pp; English.

XX

CC This DNA sequence codes for the light chain variable region (VL,  
CC see AAW87458) of humanised anti-alpha-v beta-3 vitronectin receptor  
CC monoclonal antibody D12H2LCREI. It is based on a synthetic  
CC humanised kappa chain based on a modified human REI kappa  
CC framework and complementarity determining regions from the murine  
CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody  
CC D12 (see AAW84094). Humanised antibodies of the invention can be used  
CC for passive immunotherapy of a disorder mediated by the alpha-v  
CC beta-3 receptor, e.g. cardiovascular disorders or angiogenic-  
CC related disorders, such as angiogenesis associated with diabetic  
CC retinopathy, atherosclerosis and restenosis, chronic inflammatory  
CC disorders, macular degeneration, rheumatoid arthritis and cancer,  
CC e.g. solid tumour metastasis, and diseases where bone resorption is  
CC associated with pathology such as osteoporosis, hyperparathyroidism,  
CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions  
CC produced by bone metastasis, bone loss due to immobilisation or sex  
CC hormone deficiency. They can also be used for targeted drug  
CC therapy, and for detection and diagnosis.

XX

SQ Sequence 315 BP; 81 A; 88 C; 70 G; 76 T; 0 other;

Query Match 93.9%; Score 31; DB 20; Length 315;  
Best Local Similarity 100.0%; Pred. No. 0.00087;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaaccacctacac 33  
|||||  
Db 72 ggcagccaaagtattagcaaccacctacac 102

Search completed: August 21, 2002, 10:08:40  
Job time: 10058 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:19 ; Search time 174.26 Seconds  
(without alignments)  
46.516 Million cell updates/sec

Title: US-09-339-922a-107  
Perfect score: 33  
Sequence: 1 caggccagccaaagtattagcaaccctacac 33

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents.NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	29.4	89.1	128	1	US-07-634-278-91
C 2	29.4	89.1	128	1	US-08-477-728-91
C 3	29.4	89.1	128	1	US-08-474-040-91
C 4	29.4	89.1	128	1	US-08-487-200-91
C 5	29.4	89.1	128	4	US-08-484-537-91
C 6	29.4	89.1	381	1	US-07-634-278-82
C 7	29.4	89.1	381	1	US-08-477-728-82
C 8	29.4	89.1	381	1	US-08-474-040-82
C 9	29.4	89.1	381	1	US-08-487-200-82
C 10	29.4	89.1	381	4	US-08-484-537-82
C 11	29.4	89.1	424	1	US-08-436-463-3
C 12	29.4	89.1	523	6	5453363-1
C 13	24.6	74.5	324	4	US-09-247-352-14
C 14	24.6	74.5	8858	4	US-09-247-352-6
C 15	23	69.7	324	4	US-08-737-560A-13
C 16	23	69.7	363	2	US-08-737-560A-8
C 17	20.4	61.8	321	4	US-09-247-352-7
C 18	20.4	61.8	321	4	US-09-247-352-11
C 19	18.4	55.8	812	1	US-08-053-131-178
C 20	18.4	55.8	812	1	US-08-096-762-178
C 21	18.4	55.8	812	4	US-09-042-353-41
C 22	18.4	55.8	812	4	US-08-758-417A-306
C 23	18.2	55.2	322	2	US-08-476-176B-3
C 24	18.2	55.2	322	3	US-08-127-721A-3
C 25	18.2	55.2	322	3	US-08-485-246A-3
C 26	18.2	55.2	424	2	US-08-476-176B-5
C 27	18.2	55.2	424	2	US-08-476-176B-7

28	18.2	55.2	424	2	US-08-476-176B-9	Sequence 9, Appli
29	18.2	55.2	424	3	US-08-127-721A-5	Sequence 5, Appli
30	18.2	55.2	424	3	US-08-127-721A-7	Sequence 7, Appli
31	18.2	55.2	424	3	US-08-127-721A-9	Sequence 9, Appli
32	18.2	55.2	424	3	US-08-485-246A-5	Sequence 5, Appli
33	18.2	55.2	424	3	US-08-485-246A-7	Sequence 7, Appli
34	18.2	55.2	424	3	US-08-485-246A-9	Sequence 9, Appli
C 35	18.2	55.2	4800	5	PCT-US94-07779-1	Sequence 1, Appli
C 36	18.2	55.2	7083	4	US-09-198-839-1	Sequence 1, Appli
C 37	18.2	55.2	7294	1	US-08-440-787A-1	Sequence 1, Appli
C 38	18.2	55.2	7294	1	US-08-440-787A-5	Sequence 5, Appli
C 39	18.2	55.2	7294	4	US-08-367-685-1	Sequence 1, Appli
C 40	18.2	55.2	7294	4	US-08-367-685-5	Sequence 5, Appli
C 41	18.2	55.2	7294	5	PCT-US91-071141-1	Sequence 1, Appli
C 42	18.2	55.2	7294	5	PCT-US91-071141-5	Sequence 5, Appli
C 43	18.2	55.2	7317	1	US-08-464-136-2	Sequence 2, Appli
C 44	18.2	55.2	7317	2	US-08-349-131-2	Sequence 2, Appli
C 45	18.2	55.2	7317	3	US-08-470-297A-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-07-634-278-91/c  
; Sequence 91, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-07-634-278-91

Query Match 89.1%; Score 29.4; DB 1; Length 128;  
Best Local Similarity 96.8%; Pred. No. 0.00019;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ggcagccaaagtatttagcaaacctacac 33  
|||||  
Db 95 GGCAGCCAAAGTATTAGCAACAACCTACAC 65

RESULT 2  
US-08-477-728-91/c  
; Sequence 91, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/477,728  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990

PRIOR APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 91:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)

Query Match 89.1%; Score 29.4; DB 1; Length 128;  
Best Local Similarity 96.8%; Pred. No. 0.00019;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ggcagccaaagtatttagcaaacctacac 33  
|||||  
Db 95 GGCAGCCAAAGTATTAGCAACAACCTACAC 65

RESULT 3  
US-08-474-040-91/c  
; Sequence 91, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,040  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990

PRIOR APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 91:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)

Query Match 89.1%; Score 29.4; DB 1; Length 128;  
Best Local Similarity 96.8%; Pred. No. 0.00019;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ggcagccaaagtatttagcaaacctacac 33  
|||||  
Db 95 GGCAGCCAAAGTATTAGCAACAACCTACAC 65

RESULT 4  
US-08-487-200-91/c

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; Sequence 91, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-487-200-91

Query Match      89.1%; Score 29.4; DB 1; Length 128;
Best Local Similarity 96.8%; Pred. No. 0.00019;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaaccacctacac 33
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DB 95 GGCACGCCAAAGTATTAGCAACACCTACAC 65

RESULT 5
US-08-484-537-91/c
; Sequence 91, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
```

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; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-484-537-91

Query Match      89.1%; Score 29.4; DB 4; Length 128;
Best Local Similarity 96.8%; Pred. No. 0.00019;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaaccacctacac 33
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DB 95 GGCACGCCAAAGTATTAGCAACACCTACAC 65

RESULT 6
US-07-634-278-82
; Sequence 82, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
```





FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 381 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..381  
US-08-474-040-82

Query Match 89.1%; Score 29.4; DB 1; Length 381;  
Best Local Similarity 96.8%; Pred. No. 0.00024;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 gccacgcaaaagtattagcaaccctacac 33  
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DB 132 GCCACGCCAAAGTATTAGCAACACCTACAC 162

RESULT 9  
US-08-487-200-82  
Sequence 82, Application US/08487200  
Patent No. 5693762  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,200  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002610  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 381 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..381  
US-08-487-200-82

Query Match 89.1%; Score 29.4; DB 1; Length 381;  
Best Local Similarity 96.8%; Pred. No. 0.00024;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 gccacgcaaaagtattagcaaccctacac 33  
|||||  
DB 132 GCCACGCCAAAGTATTAGCAACACCTACAC 162

RESULT 10  
US-08-484-537-82  
Sequence 82, Application US/08484537  
Patent No. 6180370  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,537  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..381
; US-08-484-537-82

Query Match      89.1%; Score 29.4; DB 4; Length 381;
Best Local Similarity 96.8%; Pred. No. 0.00024;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ggcagccaaagtattagcaaccacctacac 33
Db      132 GCCAGCCAAAGTATTAGCAACACCTACAC 162

RESULT 11
US-08-436-463-3
; Sequence 3, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23..403
; US-08-436-463-3

Query Match      89.1%; Score 29.4; DB 1; Length 424;
Best Local Similarity 96.8%; Pred. No. 0.00025;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ggcagccaaagtattagcaaccacctacac 33
Db      154 GCCAGCCAAAGTATTAGCAACACCTACAC 184

RESULT 12
5453363-1
; Patent No. 5453363
; APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF
; TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR
; ING AFTER GENETIC EXPRESSION IN PROKARYOTES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,044
; FILING DATE: 02-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 942,370
; FILING DATE: 09-SEP-1992
; APPLICATION NUMBER: 498,500
; FILING DATE: 23-MAR-1990
; APPLICATION NUMBER: 76,207
; FILING DATE: 23-OCT-1986
; SEQ ID NO:1:
; LENGTH: 5238
; 5453363-1

Query Match      89.1%; Score 29.4; DB 6; Length 5238;
Best Local Similarity 96.8%; Pred. No. 0.00042;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ggcagccaaagtattagcaaccacctacac 33
Db      78 ggcagccaaagtattagcaaccacctacac 108

RESULT 13
US-09-247-352-14
; Sequence 14, Application US/09247352
; Patent No. 6312693
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Sladak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Harris, Linda
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2a SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/247,352
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 09/026,291
; EARLIER FILING DATE: 1998-02-19
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; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 324  
; TYPE: DNA  
; ORGANISM: Human and Mouse  
US-09-247-352-14

Query Match 74.5%; Score 24.6; DB 4; Length 324;  
Best Local Similarity 87.1%; Pred. No. 0.031;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 gcccagccaaagtattagcaaccactacac 33  
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Db 72 gcccagccagagtattagcgactactacac 102

## RESULT 14

US-09-247-352-6  
; Sequence 6, Application US/09247352  
; Patent No. 6312693  
; GENERAL INFORMATION:  
; APPLICANT: Aruffo, Alejandro A.  
; APPLICANT: Sladak, Anthony W.  
; APPLICANT: Berry, Karen K.  
; APPLICANT: Harris, Linda  
; APPLICANT: Thorne, Barbara A.  
; APPLICANT: Rajorath, Jurgen  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40  
; FILE REFERENCE: DB2a SEQUENCE  
; CURRENT APPLICATION NUMBER: US/09/247,352  
; EARLIER FILING DATE: 1999-02-10  
; EARLIER FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 8858  
; TYPE: DNA  
; ORGANISM: Human and Mouse  
US-09-247-352-6

Query Match 74.5%; Score 24.6; DB 4; Length 8858;  
Best Local Similarity 87.1%; Pred. No. 0.061;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 gcccagccaaagtattagcaaccactacac 33  
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Db 1136 gcccagccagagtattagcgactactacac 1166

## RESULT 15

US-08-737-560A-13  
; Sequence 13, Application US/08737560A  
; Patent No. 5928893  
; GENERAL INFORMATION:  
; APPLICANT: KANG, Chang-Yuul  
; APPLICANT: KIM, Joong-Gon  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN  
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KANG, Chang-Yuul  
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,  
; STREET: Kwanak-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea

; ZIP: 151-057  
; ADDRESSEE: KIM, Joong-Gon  
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 135-110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage  
; COMPUTER: IBM PC/AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,560A  
; FILING DATE: 13-NOV-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: KR 95-8176  
; FILING DATE: 08-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: polynucleotide encoding 4B4-1-1  
; OTHER INFORMATION: light chain variable region  
US-08-737-560A-13

Query Match 69.7%; Score 23; DB 2; Length 324;  
Best Local Similarity 83.9%; Pred. No. 0.16;  
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 gcccagccaaagtattagcaaccactacac 33  
||||||| ||||||| || |||||  
Db 72 GCGCAGCCAGACTATTAGCGACTACTTACAC 102

Search completed: August 21, 2002, 10:52:20  
Job time: 9660 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model  
Run on: August 21, 2002, 10:49:57 ; Search time 2408.76 Seconds  
(without alignments)  
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Title: US-09-339-922A-109  
Perfect score: 33  
Sequence: 1 cagccgacgaagattagcaacttctacac 33

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

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7: gb\_ph:\*

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11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

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30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
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RESULT 1

AX060888

LOCUS

DEFINITION

AX060888

ACCESSION

AX060888.1

VERSION

GI:12406266

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

ALIGNMENTS

AX060888	Sequence 109 from Patent WO0078815.	33 bp	DNA	linear	PAT 22-JAN-2001
----------	-------------------------------------	-------	-----	--------	-----------------

synthetic construct.

synthetic construct.

artificial sequence.

1 (bases 1 to 33)

Huse, W.D. and Wu, H.

Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids

encoding same and methods of use

Patent: WO 0078815-A. 109 28-DEC-2000;

Applied Molecular Evolution (US)

Location/Qualifiers

1..33

/organism="synthetic construct"

/db\_xref="taxon:32630"

<1..>33

/note="Mutated complementarity determining region (CDR)"

/codon\_start=1

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/translation="QASQISNHLH"
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Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaacttcctacac 33
Db 1 CAGGCCAGCCAAAGTATTAGCAACTTCTCTACAC 33

RESULT 2
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LOCUS      AX060860      39 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 81 from Patent WO0078815.
ACCESSION AX060860
VERSION    AX060860.1 GI:12406238
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 39)
AUTHORS    Huse,W.D. and Wu,H.
TITLE      Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
           encoding same and methods of use
JOURNAL    Patent: WO 0078815-A 81 28-DEC-2000;
           Applied Molecular Evolution (US)
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            source          1..39
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ORIGIN

Query Match      95.2%; Score 31.4; DB 6; Length 39;
Best Local Similarity 97.0%; Pred. No. 0.00095;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaacttcctacac 33
Db 1 CAGGCCAGCCAAAGTATTAGCAACTTCTCTACAC 33

RESULT 3
AX060886
LOCUS      AX060886      33 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 107 from Patent WO0078815.
ACCESSION AX060886
VERSION    AX060886.1 GI:12406264
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   artificial sequence.
REFERENCE  1 (bases 1 to 33)
AUTHORS    Huse,W.D. and Wu,H.
TITLE      Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
           encoding same and methods of use
JOURNAL    Patent: WO 0078815-A 107 28-DEC-2000;
           Applied Molecular Evolution (US)
FEATURES   Location/Qualifiers
            source          1..33
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
            CDS              <1..>33
                        /note="Mutated complementarity determining region (CDR)"
                        /codon_start=1
                        /translation="QASQISNHLHWY"
BASE COUNT      12 a      10 c      7 g      10 t
ORIGIN

Query Match      90.3%; Score 29.8; DB 6; Length 39;
Best Local Similarity 93.9%; Pred. No. 0.0053;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaacttcctacac 33
Db 1 CAGGCCAGCCAAAGTATTAGCAACTTCTCTACAC 33

RESULT 4
AX060820
LOCUS      AX060820      39 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 41 from Patent WO0078815.
ACCESSION AX060820
VERSION    AX060820.1 GI:12406198
KEYWORDS   house mouse.
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 39)
AUTHORS    Huse,W.D. and Wu,H.
TITLE      Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
           encoding same and methods of use
JOURNAL    Patent: WO 0078815-A 41 28-DEC-2000;
           Applied Molecular Evolution (US)
FEATURES   Location/Qualifiers
            source          1..39
                        /organism="Mus musculus"
                        /db_xref="taxon:10090"
                        <1..>39
                        /note="unnamed protein product"
                        /codon_start=1
                        /protein_id="CAC24896.1"
                        /db_xref="GI:12406199"
                        /translation="QASQISNHLHWY"
BASE COUNT      13 a      12 c      7 g      7 t
ORIGIN

Query Match      90.3%; Score 29.8; DB 6; Length 39;
Best Local Similarity 93.9%; Pred. No. 0.0053;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaacttcctacac 33
Db 1 CAGGCCAGCCAAAGTATTAGCAACTTCTCTACAC 33

RESULT 5
AX060782
LOCUS      AX060782      321 bp      DNA      linear      PAT 22-JAN-2001
DEFINITION Sequence 3 from Patent WO0078815.
ACCESSION AX060782
VERSION    AX060782.1 GI:12406162
KEYWORDS   synthetic construct.
SOURCE     synthetic construct.
ORGANISM   synthetic construct.

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artificial sequence.  
1 (bases 1 to 321)  
Huse,W.D. and Wu,H.  
Anti-g(a) v7-g(b)j3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
Patent: WO 0078815-A 3 28-DEC-2000;  
Applied Molecular Evolution (US)  
Location/Qualifiers  
1..321  
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/db\_xref="taxon:32630"  
<1..>321  
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RLLIYRQSISGIPARFSGSGGTDTLTITISLPEDEFAVYYCQSGSWPHTFGGT  
KVEIK"

BASE COUNT 78 a 93 c 79 g 71 t  
ORIGIN

Query Match 90.3%; Score 29.8; DB 6; Length 321;  
Best Local Similarity 93.9%; Pred. No. 0.0052; Mismatches 0; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaacttcctacac 33  
|||||  
Db 70 CAGGCCAGCAAGTATTAGCACCTACAC 102

RESULT 6  
AX060786  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AX060786  
Sequence 7 from Patent WO0078815.  
AX060786  
AX060786.1 GI:12406166  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Huse,W.D. and Wu,H.  
Anti-g(a) v7-g(b)j3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
Patent: WO 0078815-A 7 28-DEC-2000;  
Applied Molecular Evolution (US)  
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/db\_xref="GI:12406167"  
/translation="DIVLTQSPATLSVTPGDVSLSCQASQISNHLHWYQOKSHESP  
RLLIYRQSISGIPARFSGSGGTDFALINSVETDFGMVFCQSGSGSWPHTFGGT  
KLEIK"

BASE COUNT 83 a 83 c 77 g 78 t  
ORIGIN

Query Match 90.3%; Score 29.8; DB 6; Length 321;  
Best Local Similarity 93.9%; Pred. No. 0.0052; Mismatches 0; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaacttcctacac 33  
|||||  
Db 70 CAGGCCAGCAAGTATTAGCACCTACAC 102

RESULT 7  
AX060810  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AX060810  
Sequence 31 from Patent WO0078815.  
AX060810  
AX060810.1 GI:12406189  
synthetic construct.  
synthetic construct  
artificial sequence.  
1 (bases 1 to 321)  
Huse,W.D. and Wu,H.  
Anti-g(a) v7-g(b)j3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
Patent: WO 0078815-A 31 28-DEC-2000;  
Applied Molecular Evolution (US)  
Location/Qualifiers  
1..321  
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/note="grafted antibody variable region"  
145..147  
/note="NNN-CGT OR ATG"

BASE COUNT 76 a 93 c 78 g 71 t 3 others  
ORIGIN

Query Match 90.3%; Score 29.8; DB 6; Length 321;  
Best Local Similarity 93.9%; Pred. No. 0.0052; Mismatches 0; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagccaaagtattagcaacttcctacac 33  
|||||  
Db 70 CAGGCCAGCAAGTATTAGCACCTACAC 102

RESULT 8  
MMU19309  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

MMU19309  
Mus musculus immunoglobulin kappa light chain variable region mRNA,  
clone MRL1-17, partial cds.  
U19309  
U19309.1 GI:619954  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Roark,J.H., Kuntz,C.L., Nguyen,K.A., Caton,A.J. and Erikson,J.  
Breakdown of B cell tolerance in a mouse model of systemic lupus  
erythematosus  
J. Exp. Med. 181 (3), 1157-1167 (1995)  
95173583  
2. (bases 1 to 243)  
Roark,J.H.  
Direct Submission  
Submitted (02-JAN-1995) Jessica H. Roark, Wistar Institute, 3601  
Spruce St., Philadelphia, PA 19104, USA  
Location/Qualifiers  
1..243  
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/strain="MRL-lpr/lpr"  
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/clone="MRL1-17"  
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/tissue\_type="spleen"  
/dev\_stage="adult"  
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/codon\_start=1  
/product="immunoglobulin kappa light chain variable

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region"
/protein_id="AA68563.1"
/db_xref="GI:619955"
/translation="ACRASQISNYLHWYQKSHESPRLLIKYASQISGIPSRFSGS
GSGTFTLSINSEVEDFGMYFCQSQSNWPHTFGSGT"
BASE COUNT      65 a   52 c   56 g   60 t
ORIGIN

Query Match      89.1%; Score 29.4; DB 10; Length 243;
Best Local Similarity 96.8%; Pred. No. 0.008;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcagcccaagattagcaacttctctacac 33
|||||
Db 9 GGCAGCCCAAGATTAGCAACTACCTACAC 39

RESULT 9
AF139842
LOCUS      285 bp      DNA      linear      ROD 04-NOV-1999
DEFINITION Mus musculus clone G11 immunoglobulin kappa light chain variable
region V $\kappa$ 23 (Ig) gene, partial cds.
ACCESSION AF139842
VERSION AF139842.1 GI:4732148
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 285)
Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
J. Exp. Med. 190 (5), 691-704 (1999)
JOURNAL 99406777
MEDLINE 10477553
PUBMED
REFERENCE 2 (bases 1 to 285)
AUTHORS Brard,F. and Weigert,M.
TITLES Direct Submission
JOURNAL Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES
source location/Qualifiers
1..285
/organism="Mus musculus"
/strain="MRL/Mp-lpr/lpr"
/db_xref="taxon:10090"
/chromosome="6"
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/tissue_type="tail"
/germline
/gene="Ig"
/feature="Ig"
/note="variable region"
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/gene="Ig"
/codon_start=1
/product="immunoglobulin kappa light chain variable region
V $\kappa$ 23"
/protein_id="AAD28629.1"
/db_xref="GI:4732149"
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RLLIKVASQISGIPSRFSGSGTFTLSINSEVEDFGMYFCQSQSNWP"
70..105
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/note="CDR1; complementarity determining region 1"
148..168
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/note="CDR2; complementarity determining region 2"
75 a   73 c   63 g   74 t
BASE COUNT
ORIGIN

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Query Match      89.1%; Score 29.4; DB 10; Length 285;
Best Local Similarity 96.8%; Pred. No. 0.008;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcagcccaagattagcaacttctctacac 33
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Db 72 GCCAGCCCAAGATTAGCAACTACCTACAC 102

RESULT 10
S60864
LOCUS      303 bp      mRNA      linear      ROD 15-APR-1996
DEFINITION Ab2 kappa chain V region/mab P168 [V/J junction] [mice,
MLR-lpr/lpr, mRNA Partial, 303 nt].
ACCESSION S60864
VERSION S60864.1 GI:235110
KEYWORDS
SOURCE Mus sp. MLR-lpr/lpr.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 303)
Kolzumi,T., Puccetti,A., Migliorini,P., Barrett,K.J. and
Schwartz,R.S.
Molecular heterogeneity of auto-anti-idiotypic antibodies in
MLR-lpr/lpr mice
Eur. J. Immunol. 21 (9), 2185-2193 (1991)
JOURNAL 91364791
MEDLINE
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 60864] from the original journal article.
This sequence comes from Fig.6.
FEATURES
source location/Qualifiers
1..303
/organism="Mus sp."
/db_xref="taxon:10095"
1..303
/gene="Ab2 kappa chain V region/mab P168"
77 a   80 c   66 g   80 t
BASE COUNT
ORIGIN

Query Match      89.1%; Score 29.4; DB 10; Length 303;
Best Local Similarity 96.8%; Pred. No. 0.008;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcagcccaagattagcaacttctctacac 33
|||||
Db 72 GCCAGCCCAAGATTAGCAACTACCTACAC 102

RESULT 11
MMU16184
LOCUS      324 bp      mRNA      linear      ROD 03-FEB-2000
DEFINITION Mus musculus anti-cardiolipin antibody CAR Ig light chain mRNA,
partial cds.
ACCESSION U16184
VERSION U16184.1 GI:604311
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 324)
Blank,M., Waisman,A., Mozes,E., Koike,T. and Shoenfeld,Y.
Characteristics and pathogenic role of anti-beta2-glycoprotein I
single-chain Fv domains: induction of experimental antiphospholipid
syndrome
Int. Immunol. 11 (12), 1917-1926 (1999)
JOURNAL 20059391
MEDLINE 10590257
PUBMED
REFERENCE 2 (bases 1 to 324)
AUTHORS Blank,M., Waisman,A., Mozes,E. and Shoenfeld,Y.
TITLES Pathogenic and nonpathogenic anti-cardiolipin antibodies: Binding

```



properties and v gene analysis  
Unpublished  
3 (bases 1 to 324)  
Blank.M.  
Direct Submission  
Submitted (20-OCT-1994) Miri Blank, Research Unit of Autoimmune  
Diseases, Shiba Medical Center, Tel Hashomer, 52621, Israel  
Location/Qualifiers  
1..324  
/organism="Mus musculus"  
/strain="BALB/c"  
/db\_xref="taxon:10090"  
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KLEIKS"  
BASE COUNT 86 a 81 c 71 g 86 t  
ORIGIN  
  
Query Match 89.1%; Score 29.4; DB 10; Length 324;  
Best Local Similarity 96.8%; Pred. No. 0.008;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ggcagccaaagtattagcaacttcctacac 33  
|||||  
DB 72 GGCTAGCCAAAGTATTAGCAACTTCCTACAC 102  
  
RESULT 12  
MUSIGL2VK  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
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ORGANISM  
  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
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1..330  
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translation of the corresponding V\_region. Presently  
translation qualifiers on V\_region features are illegal."  
/codon\_start=1  
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KLEIKRAD"

BASE COUNT 89 a 80 c 77 g 84 t  
ORIGIN  
  
Query Match 89.1%; Score 29.4; DB 10; Length 330;  
Best Local Similarity 96.8%; Pred. No. 0.008;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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|||||  
DB 72 GGCCAGCCAAAGTATTAGCAACTACCTACAC 102  
  
RESULT 13  
MMY16070  
LOCUS  
DEFINITION  
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VERSION  
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JOURNAL  
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/strain="Bp"  
/db\_xref="taxon:10090"  
/cell\_line="splenic lymphocyte + sp2-0-Ag14"  
/cell\_line="hybridoma Al02"  
/cell\_type="hybridoma"  
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/gene="IgL1"  
/product="immunoglobulin light chain, variable region"  
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/note="anti-scorpian hemocyanin"  
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/protein\_id="CAA76036.1"  
/db\_xref="GI:2760535"  
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KLEIKRADAAP"  
BASE COUNT 91 a 89 c 85 g 83 t  
ORIGIN  
  
Query Match 89.1%; Score 29.4; DB 10; Length 348;  
Best Local Similarity 96.8%; Pred. No. 0.008;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 ggcagccaaagtattagcaacttcctacac 33  
|||||  
DB 72 GGCCAGCCAAAGTATTAGCAACTACCTACAC 102  
  
RESULT 13  
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DEFINITION  
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KLEIKRADAAP"

## RESULT 14

MUSIGKXD  
 LOCUS MUSIGKXD 370 bp mRNA linear ROD 27-APR-1993  
 DEFINITION Mouse Ig active kappa-chain V-region, partial cds.  
 ACCESSION M93959  
 VERSION M93959.1 GI:197572  
 KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;  
 processed gene.  
 SOURCE Mus musculus CDNA to mRNA.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 370)  
 AUTHORS Takeda Y., Wise K.S. and Hoffman R.W.  
 TITLE Nucleotide sequences of immunoglobulin heavy and light chain  
 V-regions from a monoclonal autoantibody specific for a unique set  
 of small nuclear ribonucleoprotein complexes  
 Nucleic Acids Res. 20, 4099-4099 (1992)  
 JOURNAL 92375706  
 MEDLINE  
 FEATURES Location/Qualifiers

source  
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 /db\_xref="taxon:10090"  
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 /gene="Igk"  
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 /function="variable region"  
 /note="putative"  
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 /product="immunoglobulin kappa-chain"  
 /protein\_id="AAA39079.1"  
 /db\_xref="GI:554148"  
 /translation="GIMLEWISASRGDIVLTOSPATLSVTPGDKVSLSCRASOSISNY  
 LHWYQKSHESPRLLIKYVSQSIGIPSRFSGSGTDTLSINSVETEDFGMYFCQQ  
 SNSWPHTFGSGTKLEIKRADA"  
 BASE COUNT 96 a 90 c 86 g 98 t  
 ORIGIN

Query Match 89.1%; Score 29.4; DB 10; Length 370;  
 Best Local Similarity 96.8%; Pred. No. 0.008;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaacttctctacac 33  
 |||||  
 Db 108 GCCACGCAAAAGTATTAGCAACTACCTACAC 138

## RESULT 15

MMU235976  
 LOCUS MMU235976 845 bp DNA linear ROD 03-AUG-1999  
 DEFINITION Mus musculus IgV kappa fp23r gene.  
 ACCESSION AJ235976  
 VERSION AJ235976.1 GI:5327168  
 KEYWORDS IgV kappa gene; immunoglobulin; kappa light chain; variable region.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 845)  
 AUTHORS Schaeble K.F., Thiele R., Bensch A., Brensing-Kueppers J., Heim V.,  
 Kirschbaum T., Lamm R., Ohnrich M., Pourrajabi S.,  
 Roeschenthaler F., Schwendinger J., Wichelhaus D. and Zocher  
 Zschau H.G.  
 TITLE Characteristics of the immunoglobulin V kappa genes, pseudogenes,  
 relics and orphans in the mouse genome  
 Eur. J. Immunol. 29 (7), 2082-2086 (1999)  
 JOURNAL 99354924  
 MEDLINE  
 REFERENCE 2 (bases 1 to 845)  
 AUTHORS Kirschbaum T.

TITLE Direct Submission  
 JOURNAL Submitted (23-DEC-1998) T. Kirschbaum, Adolf-Butenandt-Institut  
 fuer, Physiologische Chemie, Schillerstr. 44, D-80336 Muenchen, FRG  
 FEATURES Location/Qualifiers  
 source  
 1..845  
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 68..73  
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 compared to other V kappa 23 genes; the homology ends with  
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 /db\_xref="GI:5327169"  
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 chain"  
 387..>388  
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 /number=2  
 BASE COUNT 246 a 173 c 157 g 269 t  
 ORIGIN  
 Query Match 89.1%; Score 29.4; DB 10; Length 845;  
 Best Local Similarity 96.8%; Pred. No. 0.008;  
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 ggcacgcaaaagtattagcaacttctctacac 33  
 |||||  
 Db 469 GCCACGCAAAAGTATTAGCAACTACCTACAC 499

Search completed: August 21, 2002, 10:49:58  
 Job time: 9813 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 09:56:01 ; Search time 6260.2 seconds  
(without alignments)  
71.148 Million cell updates/sec

Title: US-09-339-922A-109  
Perfect score: 33  
Sequence: 1 caggccagcaagattagcaacttctacac 33

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: em\_estba:\*
  - 2: em\_esthum:\*
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  - 4: em\_estnu:\*
  - 5: em\_estov:\*
  - 6: em\_estpl:\*
  - 7: em\_estro:\*
  - 8: em\_hic:\*
  - 9: gb\_esti:\*
  - 10: gb\_est2:\*
  - 11: gb\_hic:\*
  - 12: gb\_gss:\*
  - 13: em\_gss\_hum:\*
  - 14: em\_gss\_inv:\*
  - 15: em\_gss\_pln:\*
  - 16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	ID Description
c 1	29.4	89.1	517 12 A2846516
	29.4	89.1	772 10 B1105452
	27.8	84.2	202 10 BG144658
	27.8	84.2	738 10 BF582153
	27.8	84.2	833 10 BG966582
	27.8	84.2	835 10 B083006
	27.8	84.2	949 10 BF579007
c 9	22.4	67.9	371 10 T27081
	22.4	67.9	391 10 W81641
c 10	22.4	67.9	414 9 AA569320
	22.4	67.9	478 10 R51067
c 12	22.4	67.9	519 10 B518335
	22.4	67.9	520 9 AU158038
c 14	22.4	67.9	674 10 BG198873
	21.6	65.5	239 10 BF756995
c 16	21.6	65.5	740 10 BG397970
	21.6	65.5	823 10 BG686045

18	20.8	63.0	549	9	AW642646
19	20.8	63.0	556	10	BM004705
20	20.6	62.4	459	9	BB852173
c 21	20.6	62.4	470	10	BE848989
	20.6	62.4	639	10	BE382000
22	20.6	62.4	648	9	BB620078
23	20.6	62.4	648	9	BB620078
24	20.6	62.4	662	9	BB630699
25	20.6	62.4	745	10	BG975083
26	20.4	61.8	343	10	BE815288
27	20.4	61.8	406	10	R41697
28	20.4	61.8	591	9	AV756066
c 29	20.4	61.8	653	9	BB626942
	20.2	61.2	168	10	BG737726
31	20.2	61.2	202	9	AI010320
32	20.2	61.2	213	12	A2660650
33	20.2	61.2	532	10	BF838031
c 34	20.2	61.2	878	10	BF786148
	20.2	61.2	1005	12	CNS048VJ
36	20.2	60.6	208	9	BS575049
37	20.2	60.6	250	10	BG231232
38	20.2	60.6	290	10	BG058466
39	20.2	60.6	311	9	AW405931
40	20.2	60.6	324	9	AV693705
41	20.2	60.6	352	9	AV690753
42	20.2	60.6	367	9	AV694860
43	20.2	60.6	374	9	AV695931
44	20.2	60.6	398	10	M89293
45	20.2	60.6	413	9	AW406440

ALIGNMENTS

RESULT 1  
AZ846516/c

LOCUS 517 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0146D17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0146D17 R, DNA sequence.

ACCESSION AZ846516

VERSION AZ846516.1 GI:13016424

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 517)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0146 row: D column: 17  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 517.  
Location/Qualifiers  
1. 517  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0146D17"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"



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LOCUS      BF582153      738 bp      mRNA      linear      EST 12-DEC-2000
DEFINITION 602099743F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219402 5',
            mRNA sequence.
ACCESSION   BF582153
VERSION     BF582153.1 GI:11655865
KEYWORDS    EST.
SOURCE      house mouse.
            Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 738)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9801 row: f column: 11
            High quality sequence stop: 714.
            Location/Qualifiers
                1..738
                /organism="Mus musculus"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:4219402"
                /clone_lib="NCI_CGAP_Co24"
                /lab_host="DH10B (T1 phage-resistant)"
                /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 1.6 kb. Constructed by Life
                Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      210 a      189 c      172 g      167 t
ORIGIN
source
Query Match      84.2%; Score 27.8; DB 10; Length 738;
Best Local Similarity 93.5%; Pred. No. 0.3;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 gccacgccaagaattattagcaactctctacac 33
|||||
Db 144 GCCACGCCAAGTATTAGCAACACCTACAC 174

RESULT 5
BG966582
LOCUS      BG966582      833 bp      mRNA      linear      EST 12-JUN-2001
DEFINITION 602834412F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988955 5',
            mRNA sequence.
ACCESSION   BG966582
VERSION     BG966582.1 GI:14354219
KEYWORDS    EST.
SOURCE      house mouse.
            Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 833)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11047 row: p column: 06
            High quality sequence stop: 769.
            Location/Qualifiers
                1..833
                /organism="Mus musculus"
                /strain="FVB/N-3"
                /db_xref="taxon:10090"
                /clone="IMAGE:5006453"
                /clone_lib="NCI_CGAP_Mam2"
                /tissue_type="tumor, biopsy sample"
                /dev_stage="5 months"
                /lab_host="DH10B"
                /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                Library constructed by Life Technologies. Investigator
                providing samples: Gilbert Smith, NIH"

BASE COUNT      225 a      229 c      186 g      195 t
ORIGIN
source
Query Match      84.2%; Score 27.8; DB 10; Length 833;
Best Local Similarity 93.5%; Pred. No. 0.31;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 gccacgccaagaattattagcaactctctacac 33
|||||
Db 136 GCCACGCCAAGTATTAGCAACACCTACAC 166

RESULT 6
BI083006
LOCUS      BI083006      835 bp      mRNA      linear      EST 20-JUN-2001
DEFINITION 602874524F2 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5006453 5',
            mRNA sequence.
ACCESSION   BI083006
VERSION     BI083006.1 GI:14501336
KEYWORDS    EST.
SOURCE      house mouse.
            Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 835)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11002 row: q column: 04
            High quality sequence stop: 830.
            Location/Qualifiers
                1..833
                /organism="Mus musculus"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:4988955"
                /clone_lib="NCI_CGAP_Co24"
                /lab_host="DH10B (T1 phage-resistant)"
                /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 1.6 kb. Constructed by Life
                Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      227 a      227 c      186 g      193 t
ORIGIN
source
Query Match      84.2%; Score 27.8; DB 10; Length 833;
Best Local Similarity 93.5%; Pred. No. 0.31;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 gccacgccaagaattattagcaactctctacac 33
|||||
Db 136 GCCACGCCAAGTATTAGCAACACCTACAC 166

RESULT 6
BI083006
LOCUS      BI083006      835 bp      mRNA      linear      EST 20-JUN-2001
DEFINITION 602874524F2 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5006453 5',
            mRNA sequence.
ACCESSION   BI083006
VERSION     BI083006.1 GI:14501336
KEYWORDS    EST.
SOURCE      house mouse.
            Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 835)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11047 row: p column: 06
            High quality sequence stop: 769.
            Location/Qualifiers
                1..835
                /organism="Mus musculus"
                /strain="FVB/N-3"
                /db_xref="taxon:10090"
                /clone="IMAGE:5006453"
                /clone_lib="NCI_CGAP_Mam2"
                /tissue_type="tumor, biopsy sample"
                /dev_stage="5 months"
                /lab_host="DH10B"
                /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
                Library constructed by Life Technologies. Investigator
                providing samples: Gilbert Smith, NIH"

BASE COUNT      225 a      229 c      186 g      195 t
ORIGIN
source

```

found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM11002 row: q column: 04  
 High quality sequence stop: 830.

#### FEATURES

Location/Qualifiers  
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 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4988955"  
 /clone\_lib="NCI\_CGAP\_Co24"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: Colon; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.6 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

#### BASE COUNT

227 a 227 c 186 g 193 t

#### ORIGIN

Query Match 84.2%; Score 27.8; DB 10; Length 833;  
 Best Local Similarity 93.5%; Pred. No. 0.31;  
 Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 gccacgccaagaattattagcaactctctacac 33  
 |||||  
 Db 136 GCCACGCCAAGTATTAGCAACACCTACAC 166

#### RESULT

BI083006  
 LOCUS BI083006 835 bp mRNA linear EST 20-JUN-2001  
 DEFINITION 602874524F2 NCI\_CGAP\_Mam2 Mus musculus cDNA clone IMAGE:5006453 5',  
 mRNA sequence.  
 ACCESSION BI083006  
 VERSION BI083006.1 GI:14501336  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 835)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM11047 row: p column: 06  
 High quality sequence stop: 769.  
 Location/Qualifiers  
 1..835  
 /organism="Mus musculus"  
 /strain="FVB/N-3"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5006453"  
 /clone\_lib="NCI\_CGAP\_Mam2"  
 /tissue\_type="tumor, biopsy sample"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Gilbert Smith, NIH"

#### FEATURES

Location/Qualifiers  
 1..835  
 /organism="Mus musculus"  
 /strain="FVB/N-3"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5006453"  
 /clone\_lib="NCI\_CGAP\_Mam2"  
 /tissue\_type="tumor, biopsy sample"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Library constructed by Life Technologies. Investigator  
 providing samples: Gilbert Smith, NIH"

#### BASE COUNT

225 a 229 c 186 g 195 t

#### ORIGIN

source

```

Query Match      84.2%; Score 27.8; DB 10; Length 835;
Best Local Similarity 93.5%; Pred. No. 0.31;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaacttcctacac 33
|||||
Db 150 GGCCAGCCAAAGTATTAGCAACAACCTACAC 180

RESULT 7
BF579007
LOCUS BF579007 949 bp mRNA linear EST 12-DEC-2000
DEFINITION 602096124F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4216180 5',
mRNA sequence.
ACCESSION BF579007
VERSION BF579007.1 GI:11652719
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 949)
/note="Vector: lafmid BA; Site_1: HindIII; Site_2: NotI;
Normalized infant brain cDNA library made by Dr. M. Soares
(Columbia University), oligo-dT primed and directionally
cloned between HindIII (5') and NotI (3') sites "
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9792 row: p column: 05
High quality sequence start: 9
High quality sequence stop: 730.
Location/Qualifiers
1. .949
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4216180"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 278 a 241 c 210 g 220 t
ORIGIN

Query Match      84.2%; Score 27.8; DB 10; Length 949;
Best Local Similarity 93.5%; Pred. No. 0.32;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaacttcctacac 33
|||||
Db 149 GGCCAGCCAAAGTATTAGCAACAACCTACAC 179

RESULT 8
T27081
LOCUS T27081 371 bp mRNA linear EST 25-JUL-1996
DEFINITION NIBT258G01 Infant brain, LLNL array of Dr. M. Soares INIB Homo
sapiens cDNA clone LLAB258G01 3'end, mRNA sequence.
ACCESSION T27081
VERSION T27081.1 GI:774123
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 371)
Sikela, J.M.
Human cDNAs from infant brain
Unpublished (1993)
Contact: Sikela JM
Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
Fax: 3032707097
Email: nikki@tally.uchsc.edu
Seq primer: -21M13 Universal.
Location/Qualifiers
1. .371
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="LLAB258G01"
/clone_lib="Infant brain, LLNL array of Dr. M. Soares
INIB"
/note="Vector: lafmid BA; Site_1: HindIII; Site_2: NotI;
Normalized infant brain cDNA library made by Dr. M. Soares
(Columbia University), oligo-dT primed and directionally
cloned between HindIII (5') and NotI (3') sites "

BASE COUNT 101 a 72 c 90 g 104 t 4 others
ORIGIN

Query Match      67.9%; Score 22.4; DB 10; Length 371;
Best Local Similarity 81.2%; Pred. No. 42;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 cagccagccaaagtattagcaacttcctaca 32
|||||
Db 241 CAGCGAGCAAATTTAATAGCAACTTCCTCCA 272

RESULT 9
W81641/c
LOCUS W81641 391 bp mRNA linear EST 17-OCT-1996
DEFINITION z488e04.r1 Soares fetal heart_NDHH19W Homo sapiens cDNA clone
IMAGE:347742 5' similar to PIR:S22934 S22934 testis-specific
protein ;, mRNA sequence.
ACCESSION W81641
VERSION W81641.1 GI:1392680
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 391)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 479 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 373.
Location/Qualifiers
1. .391
/organism="Homo sapiens"
/db_xref="GDB:1273117"

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Reference: Krizman et al. (1996) Cancer Research  
56:5380-5383."

BASE COUNT 118 a 99 c 87 g 110 t  
ORIGIN

Query Match 67.9%; Score 22.4; DB 9; Length 414;  
Best Local Similarity 81.2%; Pred. No. 43;  
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 caggcagccaaagtattagcaactctctaca 32  
||||| ||| || || ||||| ||||| ||  
DB 224 CAGCGAGCAAAATTAAATAGCAACTTCTCCA 193

RESULT 11

R51067  
LOCUS R51067 478 bp mRNA linear EST 18-MAY-1995  
DEFINITION Y64b01.s1 Soares infant brain IN1B Homo sapiens cDNA clone  
IMAGE:37385 3' similar to SP:S22934 S22934 TESTIS-SPECIFIC PROTEIN  
;; mRNA sequence.

ACCESSION R51067  
VERSION R51067.1 GI:812969  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 478)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman  
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,  
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston  
R., Williamson,A., Wohldmann,P. and Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 1133  
High quality sequence stops: 384 Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1133 Std Error: 0.00  
Seq primer: Promega -21m13  
High quality sequence stop: 384.  
Location/Qualifiers  
1. .478  
/organism="Homo sapiens"  
/db\_xref="GDB:409886"  
/db\_xref="taxon:9606"  
/clone="IMAGE:37385"  
/clone\_lib="Soares infant brain IN1B"  
/sex="female"  
/rev\_stage="73 days post natal"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: whole brain; Vector: Lfamid BA; Site1: Not  
I - oligo(dT) primer [5',  
ACTGGAGAATTCGGCCGAGGAATTTTCTTTTCTTTT 3'];  
double-stranded cDNA was ligated to Hind III adaptors  
(pharmacia), digested with Not I and directionally cloned  
into the Not I and Hind III sites of the Lfamid BA vector.  
Library went through one round of normalization. Library  
constructed by Bento Soares and M.Patima Bonaldo."

BASE COUNT 115 a 95 c 124 g 137 t 7 others  
ORIGIN

Query Match 67.9%; Score 22.4; DB 10; Length 478;  
Best Local Similarity 81.2%; Pred. No. 45;

Matches 26; Conservative 0; Mismatches. 6; Indels 0; Gaps 0;

QY 1 caggccagcacaagattagcaactctctaca 32  
||||| ||| || || ||||| ||||| ||

Db 251 CAGCGGAGCAAAATTAATAGCAACTTCTCTCCA 282

## RESULT 12

BI518335  
LOCUS  
DEFINITION  
519 bp mRNA linear EST 29-AUG-2001  
603042223T1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5182660 3',  
mRNA sequence.

ACCESSION BI518335

VERSION BI518335.1 GI:15343127

KEYWORDS EST.

SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 519)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-re@mail.nih.gov](mailto:cgabbs-re@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM1455 row: n column: 05

High quality sequence start: 30

High quality sequence stop: 519.

## FEATURES

source

1..519

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5182660"

/clone\_lib="NIH\_MGC\_116"

/lab\_host="DH10B"

/note="Organ: pooled colon, kidney, stomach; Vector:

pcmv-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA

source anonymous pool of 3 colons, age 26 yo male, 49 yo

female, 71 yo male colon; 46 yo male kidney, and pool of 2

stomachs, 62 yo male and 70 yo female. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.4 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

023. Note: this is a NIH\_MGC Library."

BASE COUNT 127 a 125 c 144 g 123 t

## ORIGIN

Query Match

Best Local Similarity 67.9%; Score 22.4; DB 10; Length 519;

Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 caggccagcacaagattagcaactctctaca 32

||||| ||| || || ||||| ||||| ||

Db 201 CAGCGGAGCAAAATTAATAGCAACTTCTCTCCA 232

## RESULT 13

AU158038  
LOCUS  
DEFINITION  
520 bp mRNA linear EST 25-OCT-2000  
AU158038 PLAC1 Homo sapiens cDNA clone PLACE1010661 3', mRNA  
sequence.

ACCESSION AU158038

VERSION AU158038.1 GI:11019559

## KEYWORDS

SOURCE

Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 520)

Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,

Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano

, S. and Isogai, T.).

HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S.,

Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura

, Y., Nagai, T., Sugano, S., Isogai, T.)

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3951

Fax: 81-438-52-3952

Email: [genomics@hri.co.jp](mailto:genomics@hri.co.jp)

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

FEATURES

source

1..520

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="PLACE1010661"

/clone\_lib="PLAC1"

/tissue\_type="placenta"

/note="Vector: pWE18SF13"

BASE COUNT 132 a 124 c 115 g 133 t 16 others

ORIGIN

Query Match

Best Local Similarity 67.9%; Score 22.4; DB 9; Length 520;

Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 caggccagcacaagattagcaactctctaca 32

||||| ||| || || ||||| ||||| ||

Db 245 CAGCGGAGCAAAATTAATAGCAACTTCTCTCCA 276

||||| ||| || || ||||| ||||| ||

RESULT 14

LOCUS

BI198873/c

DEFINITION

674 bp mRNA linear EST 21-APR-2001

BI198873

ACCESSION

BI198873.1 GI:13720560

VERSION

EST.

KEYWORDS

human.

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 674)

Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,

Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,

, Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith

, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher

, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

21227151

CONTACT: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: [scain@athersys.com](mailto:scain@athersys.com)

High quality sequence stop: 674.



FEATURES  
source

Location/Qualifiers  
1. .674  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athensys RAGE Library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."  
175 a 187 c 147 g 164 t 1 others  
BASE COUNT 175 a 187 c 147 g 164 t  
ORIGIN

Query Match 67.9%; Score 22.4; DB 10; Length 674;  
Best Local Similarity 81.2%; Pred. No. 49;  
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 caggccagccaaagtattagcaacttctctaca 32  
||||| ||| || || ||||| ||||| ||  
DB 358 CAGGCGGCAAAATTAAATAGCAACTTCTCCA 327

## RESULT 15

BF756995  
LOCUS BF756995 239 bp mRNA linear EST 12-JAN-2001  
DEFINITION MR0-CT0451-021100-017-h04 CT0451 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF756995  
VERSION BF756995.1 GI:12104895  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 239)  
AUTHORS Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R., Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldman G.H., Carvalho A.F., Matsukuma A., Baia G.S., Simpson D.H., Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and Simpson A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0&t2=MR0-CT0451-021100-017-h04&t3=2000-11-02&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 11  
High quality sequence stop: 239.  
Location/Qualifiers  
1. .239  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="CT0451"  
/dev\_stage="Adult"

FEATURES  
source

/note="Organ: colon; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue

BASE COUNT 59 a 79 c 50 g 51 t  
ORIGIN  
Query Match 65.5%; Score 21.6; DB 10; Length 239;  
Best Local Similarity 85.7%; Pred. No. 78;  
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3 ggccagccaaagtattagcaacttctcta 30  
||||| || ||||| ||||| ||  
DB 173 GGCCAGTCAGAGTATTAGCAACTACTTA 200  
Search completed: August 21, 2002, 09:56:05  
Job time: 9328 sec

mRNA and cDNA amplification were performed under low stringency conditions."

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:40 ; Search time 754.01 Seconds  
(without alignments)  
75.142 Million cell updates/sec

Title: US-09-339-922a-109  
Perfect score: 33  
Sequence: 1 cagcccgccaaagtattagcaacttctctacac 33

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_032802.\*  
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*  
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11: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*  
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13: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.\*  
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16: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.\*  
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20: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	33	22	AAF28238
2	31.4	95.2	39	19	AAV49868
3	31.4	95.2	39	22	AAF28224
4	29.8	90.3	33	22	AAF28237
5	29.8	90.3	39	19	AAV49848
6	29.8	90.3	39	22	AAF28204
7	29.8	90.3	321	19	AAV49843
8	29.8	90.3	321	19	AAV49821
9	29.8	90.3	321	19	AAV49823

10	29.8	90.3	321	22	AAH74624	DNA encoding light
11	29.8	90.3	321	22	AAH74626	DNA encoding light
12	29.8	90.3	321	22	AAF28176	Vitaxin light chain
13	29.8	90.3	321	22	AAF28178	Antibody LM609 lig
14	29.8	90.3	321	22	AAF28199	DNA encoding light
15	27.8	84.2	101	20	AAV71825	Alpha-v beta-3 Mab
16	27.8	84.2	108	20	AAV71816	Alpha-v beta-3 Mab
17	27.8	84.2	128	13	AAQ26786	Oligomer jbl7 used
18	27.8	84.2	128	22	AAF56750	Humanised CMV5 ant
19	27.8	84.2	315	20	AAV71803	Humanised CMV5 ant
20	27.8	84.2	315	20	AAV71805	Humanised anti- $\alpha$ lp
21	27.8	84.2	321	20	AAV71800	Humanised anti- $\alpha$ lp
22	27.8	84.2	324	17	AAV33446	EGF receptor chime
23	27.8	84.2	324	20	AAV71798	Murine vitronectin
24	27.8	84.2	338	20	AAV71802	Vitronectin $\alpha$ -
25	27.8	84.2	381	15	AAQ64167	Sequence of mouse
26	27.8	84.2	381	22	AAF56747	Murine CMV5 antibo
27	27.8	84.2	5238	11	AAQ04654	Plasmid pBT111 enc
28	26.8	81.2	72	19	AAV49830	LM609 grafted anti
29	26.8	81.2	72	22	AAF28185	Oligonucleotide #7
30	26.8	81.2	75	19	AAV49839	LM609 grafted anti
31	26.8	81.2	75	22	AAH74633	PCR primer for lig
32	26.8	81.2	75	22	AAF28194	Grafted light chain
33	26.2	79.4	342	22	AAH27466	Murine coding sequ
34	24.6	74.5	381	21	AAZ5242	Mouse anti-verotox
35	24.6	74.5	381	21	AAZ5244	Humanised anti-ver
36	24.6	74.5	651	21	AAA44346	Human secreted exp
37	24.6	74.5	8858	20	AAZ10202	Expression vector
38	24.6	74.5	8858	24	AAH43777	Chi220 light chain
39	23	69.7	363	17	AAH38510	Light chain coding
40	23	69.7	415	21	AAH00904	Humanised antibody
41	23	69.7	415	21	AAH01262	Mouse monoclonal a
42	22.4	67.9	520	22	AAH13081	Human CDNA clone (
43	22.4	67.9	1585	22	AAH15219	Human CDNA sequenc
44	22.4	67.9	1864	22	AAH58470	Human polynucleoti
45	22.4	67.9	1900	22	AAH15178	Human CDNA sequenc

## ALIGNMENTS

RESULT 1  
AAF28238  
ID AAF28238 standard; DNA; 33 BP.  
XX  
AC AAF28238;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE DNA encoding enhanced LM609 VH CDR1 peptide.  
XX  
KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;  
XX inflammatory; cancer; retina; restenosis; osteoporosis; SS.  
XX Unidentified.  
XX  
XX WO200078815-A1.  
XX  
XX 28-DEC-2000.  
XX  
XX 23-JUN-2000; 2000WO-US17454.  
XX  
XX 24-JUN-1999; 99US-0339922.  
XX  
XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX  
XX Huse WD, Wu H;  
XX  
XX WPI; 2001-050110/06.  
XX  
XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -  
 XX  
 PS Claim 14; Page 45; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 33 BP; 11 A; 11 C; 5 G; 6 T; 0 other;  
 Query Match 100.0%; Score 33; DB 22; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 caggccagcgaagtagcaacttctctacac 33  
 Db |||||||||||||||||||||||||||||  
 1 caggccagcgaagtagcaacttctctacac 33  
 RESULT 2  
 AAV49868  
 ID AAV49868 standard; DNA; 39 BP.  
 XX  
 AC AAV49868;  
 XX  
 DT 02-NOV-1998 (first entry)  
 XX  
 DE LM609 grafted antibody V-L region CDR1 DNA fragment #2.  
 XX  
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;  
 KW complementarity determining region; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9833919-A2.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 30-JAN-1998; 98WO-US01826.  
 XX  
 PR 30-JAN-1997; 97US-0791391.  
 XX  
 PA (IXSY-) IXSYS INC.  
 XX  
 PI Glaser SM, Huse WD;  
 XX  
 DR WPI; 1998-437472/37.  
 DR P-PSDB; AAW76031.  
 XX  
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX  
 PS Disclosure; Page 42; 129pp; English.  
 XX  
 CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal  
 CC antibody LM609 heavy and light chain variable region. LM609 and the  
 CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used  
 CC to inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,  
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically  
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
 CC antibodies contain non-murine framework regions so are suitable for use  
 CC in humans. Enhanced types of LM609 have affinity more than 90 times  
 CC greater than that of parent the parent antibody.  
 XX  
 SQ Sequence 39 BP; 12 A; 10 C; 7 G; 10 T; 0 other;  
 Query Match 95.2%; Score 31.4; DB 19; Length 39;  
 Best Local Similarity 97.0%; Pred. No. 0.00014;  
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 caggccagcgaagtagcaacttctctacac 33  
 Db |||||||||||||||||||||||||  
 1 caggccagcgaagtagcaacttctctacac 33  
 RESULT 3  
 AAF28224  
 ID AAF28224 standard; DNA; 39 BP.  
 XX  
 AC AAF28224;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE DNA encoding mutant VL CDR1 peptide.  
 XX  
 KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 DR WPI; 2001-050110/06.  
 XX  
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Page 42; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 39 BP; 12 A; 10 C; 7 G; 10 T; 0 other;  
 Query Match 95.2%; Score 31.4; DB 22; Length 39;  
 Query Match 95.2%; Score 31.4; DB 22; Length 39;

Best Local Similarity 97.0%; Pred. No. 0.00014;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 caggccagcacaagattaggcaacttcctacac 33  
|||||  
Db 1 caggccagcacaagattaggcaacttcctacac 33

## RESULT 4

AAAF28237

ID AAF28237 standard; DNA; 33 BP.

XX AAF28237;

DT 03-APR-2001 (first entry)

XX DNA encoding enhanced 6H6Lh light chain CDR1.

DE LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
XX Unidentified.

OS

PN WO200078815-A1.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX 24-JUN-1999; 99US-0339922.

PR (MOLE-) APPLIED MOLECULAR EVOLUTION.  
PA Huse WD, Wu H;

PI

XX WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis -

XX Claim 16; Page 107; 132pp; English.  
XX The present invention relates to enhanced LM609 grafted antibodies

CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
CC their functional fragments. The antibodies or their functional  
CC fragments can be used in the diagnosis and treatment of  
CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
CC diseases (such as psoriasis and chronic articular rheumatism),  
CC disorders associated with inappropriate or inopportune invasion of  
CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
CC diseases (such as macular degeneration), restenosis and  
CC osteoporosis.

XX Sequence 33 BP; 12 A; 12 C; 5 G; 4 T; 0 other;  
SQ

Query Match 90.3%; Score 29.8; DB 22; Length 33;

Best Local Similarity 93.9%; Pred. No. 0.0007; 2; Indels 0; Gaps 0;

Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagcacaagattaggcaacttcctacac 33

|||||

Db 1 caggccagcacaagattaggcaacttcctacac 33

## RESULT 5

AAV49848

ID AAV49848 standard; DNA; 39 BP.

XX

AC AAV49848;

XX

XX 02-NOV-1998 (first entry)

XX LM609 grafted antibody V-L region CDR1 DNA fragment #1.

DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis; primer; V-L region; CDR;  
KW complementarity determining region; ss.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US01826.

XX 30-JAN-1997; 97US-0791391.

XX (IXSY-) IXSYS INC.

XX Glaser SM, Huse WD;

XX WPI; 1998-437472/37.

XX P-PSDB; AAW76011.

XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
PT integrin - and related grafted antibodies based on murine monoclonal  
PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
PT angiogenesis or restenosis

XX Disclosure; Page 40; 129pp; English.

XX

CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal  
CC antibody LM609 heavy and light chain variable region. LM609 and the  
CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used  
CC to inhibit binding of alphavbeta3 to a ligand and thus block  
CC integrin-mediated signal transduction. This is useful in the treatment,  
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically  
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
CC antibodies contain non-murine framework regions so are suitable for use  
CC in humans. Enhanced types of LM609 have affinity more than 90 times  
CC greater than that of parent the parent antibody.

XX Sequence 39 BP; 13 A; 12 C; 7 G; 7 T; 0 other;  
SQ

Query Match

Best Local Similarity 90.3%; Score 29.8; DB 19; Length 39;

Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caggccagcacaagattaggcaacttcctacac 33.

|||||

Db 1 caggccagcacaagattaggcaacttcctacac 33

## RESULT 6

AAAF28204

ID AAF28204 standard; DNA; 39 BP.

XX

AC AAF28204;

XX

DT 03-APR-2001 (first entry)

XX

DE DNA encoding LM609 VL CDR1 peptide.

XX

KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;

KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.

```

XX OS Unidentified.
XX PN WO200078815-A1.
XX PD 28-DEC-2000.
XX PF 23-JUN-2000; 2000WO-US17454.
XX PR 24-JUN-1999; 99US-0339922.
XX PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX PI Huse WD, Wu H;
XX DR WPI; 2001-050110/06.
XX PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
XX PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
XX PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
XX PT osteoporosis -
XX PS Disclosure; Page 40; 132pp; English.
XX CC The present invention relates to enhanced LM609 grafted antibodies
XX CC exhibiting selective binding affinity to alphavbeta3 integrin or
XX CC their functional fragments. The antibodies or their functional
XX CC fragments can be used in the diagnosis and treatment of
XX CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory
XX CC diseases (such as psoriasis and chronic articular rheumatism),
XX CC disorders associated with inappropriate or inopportune invasion of
XX CC vessels (such as diabetic retinopathy, neovascular glaucoma and
XX CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
XX CC diseases (such as macular degeneration), restenosis and
XX CC osteoporosis.
XX SQ Sequence 39 BP; 13 A; 12 C; 7 G; 7 T; 0 other;

Query Match 90.3%; Score 29.8; DB 22; Length 39;
Best Local Similarity 93.9%; Pred. No. 0.00072;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagcacaagtattagcaacttctacac 33
   |||||||
Db 1 caggccagcacaagtattagcaaccctacac 33

RESULT 7
AAV49843
ID AAV49843 standard; DNA; 321 BP.
XX AC
XX AC AAV49843;
XX DT 02-NOV-1998 (first entry)
XX DE LM609 antibody light chain variable region DNA grafted fragment.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 1..321
XX FT /*tag= a
XX FT /product= "LM609 grafted antibody light chain variable
XX FT region"
XX FT /note= "partial sequence, no start or stop codon given"
XX FT
XX FT
XX FT

```

```

PN WO9833919-A2.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-US01826.
XX PR 30-JAN-1997; 97US-0791391.
XX PA (IXSY-) IXSYS INC.
XX PI Glaser SM, Huse WD;
XX DR WPI; 1998-437472/37.
XX DR P-PSDB; AAW76006.
XX PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
XX PT integrin - and related grafted antibodies based on murine monoclonal
XX PT LM609, also related nucleic acid, used to treat, prevent or diagnose
XX PT angiogenesis or restenosis
XX PS Claim 24; Fig 7; 129pp; English.
XX CC This sequence encodes a LM609 grafted antibody variable light chain
XX CC region. LM609 and the antibody vitaxin bind selectively to integrin
XX CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
XX CC and thus block integrin-mediated signal transduction. This is useful in
XX CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
XX CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
XX CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
XX CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
XX CC etc.). The antibodies contain non-murine framework regions so are
XX CC suitable for use in humans. Enhanced types of LM609 have affinity more
XX CC than 90 times greater than that of parent the parent antibody.
XX SQ Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match 90.3%; Score 29.8; DB 19; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagcacaagtattagcaacttctacac 33
   |||||||
Db 70 caggccagcacaagtattagcaaccctacac 102

RESULT 8
AAV49821
ID AAV49821 standard; DNA; 321 BP.
XX AC
XX AC AAV49821;
XX DT 02-NOV-1998 (first entry)
XX DE Vitaxin antibody light chain variable region DNA.
XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX KW macular degeneration; osteoporosis; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 1..321
XX FT /*tag= a
XX FT /product= "vitaxin antibody light chain variable region"
XX FT /note= "partial sequence, no start or stop codon given"
XX FT
XX FT
XX FT

```

PR	30-JAN-1997;	97US-0791391.
XX	(IXSY-) IXSYS INC.	
XX	Glaser SM,	Huse WD;
PI		
XX	WFI; 1998-437472/37.	
DR	P-PSDB; AAU75004.	
XX		
PT	Humanised antibody, Vitaxin, that binds selectively to alphavbeta3	
XX	interin - and related grafted antibodies based on murine monoclonal	
PT	LM609, also related nucleic acid, used to treat, prevent or diagnose	
PT	angiogenesis or restenosis	
XX		
PS	Claim 40; Fig 2b; 129pp; English.	
XX		
CC	This sequence encodes the LM609 antibody variable light chain region.	
CC	LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3	
CC	and can be used to inhibit binding of alphavbeta3 to a ligand and thus	
CC	block integrin-mediated signal transduction. This is useful in the	
CC	treatment, prevention and diagnosis of alphavbeta3-mediated disease,	
CC	specifically angiogenesis and restenosis (but also e.g. (non-)immune	
CC	inflammation, diabetic retinopathy, neovascular glaucoma, cancer,	
CC	psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis	
CC	etc.). The antibodies contain non-murine framework regions so are	
CC	suitable for use in humans. Enhanced types of LM609 have affinity more	
CC	than 90 times greater than that of parent the parent antibody.	
XX		
SQ	Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;	
Query Match	90.3%;	Score 29.8; DB 19; Length 321;
Best Local Similarity	93.9%;	Pred. No. 0.0011;
Matches 31; Conservative	0;	Mismatches 2; Indels 0; Gaps
Qy	1 caggccgacccaagatttagcaacttcctcac 33	
Dd		
Db	70 caggccgacccaagatttagcaaccacctcac 102	
RESULT 10		
AAH74624		
ID	AAH74624 standard; DNA; 321 BP.	
XX		
AC	AAH74624;	
XX		
Dt	15-OCT-2001 (first entry)	
XX		
DE	DNA encoding light chain variable region of LM609 grafted antibody.	
XX		
Kw	Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;	
KW	chronic articular rheumatism; psoriasis; diabetic retinopathy;	
KW	neovascular glaucoma; capillary proliferation; atherosclerotic plaque;	
KW	cancer; ss.	
XX		
OS	Synthetic.	
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..321
FT		/*tag= a
FT		/transl_except= "(pos: 145..147, aa: Xaa)"
FT		/note= "Xaa is unspecified"
XX		
PN	US2001011125-A1.	
XX		
PD	02-AUG-2001.	
XX		
PF	30-JAN-1997; 97US-0790540.	
XX		
PR	30-JAN-1997; 97US-0790540.	
XX	(HUSE/) HUSE W D.	

```

XX PI Huse WD;
XX WPI; 2001-496171/54.
DR P-PSDB; AAG63588.
XX
PT New LM609 grafted antibody exhibiting selective binding affinity to
PT alphavbeta3, comprising at least one LM609 grafted heavy and light
PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT disorders or cancer
XX
PS Claim 6; Fig 1B; 25pp; English.
XX
CC The present sequence encodes the light chain variable region of the
CC grafted monoclonal antibody LM609. LM609 is a murine antibody which
CC specifically recognises the integrin alphavbeta3, and inhibits its
CC functional activity. The LM609 grafted antibody has the
CC complementarity determining regions (CDRs) substituted into a non-murine
CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC polypeptides and fragments are useful in diagnostic and therapeutic
CC purposes, such as in the production of LM609 grafted antibodies and
CC fragments having binding specificity and inhibitory activity against
CC the integrin alphavbeta3. The antibody can be used for the diagnosis
CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC disorders, chronic articular rheumatism, psoriasis, disorders
CC associated with inappropriate or inopportune invasion of vessels such
CC as diabetic retinopathy, neovascular glaucoma and capillary
CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC binding activity of alphavbeta3 that are necessary for progression of
CC an alphavbeta3-mediated disease.
XX
SQ Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match 90.3%; Score 29.8; DB 22; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagcagcaagtattagcaacttctctacac 33
Db ||||||||||||||||||| |||||
70 caggccagcagcaagtattagcaaccctctacac 102

RESULT 11
AAH74626
ID AAH74626 standard; DNA; 321 BP.
XX
AC AAH74626;
XX
DT 15-OCT-2001 (first entry)
DE DNA encoding light chain variable region of LM609 antibody.
XX
KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;
KW chronic articular rheumatism; psoriasis; diabetic retinopathy;
KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;
KW cancer; ss.
XX
OS Mus sp.
XX
PN US2001011125-A1.
XX
PD 02-AUG-2001.
XX
PF 30-JAN-1997; 97US-0790540.
XX
PR 30-JAN-1997; 97US-0790540.
XX
PA (HUSE/) HUSE W D.
XX
PI Huse WD;
XX WPI; 2001-496171/54.

```

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DR P-PSDB; AAG63590.
XX
PT New LM609 grafted antibody exhibiting selective binding affinity to
PT alphavbeta3, comprising at least one LM609 grafted heavy and light
PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory
PT disorders or cancer
XX
PS Disclosure; Fig 2B; 25pp; English.
XX
CC The present sequence encodes the light chain variable region of the
CC monoclonal antibody LM609. LM609 is a murine antibody which specifically
CC recognises the integrin alphavbeta3, and inhibits its functional activity.
CC The specification describes a LM609 grafted antibody which has the
CC complementarity determining regions (CDRs) substituted into a non-murine
CC framework. Nucleic acids encoding LM609 grafted heavy and light chain
CC polypeptides and fragments are useful in diagnostic and therapeutic
CC purposes, such as in the production of LM609 grafted antibodies and
CC fragments having binding specificity and inhibitory activity against
CC the integrin alphavbeta3. The antibody can be used for the diagnosis
CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory
CC disorders, chronic articular rheumatism, psoriasis, disorders
CC associated with inappropriate or inopportune invasion of vessels such
CC as diabetic retinopathy, neovascular glaucoma and capillary
CC proliferation in atherosclerotic plaques, or cancers), and to inhibit
CC binding activity of alphavbeta3 that are necessary for progression of
CC an alphavbeta3-mediated disease.
XX
SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 90.3%; Score 29.8; DB 22; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagcagcaagtattagcaacttctctacac 33
Db ||||||||||||||||||| |||||
70 caggccagcagcaagtattagcaaccctctacac 102

RESULT 12
AAH28176
ID AAH28176 standard; DNA; 321 BP.
XX
AC AAH28176;
XX
DT 03-APR-2001 (first entry)
DE Vitaxin light chain variable region DNA.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX

```

```
PS Disclosure; Fig 1; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;

Query Match          90.3%; Score 29.8; DB 22; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagccaaagtattagcaacctctacac 33
   |||||
Db 70 caggccagccaaagtattagcaacctctacac 102

RESULT 13
AAF28178
ID AAF28178 standard; DNA; 321 BP.
XX
AC AAF28178;
XX
DT 03-APR-2001 (first entry)
XX
DE DNA encoding light chain variable region DNA.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Fig 2; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match          90.3%; Score 29.8; DB 22; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagccaaagtattagcaacctctacac 33
   |||||
Db 70 caggccagccaaagtattagcaacctctacac 102

RESULT 14
AAF28199
ID AAF28199 standard; DNA; 321 BP.
XX
AC AAF28199;
XX
DT 03-APR-2001 (first entry)
XX
DE DNA encoding light chain variable region of LM609.
XX
KW LM609; grafted antibody; alphavbeta_3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US17454.
XX
PR 24-JUN-1999; 99US-0339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis -
XX
PS Disclosure; Fig 7; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphavbeta_3 integrin or
CC their functional fragments. The antibodies or their functional
CC fragments can be used in the diagnosis and treatment of
CC alphavbeta_3-mediated diseases such as angiogenesis, inflammatory
CC diseases (such as psoriasis and chronic articular rheumatism),
CC disorders associated with inappropriate or inopportune invasion of
CC vessels (such as diabetic retinopathy, neovascular glaucoma and
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal
CC diseases (such as macular degeneration), restenosis and
CC osteoporosis.
XX
SQ Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match          90.3%; Score 29.8; DB 22; Length 321;
Best Local Similarity 93.9%; Pred. No. 0.0011;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 caggccagccaaagtattagcaacctctacac 33
   |||||
Db 70 caggccagccaaagtattagcaacctctacac 102
```



```

RESULT 15
AAV71825/c
ID AAV71825 standard; DNA; 101 BP.
XX
XX AAV71825;
XX
XX DT 15-MAR-1999 (first entry)
XX
XX DE Alpha-v beta-3 Mab D12H2LCREI VL oligonucleotide SBA3167.
XX
XX KW Humanised antibody; monoclonal antibody; Mab; antibody engineering;
XX mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
XX cancer; metastasis; rheumatoid arthritis; atherosclerosis;
XX angiogenesis; diabetic retinopathy; inflammation;
XX macular degeneration; osteoporosis; Paget's disease;
XX hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
XX D12H2LCREI; ss.
XX
XX OS Mus sp.
XX OS Synthetic.
XX
XX PN WO9840488-A1.
XX
XX PD 17-SEP-1998.
XX
XX PF 12-MAR-1998; 98WO-US04987.
XX
XX PR 12-MAR-1997; 97US-0039609.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX PI Johanson KO, Jonak ZL, Taylor AH;
XX
XX DR WPI; 1999-034590/03.
XX
XX PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
XX immunotherapeutic treatment of e.g. diabetic retinopathy,
XX inflammatory disorders, atherosclerosis, restenosis, cancers or
XX osteoporosis
XX
XX PS Example 14; Page 51; 97pp; English.
XX
XX CC SBA3167 is one of 4 overlapping oligonucleotides (see AAV71824-27)
XX used to construct DNA (see AAV71805) encoding a region of the murine
XX D12 monoclonal antibody light chain variable region (VL) that is
XX modified in humanised D12 VL D12H2LCREI. The synthetic D12 VL
XX gene was utilised in the construction of an expression vector for
XX the humanised D12 VL (see AAW87455). D12 is a murine anti-human
XX alpha-v beta-3 vitronectin receptor monoclonal antibody. Humanised
XX D12 antibodies of the invention can be used for passive
XX immunotherapy of disorders mediated by the alpha-v beta-3
XX vitronectin receptor, e.g. restenosis and angiogenic-related
XX disorders.
XX
XX SQ Sequence 101 BP; 21 A; 20 C; 31 G; 29 T; 0 other;

Query Match 84.2%; Score 27.8; DB 20; Length 101;
Best Local Similarity 93.5%; Pred. No. 0.0067; 2; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggccagccaaagtattagcaacttcctacac 33
   |||||
Db 99 GCCCAGCCAAAGTATTAGCAACCCACTACAC 69

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Job time: 10058 sec

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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:52:20 ; Search time 174.26 Seconds  
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Searched: 383533 seqs, 122816752 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 3	27.8	84.2	128	1	US-08-474-040-91
C 4	27.8	84.2	128	1	US-08-487-200-91
C 5	27.8	84.2	128	4	US-08-484-537-91
C 6	27.8	84.2	381	1	US-07-634-278-82
C 7	27.8	84.2	381	1	US-08-477-728-82
C 8	27.8	84.2	381	1	US-08-474-040-82
C 9	27.8	84.2	381	1	US-08-487-200-82
C 10	27.8	84.2	381	4	US-08-484-537-82
C 11	27.8	84.2	424	1	US-08-436-463-3
C 12	27.8	84.2	5238	6	5453363-1
C 13	24.6	74.5	324	4	US-09-247-352-14
C 14	24.6	74.5	8858	4	US-09-247-352-6
C 15	23	69.7	324	2	US-08-737-560A-13
C 16	23	69.7	363	2	US-08-737-560A-8
C 17	20.4	61.8	321	4	US-09-247-352-7
C 18	20.4	61.8	321	4	US-09-247-352-11
C 19	19.4	58.8	1568	4	US-08-858-207A-105
C 20	18.6	56.4	1266	2	US-08-659-984A-2
C 21	18.6	56.4	1266	2	US-08-659-984A-2
C 22	18.6	56.4	1335	2	US-08-660-531-2
C 23	18.6	56.4	1335	2	US-08-659-984A-4
C 24	18.4	55.8	812	1	US-08-660-531-4
C 25	18.4	55.8	812	1	US-08-053-131-178
C 26	18.4	55.8	812	1	US-08-096-762-178
C 27	18.4	55.8	812	4	US-09-042-353-41
C 28	18.4	55.8	812	4	US-08-758-417A-306

C 28	18.2	55.2	4800	5	PCT-US94-07779-1	Sequence 1, Appli
C 29	18.2	55.2	7083	4	US-09-198-839-1	Sequence 1, Appli
C 30	18.2	55.2	7294	1	US-08-440-787A-1	Sequence 1, Appli
C 31	18.2	55.2	7294	1	US-08-440-787A-5	Sequence 5, Appli
C 32	18.2	55.2	7294	4	US-08-367-685-1	Sequence 1, Appli
C 33	18.2	55.2	7294	4	US-08-367-685-5	Sequence 5, Appli
C 34	18.2	55.2	7294	5	PCT-US91-07141-1	Sequence 1, Appli
C 35	18.2	55.2	7294	5	PCT-US91-07141-5	Sequence 5, Appli
C 36	18.2	55.2	7317	1	US-08-464-136-2	Sequence 2, Appli
C 37	18.2	55.2	7317	2	US-08-349-131-2	Sequence 2, Appli
C 38	18.2	55.2	7317	3	US-08-470-297A-2	Sequence 2, Appli
C 39	18.2	55.2	7317	5	PCT-US91-07149-2	Sequence 2, Appli
C 40	18.2	55.2	7320	1	US-08-440-787A-2	Sequence 2, Appli
C 41	18.2	55.2	7320	4	US-08-367-685-2	Sequence 2, Appli
C 42	18.2	55.2	7320	5	PCT-US91-07141-2	Sequence 2, Appli
C 43	18.2	55.2	7394	1	US-08-440-787A-6	Sequence 6, Appli
C 44	18.2	55.2	7394	4	US-08-367-685-6	Sequence 6, Appli
C 45	18.2	55.2	7394	5	PCT-US91-07141-6	Sequence 6, Appli

## ALIGNMENTS

RESULT 1  
US-07-634-278-91/C  
; Sequence 91, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELING, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (oligonucleotide)  
US-07-634-278-91

Query Match 84.2%; Score 27.8; DB 1; Length 128;  
Best Local Similarity 93.5%; Pred. No. 0.00041;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaacttctctacac 33  
|||||  
DB 95 GGCAGCCAAAGTATTAGCAACACTTACAC 65

## RESULT 2

US-08-477-728-91/c  
; Sequence 91, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (oligonucleotide)  
US-08-477-728-91

Query Match 84.2%; Score 27.8; DB 1; Length 128;  
Best Local Similarity 93.5%; Pred. No. 0.00041;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaacttctctacac 33  
|||||  
DB 95 GGCAGCCAAAGTATTAGCAACACTTACAC 65

## RESULT 3

US-08-474-040-91/c  
; Sequence 91, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (oligonucleotide)  
US-08-474-040-91

Query Match 84.2%; Score 27.8; DB 1; Length 128;  
Best Local Similarity 93.5%; Pred. No. 0.00041;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagccaaagtattagcaacttctctacac 33  
|||||  
DB 95 GGCAGCCAAAGTATTAGCAACACTTACAC 65

## RESULT 4

US-08-487-200-91/c

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; Sequence 91, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-487-200-91

Query Match      84.2%; Score 27.8; DB 1; Length 128;
Best Local Similarity 93.5%; Pred. No. 0.00041;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagcagcaagattagcaacttcctacac 33
   |||||||||||||||||||
DB 95 GGCAGCCAAAGTATTAGCAACACCTACAC 65

RESULT 5
US-08-484-537-91/c
; Sequence 91, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
```

```
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-484-537-91

Query Match      84.2%; Score 27.8; DB 4; Length 128;
Best Local Similarity 93.5%; Pred. No. 0.00041;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagcagcaagattagcaacttcctacac 33
   |||||||||||||||||||
DB 95 GGCAGCCAAAGTATTAGCAACACCTACAC 65

RESULT 6
US-07-634-278-82
; Sequence 82, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
```

STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 381 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..381  
US-07-634-278-82

Query Match 84.2%; Score 27.8; DB 1; Length 381;  
Best Local Similarity 93.5%; Pred. No. 0.00054;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 gccacgcaaaagtattagcaacttcctacac 33  
|||||  
Db 132 GCCACGCCAAAGTATTAGCAACACCTACAC 162

RESULT 7  
US-08-477-728-82  
Sequence 82, Application US/08477728  
Patent No. 5585089  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,728  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 381 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..381  
US-08-477-728-82

Query Match 84.2%; Score 27.8; DB 1; Length 381;  
Best Local Similarity 93.5%; Pred. No. 0.00054;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 gccacgcaaaagtattagcaacttcctacac 33  
|||||  
Db 132 GCCACGCCAAAGTATTAGCAACACCTACAC 162

RESULT 8  
US-08-474-040-82  
Sequence 82, Application US/08474040  
Patent No. 5693761  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,040

; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381  
US-08-474-040-82

Query Match 84.2%; Score 27.8; DB 1; Length 381;  
Best Local Similarity 93.5%; Pred. No. 0.00054;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaactctctacac 33  
|||||  
DB 132 GCCACGCCAAAGTATTAGCAACACCTTACAC 162

RESULT 9  
US-08-487-200-82  
; Sequence 82, Application US/08487200  
; Patent No. 5693762  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,200  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278

; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002610  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381  
US-08-487-200-82

Query Match 84.2%; Score 27.8; DB 1; Length 381;  
Best Local Similarity 93.5%; Pred. No. 0.00054;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcacgcaaaagtattagcaactctctacac 33  
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DB 132 GCCACGCCAAAGTATTAGCAACACCTTACAC 162

RESULT 10  
US-08-484-537-82  
; Sequence 82, Application US/08484537  
; Patent No. 6180370  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,537  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381  
US-08-484-537-82

Query Match 84.2%; Score 27.8; DB 4; Length 381;  
Best Local Similarity 93.5%; Pred. No. 0.00054;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagcgaagattagcaactctctacac 33  
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Db 132 GCCAGCAGCAAGTATTAGCAACACCTACAC 162

RESULT 11  
US-08-436-463-3  
; Sequence 3, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoto  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,463  
; FILING DATE: 26-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 341255/1992  
; FILING DATE: 28-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: KIMACHI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 424 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 23..403  
US-08-436-463-3

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Best Local Similarity 93.5%; Pred. No. 0.00056;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagcgaagattagcaactctctacac 33  
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Db 154 GCCAGCAGCAAGTATTAGCAACACCTACAC 184

RESULT 12  
5453363-1  
; Patent No. 5453363  
; APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF  
; TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR  
; ING AFTER GENETIC EXPRESSION IN PROKARYOTES  
; NUMBER OF SEQUENCES: 4  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/206,044  
; FILING DATE: 02-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 942,370  
; FILING DATE: 09-SEP-1992  
; APPLICATION NUMBER: 498,500  
; FILING DATE: 23-MAR-1990  
; APPLICATION NUMBER: 76,207  
; FILING DATE: 23-OCT-1986  
; SEQ ID NO: 1  
; LENGTH: 5238  
5453363-1

Query Match 84.2%; Score 27.8; DB 6; Length 5238;  
Best Local Similarity 93.5%; Pred. No. 0.0011;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ggcagcgaagattagcaactctctacac 33  
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Db 78 ggcagcgaagattagcaacacacacac 108

RESULT 13  
US-09-247-352-14  
; Sequence 14, Application US/09247352  
; Patent No. 6312693  
; GENERAL INFORMATION:  
; APPLICANT: Aruffo, Alejandro A.  
; APPLICANT: Siadak, Anthony W.  
; APPLICANT: Berry, Karen K.  
; APPLICANT: Thorne, Barbara A.  
; APPLICANT: Bajorath, Jurgen  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40  
; FILE REFERENCE: DB2a SEQUENCE  
; CURRENT APPLICATION NUMBER: US/09/247,352  
; CURRENT FILING DATE: 1999-02-10  
; EARLIER APPLICATION NUMBER: 09/026,291  
; EARLIER FILING DATE: 1998-02-19

; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 324  
; TYPE: DNA  
; ORGANISM: Human and Mouse  
US-09-247-352-14

Query Match 74.5%; Score 24.6; DB 4; Length 324;  
Best Local Similarity 87.1%; Pred. No. 0.015;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 72 ggcacgccaagattagcgactacttacac 102

RESULT 14  
US-09-247-352-6  
; Sequence 6, Application US/09247352  
; Patent No. 6312693  
; GENERAL INFORMATION:  
; APPLICANT: Aruffo, Alejandro A.  
; APPLICANT: Sladak, Anthony W.  
; APPLICANT: Berry, Karen K.  
; APPLICANT: Harris, Linda  
; APPLICANT: Thorne, Barbara A.  
; APPLICANT: Rajorath, Jurgen  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffrey D.  
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40  
; FILE REFERENCE: DB2a SEQUENCE  
; CURRENT APPLICATION NUMBER: US/09/247,352  
; EARLIER FILING DATE: 1999-02-10  
; EARLIER APPLICATION NUMBER: 09/026,291  
; EARLIER FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 14  
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; SEQ ID NO 6  
; LENGTH: 8858  
; TYPE: DNA  
; ORGANISM: Human and Mouse  
US-09-247-352-6

Query Match 74.5%; Score 24.6; DB 4; Length 8858;  
Best Local Similarity 87.1%; Pred. No. 0.037;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ggcacgccaagattagcaacttcctacac 33  
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Db 1136 ggcacgccaagattagcgactacttacac 1166

RESULT 15  
US-08-737-560A-13  
; Sequence 13, Application US/08737560A  
; Patent No. 5928893  
; GENERAL INFORMATION:  
; APPLICANT: KANG, Chang-Yuill  
; APPLICANT: KIM, Joong-Gon  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN  
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KANG, Chang-Yuill  
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,  
; STREET: Kwanak-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea

; ZIP: 151-057  
; ADDRESSEE: KIM, Joong-Gon  
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 135-110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage  
; COMPUTER: IBM PC/AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,560A  
; FILING DATE: 13-NOV-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: KR 95-8176  
; FILING DATE: 08-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 324 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: polynucleotide encoding 4B4-1-1  
; OTHER INFORMATION: light chain variable region  
US-08-737-560A-13

Query Match 69.7%; Score 23; DB 2; Length 324;  
Best Local Similarity 83.9%; Pred. No. 0.084;  
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ggcacgccaagattagcaacttcctacac 33  
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Db 72 ggcacgccaagattagcgactacttacac 102

Search completed: August 21, 2002, 10:52:21  
Job time: 9661 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:49:58 ; Search time 2408.76 Seconds  
(without alignments)  
182.441 Million cell updates/sec

Title: US-09-339-922A-111  
Perfect score: 21  
Sequence: 1 tatgttcccaagtcacatctct 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
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- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
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- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
CDS

AX060890 Sequence  
AX060822 Sequence  
AX060795 Sequence  
AX060804 Sequence  
AX060782 Sequence  
AX060786 Sequence  
AX060810 Sequence  
AL871173 Mus muscu  
AL627345 Mus muscu  
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U19309 Mus musculu  
U19328 Mus musculu  
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AF139843 Mus muscu  
AF137617 Mus muscu  
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X59211 Mouse immu  
X86546 M.musculus  
AF139235 Mus muscu  
L09019 Mus musculu  
L09021 Mus musculu  
X02556 Mouse mrna  
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AF087030 Mus muscu  
AF163757 Mus muscu  
X0901 M.musculus  
U16181 Mus musculu  
AJ277215 Mus muscu  
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M95941 Mouse mrna  
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M35667 Mouse lysoz  
L08211 Mouse anti-  
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AX060890 21 bp DNA linear PAT 22-JAN-2001  
Sequence 111 from Patent WO0078815.  
AX060890  
AX060890.1 GI:12406268  
synthetic construct.  
synthetic construct.  
artificial sequence.  
1 (bases 1 to 21)  
Huse,W.D. and Wu,H.  
Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
Patent: WO 0078815-A 111 28-DEC-2000;  
Applied Molecular Evolution (US)  
Location/Qualifiers  
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Db 1 TATCGTTCCAGTCCATCTCT 21

RESULT 2
AX060822 AX060822 33 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 43 from Patent WO0078815.
ACCESSION AX060822
VERSION AX060822.1 GI:12406200
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM
REFERENCE 1 (bases 1 to 33)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 43 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcggtccagtcctctct 21
|||||
Db 13 TATCGTTCCAGTCCATCTCT 33

RESULT 3
AX060795 AX060795 84 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 16 from Patent WO0078815.
ACCESSION AX060795
VERSION AX060795.1 GI:12406175
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 84)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 16 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
Location/Qualifiers
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcggtccagtcctctct 21
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Db 19 TATCGTTCCAGTCCATCTCT 39

RESULT 4
AX060804 AX060804 84 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 25 from Patent WO0078815.
ACCESSION AX060804
VERSION AX060804.1 GI:12406184
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 84)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 25 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
Location/Qualifiers
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Query Match      100.0%; Score 21; DB 6; Length 84;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcggtccagtcctctct 21
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Db 19 TATCGTTCCAGTCCATCTCT 39

RESULT 5
AX060782 AX060782 321 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 3 from Patent WO0078815.
ACCESSION AX060782
VERSION AX060782.1 GI:12406162
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 321)
AUTHORS Huse, W.D. and Wu, H.
TITLE Anti-g(a) v2-g(b)3? recombinant human antibodies, nucleic acids
encoding same and methods of use
JOURNAL Patent: WO 0078815-A 3 28-DEC-2000;
Applied Molecular Evolution (US)
FEATURES
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Db 148 TATCGTTCCCGAGTCCATCTCT 168

RESULT 6
LOCUS   AX060786               321 bp    DNA    linear    PAT 22-JAN-2001
DEFINITION   Sequence 7 from Patent W00078815.
ACCESSION   AX060786
VERSION     AX060786.1  GI:12406166
KEYWORDS     house mouse.
SOURCE      Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 321)
AUTHORS     Huse,W.D. and Wu,H.
TITLE       Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
            encoding same and methods of use
JOURNAL     Patent: WO 0078815-A 7 28-DEC-2000;
            Applied Molecular Evolution (US)
FEATURES    Location/Qualifiers
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BASE COUNT      78 a   93 c   79 g   71 t   3 others
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Db 148 TATCGTTCCCGAGTCCATCTCT 168

RESULT 6
LOCUS   AX060786               321 bp    DNA    linear    PAT 22-JAN-2001
DEFINITION   Sequence 7 from Patent W00078815.
ACCESSION   AX060786
VERSION     AX060786.1  GI:12406166
KEYWORDS     house mouse.
SOURCE      Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 321)
AUTHORS     Huse,W.D. and Wu,H.
TITLE       Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
            encoding same and methods of use
JOURNAL     Patent: WO 0078815-A 7 28-DEC-2000;
            Applied Molecular Evolution (US)
FEATURES    Location/Qualifiers
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Db 148 TATCGTTCCCGAGTCCATCTCT 168

Query Match      100.0%; Score 21; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
LOCUS   AX060810               321 bp    DNA    linear    PAT 22-JAN-2001
DEFINITION   Sequence 31 from Patent W00078815.
ACCESSION   AX060810
VERSION     AX060810.1  GI:12406189
KEYWORDS     synthetic construct.
SOURCE      synthetic construct
ORGANISM    artificial sequence.

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REFERENCE      1 (bases 1 to 321)
AUTHORS       Huse,W.D. and Wu,H.
TITLE         Anti-g(a) v7-g(b)3? recombinant human antibodies, nucleic acids
            encoding same and methods of use
JOURNAL       Patent: WO 0078815-A 31 28-DEC-2000;
            Applied Molecular Evolution (US)
FEATURES      Location/Qualifiers
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BASE COUNT      76 a   93 c   78 g   71 t   3 others
ORIGIN
      1 tatcgttcccgagtcctctct 21
      |||||||
Db 148 TATCGTTCCCGAGTCCATCTCT 168

RESULT 8
LOCUS   AL671173/C            199080 bp    DNA    linear    HTG 08-FEB-2002
DEFINITION   Mus musculus chromosome 4 clone RP23-426N4, *** SEQUENCING IN
            PROGRESS ***, in unordered pieces.
ACCESSION   AL671173
VERSION     AL671173.3  GI:18643846
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (sites)
AUTHORS       Plumb,B.
TITLE         Direct Submission
JOURNAL       Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
            On Feb 10, 2002 this sequence version replaced gi:18477144.
COMMENT       ----- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            ----- Project Information
            Center project name: BM426N4
            ----- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 74% of reads
            Chemistry: Dye-terminator; 25% of reads
            Consensus quality: 196691 bases at least Q40
            Consensus quality: 197461 bases at least Q30
            Consensus quality: 197868 bases at least Q20
            Insert size: 198280; sum-of-contigs
            Insert size: 205652; 5.0% error; agarose-fp
            Quality coverage: 7.13x in Q20 bases; sum-of-contigs Quality
            coverage: 7.00x in Q20 bases; agarose-fp
            -----
            * NOTE: This is a 'working draft' sequence.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            Location/Qualifiers
            source          1..199080
                        /organism="Mus musculus"
                        /db_xref="taxon:10090"

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/clone_lib="RPC1-23"
1. .3299
/feature="assembly_fragment:00717"
fragment_chain:1"
3400. .46221
/feature="assembly_fragment:00198"
fragment_chain:1"
46322. .84635
/feature="assembly_fragment:01999"
fragment_chain:1"
84736. .94486
/feature="assembly_fragment:02694"
fragment_chain:1"
94587. .96789
/feature="assembly_fragment:01661"
fragment_chain:1"
96890. .119792
/feature="assembly_fragment:00161"
fragment_chain:2"
119893. .125701
/feature="assembly_fragment:00140"
fragment_chain:2"
125802. .196306
/feature="assembly_fragment:00002"
196407. .199080
/feature="assembly_fragment:01500"
815 others

BASE COUNT 52895 a 47980 c 46823 g 50567 t
ORIGIN

Query Match 85.7%; Score 18; DB 2; Length 199080;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgttcacagtcacatctct 21
|||||
Db 123307 CGTTCACAGTCACATCTCT 123290

RESULT 9
AL627345/c
LOCUS
DEFINITION Mus musculus chromosome 4 clone RP23-169E7, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
ACCESSION AL627345
VERSION AL627345.4 GI:16596763
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
Burton, J.
Direct Submission
TITLE Submitted (30-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Nov 2, 2001 this sequence version replaced gi:16596752.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bml69E7
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 1% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 208062 bases at least Q40

```

Consensus quality: 209911 bases at least Q30  
Consensus quality: 211313 bases at least Q20  
Insert size: 212988; sum-of-contigs  
Insert size: 237457; 1.8% error; agarose-fp  
Quality coverage: 7.10x in Q20 bases; sum-of-contigs Quality  
coverage: 6.79x in Q20 bases; agarose-fp  
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\* NOTE: This is a 'working draft' sequence.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

FEATURES  
source  
1. .216188  
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/db\_xref="taxon:10090"  
/chromosome="4"  
/clone="RP23-169E7"  
/clone\_lib="RPC1-23"  
1. .13211  
/feature="assembly\_fragment:04054"  
clone\_end:SP6  
vector\_side:left  
13312. .37041  
/feature="assembly\_fragment:05232"  
fragment\_chain:1"  
37142. .39300  
/feature="assembly\_fragment:02127"  
fragment\_chain:1"  
39401. .45603  
/feature="assembly\_fragment:01795"  
fragment\_chain:1"  
45704. .48389  
/feature="assembly\_fragment:05387"  
fragment\_chain:1"  
48490. .51610  
/feature="assembly\_fragment:05684"  
fragment\_chain:1"  
51711. .57795  
/feature="assembly\_fragment:00041"  
fragment\_chain:1"  
57896. .62317  
/feature="assembly\_fragment:05227"  
fragment\_chain:1"  
62418. .66250  
/feature="assembly\_fragment:00195"  
fragment\_chain:1"  
66351. .72994  
/feature="assembly\_fragment:02274"  
fragment\_chain:1"  
73095. .76869  
/feature="assembly\_fragment:05274"  
fragment\_chain:1"  
76970. .81417  
/feature="assembly\_fragment:03583"  
fragment\_chain:2"  
81518. .95713  
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fragment\_chain:2"  
95814. .108724  
/feature="assembly\_fragment:05397"  
fragment\_chain:2"  
108825. .114591  
/feature="assembly\_fragment:05157"  
fragment\_chain:2"  
114692. .119312  
/feature="assembly\_fragment:01061"  
fragment\_chain:2"  
119413. .122148  
/feature="assembly\_fragment:02286"  
fragment\_chain:3"  
12249. .124750  
/feature="assembly\_fragment:02147"  
fragment\_chain:3"

misc\_feature 124851..133431  
/note="assembly\_fragment:00673  
fragment\_chain:3"  
13332..135549  
/note="assembly\_fragment:04205  
fragment\_chain:3"  
13560..140504  
/note="assembly\_fragment:01738  
fragment\_chain:4"  
140605..142781  
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fragment\_chain:4"  
142882..150571  
/note="assembly\_fragment:02230  
fragment\_chain:4"  
150672..156185  
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fragment\_chain:5"  
156286..159860  
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fragment\_chain:5"  
159961..162907  
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fragment\_chain:5"  
163008..167874  
/note="assembly\_fragment:03918  
fragment\_chain:6"  
167975..178909  
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fragment\_chain:6"  
179010..186318  
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fragment\_chain:6"  
186419..189450  
/note="assembly\_fragment:01228  
fragment\_chain:7"  
189551..196619  
/note="assembly\_fragment:02401  
fragment\_chain:7"  
196720..212969  
/note="assembly\_fragment:04261"  
213070..216188  
/note="assembly\_fragment:02718  
clone\_end:17  
vector\_side:right"  
BASE COUNT 51159 a 53937 c 54749 g 53129 t 3214 others  
ORIGIN

Query Match 85.7%; Score 18; DB 2; Length 216188;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 cgttccagtcacatctct 21  
|||||  
Db 215029 CgTTCcAGTCcATCTCT 215012

RESULT 10  
AX060862 AX060862 33 bp DNA linear PAT 22-JAN-2001  
LOCUS  
DEFINITION Sequence 83 from Patent WO0078815.  
ACCESSION AX060862  
VERSION AX060862.1 GI:12406240  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Huse, W.D. and Wu, H.  
TITLE Anti'-g(a) v2.g(b)3? recombinant human antibodies, nucleic acids  
encoding same and methods of use  
JOURNAL Patent: WO 0078815-A 83 28-DEC-2000;

FEATURES Applied Molecular Evolution (US)  
source Location/Qualifiers  
1..33  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
CDS  
<1..>33  
/note="Mutated complementarity determining region (CDR)"  
/codon\_start=1  
/transl\_table=11  
/protein\_id="CAC34917.1"  
/db\_xref="GI:12406241"  
/translation="LLIRYSQSIS"  
BASE COUNT 4 a 13 c 2 g 14 t  
ORIGIN  
Query Match 84.8%; Score 17.8; DB 6; Length 33;  
Best Local Similarity 90.5%; Pred. No. 1.4e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 tatcgttccagtcacatctct 21  
|||||  
Db 13 TATTCTTCCcAGTCcATCTCT 33  
RESULT 11  
MDIGKVAV  
LOCUS  
DEFINITION M.domesticus Igk variable region. 236 bp mRNA linear ROD 05-NOV-1994  
ACCESSION Z22072  
VERSION Z22072.1 GI:297637  
KEYWORDS anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin.  
SOURCE western European house mouse.  
ORGANISM Mus musculus domesticus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 236)  
AUTHORS Tillman, D.M., Jou, N.T., Hill, R.J. and Marion, T.N.  
TITLE Both IgM and IgG anti-DNA antibodies are the products of clonally  
selective B cell stimulation in (NZB x NZW)F1 mice  
JOURNAL J. Exp. Med. 176 (3), 761-779 (1992)  
MEDLINE 92381444  
REFERENCE 2 (bases 1 to 236)  
AUTHORS Marion, T.N.  
TITLE Direct Submission  
JOURNAL Submitted (23-MAR-1993) Tony N. Marion, Microbiology and  
Immunology, University of Tennessee, Memphis, 858 Madison Avenue,  
Memphis, TN, 38163, USA  
FEATURES Location/Qualifiers  
source  
1..236  
/organism="Mus musculus domesticus"  
/strain="(NZB x NZW)F1"  
/isolate="mouse #165"  
/db\_xref="taxon:10092"  
/chromosome="6"  
/sex="Female"  
/cell\_line="165.60"  
/cell\_type="hybridoma"  
/tissue\_type="spleen"  
/dev\_stage="somatic variant"  
1..236  
/gene="Igk"  
CDS  
<1..>236  
/gene="Igk"  
/function="kappa light chain variable region for anti-DNA  
antibody; Vk23 family"  
/codon\_start=1  
/product="immunoglobulin variable region"  
/protein\_id="CAA80046.1"  
/db\_xref="GI:297638"  
/translation="LATYTGINKNHSLOGFSSMLPSPSLGSPPGSVAVDQGISL  
SVSTVRLKILEISVNRVTAGLRSRVSPWSKS"  
BASE COUNT 68 a 57 c 53 g 58 t

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ORIGIN
Query Match      84.8%; Score 17.8; DB 10; Length 236;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21
   ||| |||||||||||||||
DB 63 TATGCTTCCAGTCCATCTCT 83

RESULT 12
MMU19328
LOCUS      MMU19328
DEFINITION Mus musculus immunoglobulin kappa light chain variable region mRNA,
clone MRL1-17, partial cds.
ACCESSION U19309
VERSION   U19309.1
KEYWORDS  GI:619954
SOURCE    house mouse.
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 243)
AUTHORS   Roark,J.H., Kuntz,C.L., Nguyen,K.A., Caton,A.J. and Erikson,J.
TITLE     Breakdown of B cell tolerance in a mouse model of systemic lupus
erythematosus
JOURNAL   J. Exp. Med. 181 (3), 1157-1167 (1995)
MEDLINE   95173583
AUTHORS   Roark,J.H.
TITLE     Direct Submission
JOURNAL   Submitted (02-JAN-1995) Jessica H. Roark, Wistar Institute, 3601
Spruce St., Philadelphia, PA 19104, USA
FEATURES   Location/Qualifiers
            source
              1..243
                /organism="Mus musculus"
                /strain="MRL-lpr/lpr"
                /db_xref="taxon:10090"
                /clone="MRL1-17"
                /cell_type="splenic B cell hybridoma"
                /tissue_type="spleen"
                /dev_stage="adult"
                <!.>243
                /codon_start=1
                /product="immunoglobulin kappa light chain variable
region"
                /protein_id="AAAG8563.1"
                /db_xref="GI:619955"
                /translation="ACRASQISNYLHWYQKSHSPRLLIKVASQSIGIPSRFSGS
GSGDTFLINSVETEDFGMYFCQSNWPHFGSGT"
BASE COUNT 65 a 62 c 56 g 60 t
ORIGIN

CDS
Query Match      84.8%; Score 17.8; DB 10; Length 276;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21
   ||| |||||||||||||||
DB 118 TATGCTTCCAGTCCATCTCT 138

RESULT 14
AF139842
LOCUS      AF139842
DEFINITION Mus musculus clone GL1 immunoglobulin kappa light chain variable
region VK23 (Ig) gene, partial cds.
ACCESSION  AF139842
VERSION     AF139842.1
KEYWORDS    GI:4732148
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 285)
AUTHORS     Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
TITLE       Somatic mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
JOURNAL     J. Exp. Med. 190 (5), 691-704 (1999)
MEDLINE     99406777
PUBMED      10477553
REFERENCE 2 (bases 1 to 285)
AUTHORS     Brard,F. and Weigert,M.
TITLE       Direct Submission
JOURNAL     Submitted (01-APR-1999) Molecular Biology, Princeton University,
Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES    Location/Qualifiers
            source
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                /organism="Mus musculus"
                /strain="MRL/Mp-lpr/lpr"

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/db_xref="taxon:10090"
/chromosome="6"
/clone="GL1"
/tissue_type="tail"
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/gene="Ig"
/note="variable region"
<!.>285
/gene="Ig"
/codon_start=1
/product="immunoglobulin kappa light chain variable region
Vk23"
/protein_id="AAD28629.1"
/db_xref="GI:4732149"
/translation="DIVLTQSPATLSVTPGDVSLSCRASQISNLYLHWYQKSHESP
RLIKYASQISGIPSRFSGSGTDTLSINSVETEDFGMFCQSNWP"
70.105
/gene="Ig"
/note="CDR1; complementarity determining region 1"
148.168
/gene="Ig"
/note="CDR2; complementarity determining region 2"
75 a 73 c 63 g 74 t
BASE COUNT 75 a 73 c 63 g 74 t
ORIGIN
Query Match 84.8%; Score 17.8; DB 10; Length 285;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgtccagtcctctct 21
||| ||||| ||||| |||||
Db 148 TATGCTTCCAGTCCATCTCT 168

RESULT 15
AF139843 286 bp DNA linear ROD 04-NOV-1999
LOCUS Mus musculus clone GL2 immunoglobulin kappa light chain variable
DEFINITION region Vk23 (Ig) gene, partial cds.
ACCESSION AF139843
VERSION AF139843.1 GI:4732150
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 286)
Brard,F., Shannon,M., Prak,E.L., Litwin,S. and Weigert,M.
Somatc mutation and light chain rearrangement generate
autoimmunity in anti-single-stranded DNA transgenic MRL/lpr mice
J. Exp. Med. 190 (5), 691-704 (1999)
99406777
MEDLINE
PUBMED 10477553
2 (bases 1 to 286)
Brard,F. and Weigert,M.
Direct Submission
TITLE Submitted (01-APR-1999) Molecular Biology, Princeton University,
JOURNAL Washington Road, Room 401, Princeton, NJ 08544, USA
FEATURES
source
Location/Qualifiers
1..286
/organism="Mus musculus"
/strain="MRL/Mp-lpr/lpr"
/db_xref="taxon:10090"
/chromosome="6"
/clone="GL2"
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/germline
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/gene="Ig"
/note="variable region"
<!.>286
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Vk23"
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/db_xref="GI:4732151"
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RLIKYASQISGIPSRFSGSGTDTLSINSVETEDFGMFCQSNWP"
70.105
/gene="Ig"
/note="CDR1; complementarity determining region 1"
148.168
/gene="Ig"
/note="CDR2; complementarity determining region 2"
75 a 75 c 62 g 74 t
BASE COUNT 75 a 75 c 62 g 74 t
ORIGIN
Query Match 84.8%; Score 17.8; DB 10; Length 286;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgtccagtcctctct 21
||| ||||| ||||| |||||
Db 148 TATGCTTCCAGTCCATCTCT 168

Search completed: August 21, 2002, 10:50:08
Job time: 9823 sec
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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	17.8	84.8	236	10	BG089048	ut61b10.Y
2	17.8	84.8	369	12	AQ138719	HS-3073.A
C 3	17.8	84.8	738	10	BF582153	60209743
4	17.8	84.8	835	10	BG966582	602834412
5	17.8	84.8	835	10	B1083006	BG083006
C 6	16.8	80.0	320	9	AI452179	mp82g11.x
C 7	16.8	80.0	388	10	BE688887	B5688887
C 8	16.8	80.0	397	9	AU062862	au062862
C 9	16.8	80.0	455	10	BF715275	BF715275
10	16.8	80.0	460	9	AW179330	pm4-ST012
11	16.8	80.0	461	9	AI530706	AI530706
12	16.8	80.0	470	9	AA120431	mp82g11.y
13	16.8	80.0	474	9	AI007215	AI120431.x
C 14	16.8	80.0	545	10	BI509406	AI007215
C 15	16.8	80.0	625	12	BH319848	ua73h11.r
C 16	16.8	80.0	634	10	BG923521	BI509406
C 17	16.8	80.0	637	12	BH037505	BH319848
						CH2330-63K
						BG923521
						mp82818208
						RPCI-24-2

the

BG0809048 236 bp mRNA linear EST 26-JAN-2000  
 uc61bl10.y1 Soares\_mouse\_NMGB\_bcell Mus musculus cDNA clone  
 IMAGE:332299 5' similar to SW:KV51-MOUSE P01642 IG KAPPA CHAIN V-V  
 REGION LR PRECURSOR ;, mRNA sequence.  
 BG080908  
 BG0809048.1 GI:12571611  
 EST.  
 house mouse.  
 Mus musculus  
 Euteleostomi; Euteleostomi; Euteleostomi; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 236)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 MGI:1076463  
 Seq primer: -40RP from Gibco.  
 Location/Qualifiers  
 1..236  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:332299"  
 /clone\_lib="Soares\_mouse\_NMGB\_bcell"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: germinal B-cell; Vector: pT7T3D-Pac  
 (Pharmacia) with a modified polylinker; Site\_1: Not I;  
 Site\_2: Eco RI; 1st strand cDNA was primed with a Not I -  
 oligo(dT) primer [5',  
 TGTACCAACTGAGTGGAGCGCCCGTGTGTGTGTGTGTGTGTGTGTGTGT  
 T 3']; double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pT7T3 vector.  
 Library is normalized; constructed by Bento Soares and



```

BASE COUNT      66 a      54 c      58 g      58 t
ORIGIN
M.Fatima Bonaldo."

Query Match      84.8%; Score 17.8; DB 10; Length 236;
Best Local Similarity 90.5%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttccagtcacatctct 21
   ||| ||||| ||||| |||||
Db 55 TATGCTTCCAGTCACATCTCT 75

RESULT 2
AQ138719/c
LOCUS
DEFINITION
HS_3073_A2_G11_MR_CIT_Approved_Human_Genomic_Sperm_Library_D_Homo
sapiens genomic clone Plate-3073 Col-22 Row-M, DNA sequence.
ACCESSION
AQ138719
VERSION
AQ138719.1 GI:3529372
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 369)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3073 row: M column: 22
Class: BAC ends
High quality sequence stop: 369.
Location/Qualifiers
1..369
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate-3073 Col-22 Row-M"
/sex="male"
/notes="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

BASE COUNT      152 a      55 c      125 g      37 t
ORIGIN

Query Match      84.8%; Score 17.8; DB 12; Length 369;
Best Local Similarity 90.5%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttccagtcacatctct 21
   |||| | ||||| |||||
Db 285 TATCGGTCTCAGTCACATCTCT 265

RESULT 3
BF582153
LOCUS
DEFINITION- 602099743F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219402 5',
^ mRNA sequence.
ACCESSION
BF582153

```

---

```

VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/.
1 (bases 1 to 738)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9801 row: f column: 11
High quality sequence stop: 714.
Location/Qualifiers
1..738
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4219402"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      210 a      189 c      172 g      167 t
ORIGIN

Query Match      84.8%; Score 17.8; DB 10; Length 738;
Best Local Similarity 90.5%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttccagtcacatctct 21
   ||| ||||| ||||| |||||
Db 220 TATGCTTCCAGTCACATCTCT 240

RESULT 4
BG966582
LOCUS
DEFINITION
602834412F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:498955 5',
^ mRNA sequence.
ACCESSION
BG966582
VERSION
BG966582.1 GI:14354219
KEYWORDS
EST.
SOURCE
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 833)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1002 row: g column: 04
High quality sequence stop: 830.

```

QY 1 tategttcccgagtcacatctct 21  
 ||| ||||| ||||| |||||  
 Db 226 TATGCTTCCCGAGTCCATCTCT 246  
  
 RESULT 6  
 AI452179/c  
 LOCUS linear EST 09-MAR-1999  
 DEFINITION 320 bp mRNA Mus musculus cDNA clone IMAGE:575780  
 3', mRNA sequence.  
 ACCESSION AI452179  
 VERSION AI452179  
 KEYWORDS GI:4300111  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 320)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapsr@mail.nih.gov](mailto:cgapsr@mail.nih.gov)  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 This clone was previously sequenced on the 5' end only, this new  
 data is from the 3' end  
 High quality sequence stop: 319.  
 FEATURES  
 Location/Qualifiers  
 1..320  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:575780"  
 /clone\_lib="Soares\_thymus\_2Ndbt"  
 /sex="male"  
 /tissue.type="Thymus"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"  
 /note="Vector: pT773D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5',  
 TCTTACCATCTGAAGTCGGACGGCGGTTTTTTTTTTTTTTTTTTTT  
 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. RNA  
 provided by Dr. Bertrand Jordan. Library went through two  
 rounds of normalization, and was constructed by Bento  
 Soares and M.Fatima Bonaldo."  
 BASE COUNT 83 a 65 c 68 g 104 t  
 ORIGIN  
  
 Query Match 80.0%; Score 16.8; DB 9; Length 320;  
 Best Local Similarity 90.0%; Pred. No. 1.3e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
 QY 2 atcgttcccgagtcacatctct 21  
 ||| | ||||| |||||  
 Db 179 ATCTGCCCGAGTCCATCTCT 160  
  
 RESULT 7  
 BE68887/c  
 LOCUS linear EST 11-SEP-2000  
 DEFINITION 388 bp mRNA Mus musculus cDNA clone  
 IMAGE:3419045 3', mRNA sequence.  
 ACCESSION BE68887  
 VERSION BE68887  
 KEYWORDS GI:10076511  
 SOURCE house mouse.

```

ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 388)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Other_ESTs: uw39d03.y1
            Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1094857
            High quality sequence stop: 351.

FEATURES      Location/Qualifiers
            1..388
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="IMAGE:3419045"
            /clone_lib="Soares_thymus_2NbMT"
            /sex="male"
            /tissue_type="thymus"
            /dev_stage="4 weeks"
            /lab_host="DH10B"
            /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
            polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
            was primed with a Not I - oligo(dT) primer [5',
            TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGT
            3']; double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not I
            and Eco RI sites of the modified pT7T3 vector. RNA
            provided by Dr. Bertrand Jordan. Library went through two
            rounds of normalization, and was constructed by Bento
            Soares and M.Fatima Bonaldo."

BASE COUNT    93 a 88 c 84 g 123 t
ORIGIN

Query Match      80.0%; Score 16.8; DB 10; Length 388;
Best Local Similarity 90.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 atcgtcccgagtcctctct 21
||||| ||||| ||||| |||||
Db 179 ATCTTCCCGCAGTCCATCTCT 160

RESULT 8
LOCUS      AU062862
DEFINITION AU062862 Rice callus Oryza sativa cDNA clone C51207_1A, mRNA
sequence.
ACCESSION AU062862
VERSION AU062862.1 GI:4878563
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 397)
Sasaki, T. and Minobe, Y.
Rice cDNA from callus
Unpublished (1994)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/

PROJECT = 'RGP'
Location/Qualifiers
1..397
/organism="Oryza sativa"
/strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="C51207_1A"
/clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid."
BASE COUNT    70 a 94 c 101 g 124 t 8 others
ORIGIN

Query Match      80.0%; Score 16.8; DB 9; Length 397;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tatcgtcccgagtcctctct 21
||||| ||||| ||||| |||||
Db 122 TATCTTTCCATCCATCTCT 142

RESULT 9
LOCUS      BF715275/c
DEFINITION BF715275 mab06f07.x1 Soares_thymus_2NbMT Mus musculus cDNA clone
IMAGE:3825564 3', mRNA sequence.
ACCESSION BF715275
VERSION BF715275.1 GI:12014547
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
1 (bases 1 to 455)
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1461916.

FEATURES      Location/Qualifiers
            1..455
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="IMAGE:3825564"
            /clone_lib="Soares_thymus_2NbMT"
            /sex="male"
            /tissue_type="Thymus"
            /dev_stage="4 weeks"
            /lab_host="DH10B"
            /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
            polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
            was primed with a Not I - oligo(dT) primer [5',
            TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGT
            3']; double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not I
            and Eco RI sites of the modified pT7T3 vector. RNA
            provided by Dr. Bertrand Jordan. Library went through two
            rounds of normalization, and was constructed by Bento
            Soares and M.Fatima Bonaldo."

BASE COUNT    106 a 111 c 99 g 139 t
ORIGIN

Query Match      80.0%; Score 16.8; DB 10; Length 455;

```

Best Local Similarity 90.0%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcgtccagtcctctct 21  
||| | ||||| |||||

Db 179 ATCTGCCAGTCCATCTCT 160

RESULT 10  
AW179330  
LOCUS mp82g11.y1 Soares\_thymus\_2NbMT Mus musculus cDNA clone IMAGE:575780  
DEFINITION PM4-ST0120-100999-001-c09 ST0120 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW179330  
VERSION AW179330.1 GI:6445367  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 460)  
HCGP <http://www.ludwig.org.br/ORESTES>.  
The FAPESP/LICR Human Cancer Genome Project  
Contact: Simpson A.J.G.  
Unpublished (1999)  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM4&t2=PM4-ST0120-100999-001-c09&t3=1999-09-10&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence stop: 229.

FEATURES  
source  
1. .460  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="ST0120"  
/dev\_stage="Adult"  
/note="Organ: stomach; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 116 a 125 c 104 g 115 t  
ORIGIN  
Location/Qualifiers

Query Match 80.0%; Score 16.8; DB 9; Length 460;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgtccagtcctctc 20  
||| | ||||| |||||

Db 212 TATGCTCCAGTCCATCTC 231

RESULT 11  
AI530706  
LOCUS mp82g11.y1 Soares\_thymus\_2NbMT Mus musculus cDNA clone IMAGE:575780  
DEFINITION PM4-ST0120-100999-001-c09 ST0120 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AI530706  
VERSION AI530706.1 GI:4444841  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 460)  
HCGP <http://www.ludwig.org.br/ORESTES>.  
The FAPESP/LICR Human Cancer Genome Project  
Contact: Simpson A.J.G.  
Unpublished (1999)  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM4&t2=PM4-ST0120-100999-001-c09&t3=1999-09-10&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence stop: 229.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
1. .461  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:575780"  
/clone\_lib="Soares\_thymus\_2NbMT"  
/sex="male"  
/tissue\_type="Thymus"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/note="Vector: p7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAAGTCGAGCGCGCTTTTGTGTGTGTGTGTGTGTGTGT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7T3 vector. RNA  
provided by Dr. Bertrand Jordan. Library went through two  
rounds of normalization, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 107 a 110 c 129 g 115 t  
ORIGIN  
Location/Qualifiers

Query Match 80.0%; Score 16.8; DB 9; Length 461;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcgtccagtcctctct 21  
||| | ||||| |||||

Db 379 ATCTGCCAGTCCATCTCT 398

RESULT 12  
AA120431  
LOCUS mp82g11.r1 Soares\_thymus\_2NbMT Mus musculus cDNA clone IMAGE:575780  
DEFINITION 5', mRNA sequence.  
ACCESSION AA120431  
VERSION AA120431.1 GI:1675436  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 470)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Mortis, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
1. .461  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:575780"  
/clone\_lib="Soares\_thymus\_2NbMT"  
/sex="male"  
/tissue\_type="Thymus"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/note="Vector: p7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAAGTCGAGCGCGCTTTTGTGTGTGTGTGTGTGTGTGT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7T3 vector. RNA  
provided by Dr. Bertrand Jordan. Library went through two  
rounds of normalization, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 107 a 110 c 129 g 115 t  
ORIGIN  
Location/Qualifiers

Query Match 80.0%; Score 16.8; DB 9; Length 461;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcgtccagtcctctct 21  
||| | ||||| |||||

Db 379 ATCTGCCAGTCCATCTCT 398

RESULT 12  
AA120431  
LOCUS mp82g11.r1 Soares\_thymus\_2NbMT Mus musculus cDNA clone IMAGE:575780  
DEFINITION 5', mRNA sequence.  
ACCESSION AA120431  
VERSION AA120431.1 GI:1675436  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 470)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Mortis, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
1. .461  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:575780"  
/clone\_lib="Soares\_thymus\_2NbMT"  
/sex="male"  
/tissue\_type="Thymus"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/note="Vector: p7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAAGTCGAGCGCGCTTTTGTGTGTGTGTGTGTGTGTGT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7T3 vector. RNA  
provided by Dr. Bertrand Jordan. Library went through two  
rounds of normalization, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 107 a 110 c 129 g 115 t  
ORIGIN  
Location/Qualifiers

Query Match 80.0%; Score 16.8; DB 9; Length 461;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcgtccagtcctctct 21  
||| | ||||| |||||

Db 379 ATCTGCCAGTCCATCTCT 398

RESULT 12  
AA120431  
LOCUS mp82g11.r1 Soares\_thymus\_2NbMT Mus musculus cDNA clone IMAGE:575780  
DEFINITION 5', mRNA sequence.  
ACCESSION AA120431  
VERSION AA120431.1 GI:1675436  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 470)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Mortis, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
1. .461  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:575780"  
/clone\_lib="Soares\_thymus\_2NbMT"  
/sex="male"  
/tissue\_type="Thymus"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/note="Vector: p7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAAGTCGAGCGCGCTTTTGTGTGTGTGTGTGTGTGTGT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7T3 vector. RNA  
provided by Dr. Bertrand Jordan. Library went through two  
rounds of normalization, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 107 a 110 c 129 g 115 t  
ORIGIN  
Location/Qualifiers

Query Match 80.0%; Score 16.8; DB 9; Length 461;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atcgtccagtcctctct 21  
||| | ||||| |||||

Db 379 ATCTGCCAGTCCATCTCT 398

RESULT 12  
AA120431  
LOCUS mp82g11.r1 Soares\_thymus\_2NbMT Mus musculus cDNA clone IMAGE:575780  
DEFINITION 5', mRNA sequence.  
ACCESSION AA120431  
VERSION AA120431.1 GI:1675436  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 470)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Mortis, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:350428

Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 453.

#### FEATURES source

```

Location/Qualifiers
1. .470
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:575780"
/clone_lib="Soares_thymus_2NbMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/Note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT      110 a 109 c 133 g 118 t
ORIGIN

```

Query Match 80.0%; Score 16.8; DB 9; Length 470;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 atcgttccagtcacatctct 21
|||||
Db 380 ATCTTGCCAGTCCATCTCT 399

```

#### RESULT 13 AI007215

```

LOCUS      AI007215      474 bp      mRNA      linear      EST 12-JUN-1998
DEFINITION ua73h11.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
IMAGE:1363173 5', mRNA sequence.

```

```

ACCESSION  AI007215
VERSION     AI007215.1  GI:3216772
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus

```

#### REFERENCE AUTHORS

1 (bases 1 to 474)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

The WashU-HHMI Mouse EST Project  
Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:896393

Seq primer: -28m13 rev2 ET from Amersham.

#### FEATURES source

```

Location/Qualifiers
1. .474
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:1363173"
/clone_lib="Soares_thymus_2NbMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/Note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT      111 a 111 c 133 g 119 t
ORIGIN

```

Query Match 80.0%; Score 16.8; DB 9; Length 474;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 2 atcgttccagtcacatctct 21
|||||
Db 379 ATCTTGCCAGTCCATCTCT 398

```

#### RESULT 14 BI509406/c

```

LOCUS      BI509406      545 bp      mRNA      linear      EST 29-AUG-2001
DEFINITION BB170016A20C04 Bee Brain Normalized/Subtracted Library, BB17 Apis
mellifera cDNA clone BB170016A20C04 5', mRNA sequence.

```

```

ACCESSION  BI509406
VERSION     BI509406.1  GI:15359780
KEYWORDS   EST.
SOURCE     honeybee.
ORGANISM   Apis mellifera

```

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata  
; Apoidea; Apidae; Apis.

1 (bases 1 to 545)

Whitfield,C.W., Soares,B., Robertson,H.M., Pardinas,J., Liu,L.,  
Smoller,D. and Robinson,G.E.

An Expressed Sequence Tag Resource for Studies of Brain and

Behavior in the Honey Bee

Unpublished (2001)

Contact: Gene E. Robinson

Department of Entomology

University of Illinois

505 S. Goodwin Ave., Urbana, IL 61801, USA

Tel: 217 265 0309

Fax: 217 244 3499

Email: generob@life.uiuc.edu

This research was funded by the University of Illinois Critical  
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation  
Award in Functional Genomics to G.E. Robinson and an NSF

Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.

REPEAT IN THE SEQUENCE

Low complexity STRAND (+) ELEMENT A-rich LOCATION [454,540].

PCR Primers

FORWARD: TAATACGACTCACTATAGGG

BACKWARD: ATTAACCTCACTAAG

Insert Length: 545 Std Error: 0.00

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Seq primer: AGCGATAACAATTTCACACAGGA

High quality sequence stop: 545.

Location/Qualifiers
1. .625
/organism="Rattus norvegicus"
/strain="BN/SSNHsd/MCW"

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 10:08:40 ; Search time 754.01 seconds

(without alignments)  
47.818 Million cell updates/sec

Title: us-09-339-922a-111

Perfect score: 21

Sequence: 1 tatcgttccagtcctctct 21

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

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2: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
3: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
4: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
5: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*  
6: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*  
7: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*  
8: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*  
9: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*  
10: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*  
11: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*  
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23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	22	AAV28239
2	21	100.0	33	19	AAV49849
3	21	100.0	33	22	AAV28205
4	21	100.0	84	19	AAV49840
5	21	100.0	84	19	AAV49831
6	21	100.0	84	22	AAH74634
7	21	100.0	84	22	AAH74634
8	21	100.0	84	22	AAH74634
9	21	100.0	321	19	AAV49843

10	21	100.0	321	19	AAV49821	Vitaxin antibody 1
11	21	100.0	321	19	AAV49823	LM609 antibody lig
12	21	100.0	321	22	AAH74624	DNA encoding light
13	21	100.0	321	22	AAH74626	DNA encoding light
14	21	100.0	321	22	AAH74626	Vitaxin light chain
15	21	100.0	321	22	AAH74626	Antibody LM609 lig
16	21	100.0	321	22	AAH74626	DNA encoding light
17	17.8	84.8	33	19	AAV49869	LM609 grafted anti
18	17.8	84.8	33	22	AAH74626	DNA encoding mutan
19	17.8	84.8	114	20	AAV71817	Alpha-v beta-3 MAB
20	17.8	84.8	315	20	AAV71803	JK gene segment.
21	17.8	84.8	315	20	AAV71805	Humanised anti-alp
22	17.8	84.8	321	20	AAV71800	Humanised anti-alp
23	17.8	84.8	324	17	AAH73446	EGF receptor chime
24	17.8	84.8	324	20	AAV71798	Murine vitronectin
25	17.8	84.8	338	20	AAV71802	Vitronectin alpha-
26	17.8	84.8	342	22	AAH74666	Murine coding sequ
27	17.8	84.8	381	15	AAQ64167	Sequence of mouse
28	17.8	84.8	381	22	AAH58747	Murine CMV5 antibo
29	17.8	84.8	5238	11	AAQ04654	Plasmid pBT111 enc
30	16.8	80.0	101	20	AAV71825	Alpha-v beta-3 MAB
31	16.8	80.0	308	22	AAK49560	Human bone marrow
32	16.8	80.0	384	21	AAZ39321	Nucleotide sequenc
33	16.8	80.0	573	22	AAK36602	Human bone marrow
34	16.8	80.0	753	21	AAK38914	Arabidopsis thalia
35	16.8	80.0	1632	21	AAK50082	Arabidopsis thalia
36	16.2	77.1	363	17	AAH38510	Light chain coding
37	16.2	77.1	381	21	AAZ35242	Mouse anti-verotox
38	16.2	77.1	381	21	AAZ35244	Humanised anti-ver
39	16.2	77.1	415	21	AAH00904	Humanised antibody
40	16.2	77.1	415	21	AAH00906	Humanised antibody
41	16.2	77.1	415	21	AAH01262	Mouse monoclonal a
42	16.2	77.1	465	21	AAH46877	DNA encoding the k
43	16.2	77.1	510	23	AAH76374	DNA encoding novel
44	16.2	77.1	651	21	AAA44346	Human secreted exp
45	16.2	77.1	8858	20	AAZ10202	Expression vector

#### ALIGNMENTS

RESULT 1  
AAV28239  
ID AAV28239 standard; DNA; 21 BP.  
XX  
AC AAV28239;  
XX  
DT 03-APR-2001 (first entry)  
XX  
DE DNA encoding enhanced 6H6LH light chain CDR2.  
XX  
KW LM609; grafted antibody; alphaVbeta3 integrin; angiogenesis;  
XX inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
XX  
OS Unidentified.  
XX  
PW WO200078815-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 23-JUN-2000; 2000WO-US17454.  
XX  
PR 24-JUN-1999; 99US-0339922.  
XX  
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
XX  
PI Huse WD, Wu H;  
XX  
DR WPI; 2001-050110/06.  
XX  
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
XX to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
XX angiogenesis, inflammatory diseases e.g. psoriasis, cancers and

PT osteoporosis -  
 PS Claim 16; Page 107; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 21 BP; 3 A; 8 C; 2 G; 8 T; 0 other;  
 Query Match 100.0%; Score 21; DB 22; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.43;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 tatcgttccagtcacatctct 21  
 Db 1 tatcgttccagtcacatctct 21  
 RESULT 2  
 AAV49849  
 ID AAV49849 standard; DNA; 33 BP.  
 XX  
 AC AAV49849;  
 XX  
 DT 02-NOV-1998 (first entry)  
 XX  
 DE LM609 grafted antibody V-L region CDR2 DNA fragment #1.  
 XX  
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;  
 KW complementarity determining region; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9833919-A2.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 30-JAN-1998; 98WO-US01826.  
 XX  
 PR 30-JAN-1997; 97US-0791391.  
 XX  
 PA (IXSY-) IXSYS INC.  
 XX  
 PI Glaser SM, Huse WD;  
 XX  
 DR WPI; 1998-437472/37.  
 XX  
 XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX  
 PS Disclosure; Page 40; 129pp; English.  
 XX  
 CC AAV49844-V49877 are nucleotide fragments of the grafted monoclonal  
 CC antibody LM609 heavy and light chain variable region. LM609 and the  
 CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be used  
 CC to inhibit binding of alphavbeta3 to a ligand and thus block  
 CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically  
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,  
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,  
 CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The  
 CC antibodies contain non-murine framework regions so are suitable for use  
 CC in humans. Enhanced types of LM609 have affinity more than 90 times  
 CC greater than that of parent the parent antibody.  
 XX  
 SQ Sequence 33 BP; 4 A; 13 C; 3 G; 13 T; 0 other;  
 Query Match 100.0%; Score 21; DB 19; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 0.45;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 tatcgttccagtcacatctct 21  
 Db 13 tatcgttccagtcacatctct 33  
 RESULT 3  
 AAF28205  
 ID AAF28205 standard; DNA; 33 BP.  
 XX  
 AC AAF28205;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE DNA encoding LM609 VL CDR2 peptide.  
 XX  
 KW LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078615-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 DR WPI; 2001-050110/06.  
 XX  
 DE Enhanced LM609 grafted antibodies exhibiting selective binding affinity.  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 PS Disclosure; Page 40; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 SQ Sequence 33 BP; 4 A; 13 C; 3 G; 13 T; 0 other;  
 Query Match 100.0%; Score 21; DB 22; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 0.45;



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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctcgttccagtcctctct 21
   |||||||
Db 13 tctcgttccagtcctctct 33

RESULT 4
AAV49840
ID AAV49840 standard; DNA; 84 BP.
XX
AC AAV49840;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody light chain variable region oligonucleotide #3.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Example 5; Page 80; 129pp; English.
XX
XX AAV49838-V49842 are oligonucleotides used in the construction of grafted
CC LM609 monoclonal antibody light chain variable regions. LM609 and the
CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be
CC used to inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 84 BP; 17 A; 25 C; 20 G; 22 T; 0 other;

Query Match 100.0%; Score 21; DB 19; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctcgttccagtcctctct 21
   |||||||
Db 19 tctcgttccagtcctctct 39

RESULT 5
AAV49840
ID AAV49840 standard; DNA; 84 BP.
XX
AC AAV49840;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody light chain variable region oligonucleotide #3.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Example 5; Page 80; 129pp; English.
XX
XX AAV49838-V49842 are oligonucleotides used in the construction of grafted
CC LM609 monoclonal antibody light chain variable regions. LM609 and the
CC antibody vitaxin bind selectively to integrin alphavbeta3 and can be
CC used to inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 84 BP; 17 A; 25 C; 20 G; 22 T; 0 other;

Query Match 100.0%; Score 21; DB 19; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctcgttccagtcctctct 21
   |||||||
Db 19 tctcgttccagtcctctct 39

RESULT 6
AAH74634
ID AAH74634 standard; DNA; 84 BP.
XX
AC AAH74634;
XX
DT 15-OCT-2001 (first entry)
XX
DE PCR primer for light chain variable region of LM609 antibody.

```

```

AAV49831
ID AAV49831 standard; DNA; 84 BP.
XX
AC AAV49831;
XX
DT 02-NOV-1998 (first entry)
XX
DE LM609 grafted antibody variable region oligonucleotide #8.
XX
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN WO9833919-A2.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US01826.
XX
PR 30-JAN-1997; 97US-0791391.
XX
PA (IXSY-) IXSYS INC.
XX
PI Glaser SM, Huse WD;
XX
XX WPI; 1998-437472/37.
XX
XX Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
XX
PS Example 2; Page 65; 129pp; English.
XX
XX AAV49824-V49833 are oligonucleotides used in the construction of grafted
CC LM609 monoclonal antibody heavy and light chain variable regions. LM609
CC and the antibody vitaxin bind selectively to integrin alphavbeta3 and
CC can be used to inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis,
CC rheumatoid arthritis, macular degeneration, osteoporosis etc.). The
CC antibodies contain non-murine framework regions so are suitable for use
CC in humans. Enhanced types of LM609 have affinity more than 90 times
CC greater than that of parent the parent antibody.
XX
SQ Sequence 84 BP; 16 A; 25 C; 20 G; 21 T; 2 other;

Query Match 100.0%; Score 21; DB 19; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctcgttccagtcctctct 21
   |||||||
Db 19 tctcgttccagtcctctct 39

RESULT 6
AAH74634
ID AAH74634 standard; DNA; 84 BP.
XX
AC AAH74634;
XX
DT 15-OCT-2001 (first entry)
XX
DE PCR primer for light chain variable region of LM609 antibody.

```

XX Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer; PCR primer; ss.  
 XX Mus sp.  
 OS  
 XX US2001011125-A1.  
 PN  
 XX  
 PD 02-AUG-2001.  
 XX  
 XX 30-JAN-1997; 97US-0790540.  
 PF  
 XX 30-JAN-1997; 97US-0790540.  
 PR  
 XX (HUSE/) HUSE W D.  
 PA  
 XX Huse WD;  
 PI  
 XX WPI; 2001-496171/54.  
 DR  
 XX New LM609 grafted antibody exhibiting selective binding affinity to  
 XX alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer -  
 XX  
 XX Example 2; Page 17; 25pp; English.  
 PS  
 XX PCR primers AAH74632-36 were used to amplify DNA encoding fragments  
 CC of the light chain variable region of the monoclonal antibody LM609.  
 CC LM609 is a murine antibody which specifically recognises the integrin  
 CC alphavbeta3, and inhibits its functional activity. The specification  
 CC describes a LM609 grafted antibody which has the complementarity  
 CC determining regions (CDRs) substituted into a non-murine framework.  
 CC Nucleic acids encoding LM609 grafted heavy and light chain polypeptides  
 CC and fragments are useful in diagnostic and therapeutic purposes, such  
 CC as in the production of LM609 grafted antibodies and fragments having  
 CC binding specificity and inhibitory activity against the integrin  
 CC alphavbeta3. The antibody can be used for the diagnosis or treatment  
 CC of alphavbeta3-mediated diseases (e.g. inflammatory disorders, chronic  
 CC articular rheumatism, psoriasis, disorders associated with inappropriate  
 CC or inopportune invasion of vessels such as diabetic retinopathy,  
 CC neovascular glaucoma and capillary proliferation in atherosclerotic  
 CC plaques, or cancers), and to inhibit binding activity of alphavbeta3  
 CC that are necessary for progression of an alphavbeta3-mediated disease.  
 XX  
 XX Sequence 84 BP; 17 A; 25 C; 20 G; 22 T; 0 other;  
 SQ

Query Match 100.0%; Score 21; DB 22; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 0.49;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21  
 |||||  
 Db 19 tatcgttccagtcctctct 39

RESULT 7  
 AAF28186  
 ID AAF28186 standard; DNA; 84 BP.  
 XX  
 AC AAF28186;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Grafted light chain variable region oligonucleotide #8.  
 XX  
 XX LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
 KW  
 XX Unidentified.  
 OS

XX WO200078815-A1.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 23-JUN-2000; 2000WO-US17454.  
 PF  
 XX 24-JUN-1999; 99US-0339922.  
 PR  
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 PA  
 XX Huse WD, Wu H;  
 PI  
 XX WPI; 2001-050110/06.  
 DR  
 XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis -  
 XX  
 XX Example 2; Page 67; 132pp; English.  
 PS  
 XX The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta\_3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.  
 XX  
 XX Sequence 84 BP; 16 A; 25 C; 20 G; 21 T; 2 other;  
 SQ

Query Match 100.0%; Score 21; DB 22; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 0.49;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21  
 |||||  
 Db 19 tatcgttccagtcctctct 39

RESULT 8  
 AAF28195  
 ID AAF28195 standard; DNA; 84 BP.  
 XX  
 AC AAF28195;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Grafted light chain variable region oligonucleotide #3.  
 XX  
 XX LM609; grafted antibody; alphavbeta\_3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ss.  
 KW  
 XX Unidentified.  
 OS  
 XX WO200078815-A1.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 23-JUN-2000; 2000WO-US17454.  
 PF  
 XX 24-JUN-1999; 99US-0339922.  
 PR  
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 PA  
 XX Huse WD, Wu H;  
 PI  
 XX

WPT; 2001-0501110/06.

Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -

Example 4; Page 81; 132pp; English.

The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to alphavbeta\_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of alphavbeta\_3-mediated diseases such as angiogenesis, inflammatory diseases (such as psoriasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and osteoporosis.

Sequence 84 BP; 17 A; 25 C; 20 G; 22 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 84;  
Best Local Similarity 100.0%; Pred. NO. 0.49;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tatcgttccagtcacatctct 21  
|||||  
Db 19 tatcgttccagtcacatctct 39

RESULT 9  
AAV49843  
ID AAV49843 standard; DNA; 321 BP.  
XX AAV49843;  
XX  
XX  
DT 02-NOV-1998 (first entry)  
XX  
XX LM609 antibody light chain variable region DNA grafted fragment.  
XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
KW macular degeneration; osteoporosis; ss.  
XX  
OS Mus sp.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 1..321  
FT FT /\*tag= a  
FT FT /product= "LM609 grafted antibody light chain variable region"  
FT FT /note= "partial sequence, no start or stop codon given"  
XX  
PN W09833919-A2.  
XX  
XX  
XX 06-AUG-1998.  
XX  
XX 30-JAN-1998; 98WO-US01826.  
XX  
XX 30-JAN-1997; 97US-0791391.  
XX  
XX (IXSY-) IXSYS INC.  
XX  
XX Glaser SM, Huse WD;  
XX  
XX WPT; 1998-437472/37.  
DR P-PSDB; AAW76006.  
XX

PT angiogenesis or restenosis  
 XX Claim 6; Fig 1b; 129pp; English.  
 XX This sequence encodes the vitaxin antibody variable light chain region.  
 CC Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3  
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
 CC block integrin-mediated signal transduction. This is useful in the  
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
 CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.  
 XX Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;  
 SQ

Query Match 100.0%; Score 21; DB 19; Length 321;  
 Best Local Similarity 100.0%; Pred. No. 0.57;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgttcccagtcctctct 21  
 |||||  
 Db 148 tatcgttcccagtcctctct 168

RESULT 11  
 AAV49823  
 ID AAV49823 standard; DNA; 321 BP.  
 XX  
 AC AAV49823;  
 XX  
 DT 02-NOV-1998 (first entry)  
 XX  
 DE LM609 antibody light chain variable region DNA fragment.  
 XX  
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;  
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
 KW macular degeneration; osteoporosis; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..321  
 FT /\*tag= a  
 FT /product= "LM609 antibody light chain variable region"  
 FT /note= "partial sequence, no start or stop codon given"

XX WO9833919-A2.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 30-JAN-1998; 98WO-0501826.  
 XX  
 PR 30-JAN-1997; 97US-0791391.  
 XX  
 PA (IXSY-) IXSYS INC.  
 XX  
 PI Glaser SM, Huse WD;  
 XX  
 DR WPI; 1998-437472/37.  
 DR P-PSDB; AAV75004.  
 XX  
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3  
 PT integrin - and related grafted antibodies based on murine monoclonal  
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
 PT angiogenesis or restenosis  
 XX  
 PS Claim 40; Fig 2b; 129pp; English.

XX This sequence encodes the LM609 antibody variable light chain region.  
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3  
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus  
 CC block integrin-mediated signal transduction. This is useful in the  
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,  
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune  
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,  
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis  
 CC etc.). The antibodies contain non-murine framework regions so are  
 CC suitable for use in humans. Enhanced types of LM609 have affinity more  
 CC than 90 times greater than that of parent the parent antibody.  
 XX Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;  
 SQ

Query Match 100.0%; Score 21; DB 19; Length 321;  
 Best Local Similarity 100.0%; Pred. No. 0.57;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgttcccagtcctctct 21  
 |||||  
 Db 148 tatcgttcccagtcctctct 168

RESULT 12  
 AAH74624  
 ID AAH74624 standard; DNA; 321 BP.  
 XX  
 AC AAH74624;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX  
 DE DNA encoding light chain variable region of LM609 grafted antibody.  
 XX  
 KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer; ss.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..321  
 FT /\*tag= a  
 FT /transl\_except= "(pos: 145..147, aa: Xaa)"  
 FT /note= "Xaa is unspecified"

XX US2001011125-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 30-JAN-1997; 97US-0790540.  
 XX  
 PR 30-JAN-1997; 97US-0790540.  
 XX  
 PA (HUSE/) HUSE W D.  
 XX  
 PI Huse WD;  
 XX  
 DR WPI; 2001-496171/54.  
 DR P-PSDB; AAG63588.  
 XX  
 PT New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer  
 XX  
 PS Claim 6; Fig 1B; 25pp; English.  
 XX  
 CC The present sequence encodes the light chain variable region of the  
 CC grafted monoclonal antibody LM609. LM609 is a murine antibody which

CC specifically recognises the integrin alphavbeta3, and inhibits its  
 CC functional activity. The LM609 grafted antibody has the  
 CC complementary determining regions (CDRs) substituted into a non-murine  
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain  
 CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis  
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
 CC disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 CC an alphavbeta3-mediated disease.

XX  
 SQ Sequence 321 BP; 76 A; 93 C; 78 G; 71 T; 3 other;

Query Match 100.0%; Score 21; DB 22; Length 321;  
 Best Local Similarity 100.0%; Pred. No. 0.57;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgttcccagtcctctct 21  
 |||||  
 Db 148 tatcgttcccagtcctctct 168

RESULT 13  
 AAH74626  
 ID AAH74626 standard; DNA; 321 BP.  
 XX  
 AC AAH74626;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX  
 DE DNA encoding light chain variable region of LM609 antibody.  
 XX  
 KW Grafted antibody; LM609; integrin; alphavbeta3; inflammatory disorder;  
 KW chronic articular rheumatism; psoriasis; diabetic retinopathy;  
 KW neovascular glaucoma; capillary proliferation; atherosclerotic plaque;  
 KW cancer; ss.

OS Mus sp.  
 XX  
 PN US2001011125-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 30-JAN-1997; 97US-0790540.  
 XX  
 PR 30-JAN-1997; 97US-0790540.  
 XX  
 PA (HUSE/) HUSE W D.  
 XX  
 PI Huse WD;  
 XX  
 WPI; 2001-496171/54.  
 DR P-PSDB; AAG63590.  
 XX

PT New LM609 grafted antibody exhibiting selective binding affinity to  
 PT alphavbeta3, comprising at least one LM609 grafted heavy and light  
 PT chain polypeptide, useful for diagnosing and treating e.g. inflammatory  
 PT disorders or cancer -  
 XX  
 PS Disclosure; Fig 2B; 25pp; English.  
 XX  
 CC The present sequence encodes the light chain variable region of the  
 CC monoclonal antibody LM609. LM609 is a murine antibody which specifically  
 CC recognises the integrin alphavbeta3, and inhibits its functional activity.  
 CC The specification describes a LM609 grafted antibody which has the  
 CC complementary determining regions (CDRs) substituted into a non-murine  
 CC framework. Nucleic acids encoding LM609 grafted heavy and light chain

CC polypeptides and fragments are useful in diagnostic and therapeutic  
 CC purposes, such as in the production of LM609 grafted antibodies and  
 CC fragments having binding specificity and inhibitory activity against  
 CC the integrin alphavbeta3. The antibody can be used for the diagnosis  
 CC or treatment of alphavbeta3-mediated diseases (e.g. inflammatory  
 CC disorders, chronic articular rheumatism, psoriasis, disorders  
 CC associated with inappropriate or inopportune invasion of vessels such  
 CC as diabetic retinopathy, neovascular glaucoma and capillary  
 CC proliferation in atherosclerotic plaques, or cancers), and to inhibit  
 CC binding activity of alphavbeta3 that are necessary for progression of  
 CC an alphavbeta3-mediated disease.

XX  
 SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 321;  
 Best Local Similarity 100.0%; Pred. No. 0.57;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tatcgttcccagtcctctct 21  
 |||||  
 Db 148 tatcgttcccagtcctctct 168

RESULT 14  
 AAF28176  
 ID AAF28176 standard; DNA; 321 BP.  
 XX  
 AC AAF28176;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Vitaxin light chain variable region DNA.  
 XX  
 KW LM609; grafted antibody; alphavbeta3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US17454.  
 XX  
 PR 24-JUN-1999; 99US-0339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 WPI; 2001-050110/06.

Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 osteoporosis -

PS Disclosure; Fig 1; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta3 integrin or  
 CC their functional fragments. The antibodies or their functional  
 CC fragments can be used in the diagnosis and treatment of  
 CC alphavbeta3-mediated diseases such as angiogenesis, inflammatory  
 CC diseases (such as psoriasis and chronic articular rheumatism),  
 CC disorders associated with inappropriate or inopportune invasion of  
 CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
 CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
 CC diseases (such as macular degeneration), restenosis and  
 CC osteoporosis.

XX  
 SQ Sequence 321 BP; 78 A; 93 C; 79 G; 71 T; 0 other;

Job time: 10059 sec

Query Match 100.0%; Score 21; DB 22; Length 321;  
Best Local Similarity 100.0%; Pred. No. 0.57;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tatcgttccagtcctctct 21  
|||||  
Db 148 tatcgttccagtcctctct 168

## RESULT 15

AAF28178  
ID AAF28178 standard; DNA; 321 BP.

XX  
AC AAF28178;

XX 03-APR-2001 (first entry)

XX Antibody LM609 light chain variable region DNA.

XX LM609; grafted antibody; alphaVbeta<sub>3</sub> integrin; angiogenesis;  
KW inflammatory; cancer; retina; restenosis; osteoporosis; ds.

XX Unidentified.

OS  
PN WO200078815-A1.

XX  
PD 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17454.

XX  
PR 24-JUN-1999; 99US-0339922.

XX (MOLE-) APPLIED MOLECULAR EVOLUTION.

XX  
PI Huse WD, Wu H;

XX  
DR WPI; 2001-050110/06.

XX Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
PT to alpha(V)beta<sub>3</sub> integrin, useful in the diagnosis and treatment of  
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
PT osteoporosis -

XX  
PS Disclosure; Fig 2; 132pp; English.

XX The present invention relates to enhanced LM609 grafted antibodies  
CC exhibiting selective binding affinity to alphaVbeta<sub>3</sub> integrin or  
CC their functional fragments. The antibodies or their functional  
CC fragments can be used in the diagnosis and treatment of  
CC alphaVbeta<sub>3</sub>-mediated diseases such as angiogenesis, inflammatory  
CC diseases (such as psoriasis and chronic articular rheumatism),  
CC disorders associated with inappropriate or inopportune invasion of  
CC vessels (such as diabetic retinopathy, neovascular glaucoma and  
CC cancer disorders such as tumours and Kaposi's sarcoma), retinal  
CC diseases (such as macular degeneration), restenosis and  
CC osteoporosis.

XX  
SQ Sequence 321 BP; 83 A; 83 C; 77 G; 78 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 321;  
Best Local Similarity 100.0%; Pred. No. 0.57;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tatcgttccagtcctctct 21  
|||||  
Db 148 tatcgttccagtcctctct 168

Search completed: August 21, 2002, 10:08:41

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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29.601 Million cell updates/sec

Title: US-09-339-922A-111

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Scoring table:

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Maximum Match 100%

Listing first 45 summaries

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#### SUMMARIES

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4	17.8	84.8	381	1	US-08-487-200-82
5	17.8	84.8	381	4	US-08-484-537-82
6	17.8	84.8	424	1	US-08-436-463-3
7	17.8	84.8	5238	6	5453363-1
8	16.2	77.1	324	2	US-08-737-560A-13
9	16.2	77.1	324	4	US-09-247-352-14
10	16.2	77.1	363	2	US-08-737-560A-8
11	16.2	77.1	8858	4	US-09-247-352-6
12	15.8	75.2	1100	3	US-09-094-103-3
13	15.8	75.2	1172	3	US-09-094-103-1
14	15.2	72.4	80161	3	US-09-036-987A-1
15	15.2	72.4	80161	4	US-09-370-700-1
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17	15	71.4	113	1	US-08-477-728-92
18	15	71.4	113	1	US-08-474-040-92
19	15	71.4	113	1	US-08-487-200-92
20	15	71.4	113	4	US-08-484-537-92
21	14.6	69.5	49	2	US-08-980-071-74
22	14.6	69.5	49	3	US-09-314-093-74
23	14.6	69.5	49	4	US-09-337-635-74
24	14.6	69.5	703	4	US-08-998-416-828
25	14.6	69.5	966	3	US-08-748-506-5
26	14.6	69.5	966	3	US-08-748-506-7
27	14.6	69.5	966	3	US-08-748-506-8

28	14.6	69.5	3441	2	US-08-525-864A-1	Sequence 1, Appli
29	14.6	69.5	3907	3	US-08-475-742-1	Sequence 1, Appli
30	14.6	69.5	7379	4	US-09-341-587-5	Sequence 5, Appli
31	14.4	68.6	445	3	US-09-188-930-233	Sequence 233, App
32	14.4	68.6	2622	4	US-09-130-616-170	Sequence 170, App
33	14.4	68.6	3111	2	US-09-014-969-12	Sequence 12, Appl
34	14.4	68.6	5049	1	US-08-336-345-1	Sequence 1, Appli
35	14.4	68.6	5049	1	US-08-336-345-2	Sequence 2, Appli
36	14.4	68.6	5049	2	US-08-647-655-1	Sequence 1, Appli
37	14.4	68.6	5049	2	US-08-647-655-2	Sequence 2, Appli
38	14.4	68.6	35081	2	US-08-752-760A-1	Sequence 1, Appli
39	14.2	67.6	540	1	US-08-117-083-18	Sequence 18, Appl
40	14.2	67.6	642	4	US-09-385-982-386	Sequence 386, App
41	14.2	67.6	789	1	US-08-436-748-4	Sequence 4, Appli
42	14.2	67.6	789	3	US-08-483-857-3	Sequence 3, Appli
43	14.2	67.6	1237	1	US-08-197-792-40	Sequence 40, Appl
44	14.2	67.6	1237	1	US-08-459-850-40	Sequence 40, Appl
45	14.2	67.6	1237	1	US-08-459-214-40	Sequence 40, Appl

#### ALIGNMENTS

RESULT 1  
US-07-634-278-82  
; Sequence 82, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 118233-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381  
US-07-634-278-82

Query Match 84.8%; Score 17.8; DB 1; Length 381;  
Best Local Similarity 90.5%; Pred. No. 4;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgtccagtcacatctct 21  
||| ||||| ||||| |||||  
Db 208 TATGCTTCCAGTCCATCTCT 228

RESULT 2  
US-08-477-728-82  
; Sequence 82, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381  
US-08-477-728-82

Query Match 84.8%; Score 17.8; DB 1; Length 381;  
Best Local Similarity 90.5%; Pred. No. 4;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgtccagtcacatctct 21  
||| ||||| ||||| |||||  
Db 208 TATGCTTCCAGTCCATCTCT 228

RESULT 3  
US-08-474-040-82  
; Sequence 82, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLEI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381  
US-08-474-040-82

Query Match 84.8%; Score 17.8; DB 1; Length 381;  
Best Local Similarity 90.5%; Pred. No. 4;



Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21  
Db 208 TATGCTTCCAGTCCATCTCT 228

RESULT 4  
US-08-487-200-82  
; Sequence 82, Application US/08487200  
; Patent No. 5693762  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,200  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002610  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381  
US-08-487-200-82

Query Match 84.8%; Score 17.8; DB 1; Length 381;  
Best Local Similarity 90.5%; Pred. No. 4;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21

Db 208 TATGCTTCCAGTCCATCTCT 228

RESULT 5  
US-08-484-537-82  
; Sequence 82, Application US/08484537  
; Patent No. 6180370  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,537  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 381 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..381  
US-08-484-537-82

Query Match 84.8%; Score 17.8; DB 4; Length 381;  
Best Local Similarity 90.5%; Pred. No. 4;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21  
Db 208 TATGCTTCCAGTCCATCTCT 228

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RESULT 6
US-08-436-463-3
; Sequence 3, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoto
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-PELVINE HERPES VIRUS-1 RECOMBINANT
; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,463
; FILING DATE: 26-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 341255/1992
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: KIMACHI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23..403
US-08-436-463-3

Query Match 84.8%; Score 17.8; DB 1; Length 424;
Best Local Similarity 90.5%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgttccagtcacatctct 21
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Db 230 TATGCTTCCAGTCACATCTCT 250

RESULT 7
5453363-1
; Patent No. 5453363
; APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF
; TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR
; ING AFTER GENETIC EXPRESSION IN PROKARYOTES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,044
; FILING DATE: 02-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 942,370
; FILING DATE: 09-SEP-1992
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; APPLICATION NUMBER: 498,500
; FILING DATE: 23-MAR-1990
; APPLICATION NUMBER: 76,207
; FILING DATE: 23-OCT-1986
; SEQ ID NO:1:
; LENGTH: 5238
5453363-1

Query Match 84.8%; Score 17.8; DB 6; Length 5238;
Best Local Similarity 90.5%; Pred. No. 5.2;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgttccagtcacatctct 21
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Db 154 tatcgttccagtcacatctct 174

RESULT 8
US-08-737-560A-13
; Sequence 13, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: KIM, Joong-Gon
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuil
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgu Jung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: polynucleotide encoding 4B4-1-1
; OTHER INFORMATION: light chain variable region
US-08-737-560A-13
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Query Match 77.1%; Score 16.2; DB 2; Length 324;  
Best Local Similarity 85.7%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21  
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Db 148 TATGCTTCCCAATCCATCTCT 168

RESULT 9  
US-09-247-352-14  
; Sequence 14, Application US/09247352  
; Patent No. 6312693  
; GENERAL INFORMATION:  
; APPLICANT: Aruffo, Alejandro A.  
; APPLICANT: Siadak, Anthony W.  
; APPLICANT: Berry, Karen K.  
; APPLICANT: Harris, Linda  
; APPLICANT: Thorne, Barbara A.  
; APPLICANT: Bajorath, Jurgen  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffry D.  
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40  
; FILE REFERENCE: DB2a SEQUENCE  
; CURRENT APPLICATION NUMBER: US/09/247,352  
; EARLIER FILING DATE: 1999-02-10  
; EARLIER FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 324  
; TYPE: DNA  
; ORGANISM: Human and Mouse  
US-09-247-352-14

Query Match 77.1%; Score 16.2; DB 4; Length 324;  
Best Local Similarity 85.7%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21  
||| ||||| ||||| |||||  
Db 148 tatcgttccagtcctctct 168

RESULT 10  
US-08-737-560A-8  
; Sequence 8, Application US/08737560A  
; Patent No. 5928893  
; GENERAL INFORMATION:  
; APPLICANT: KANG, Chang-Yuill  
; APPLICANT: KIM, Joong-Gon  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN  
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KANG, Chang-Yuill  
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,  
; STREET: Kwanak-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 151-057  
; ADDRESSEE: KIM, Joong-Gon  
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu  
; CITY: Seoul  
; STATE: Seoul  
; COUNTRY: Republic of Korea  
; ZIP: 135-110  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage  
; COMPUTER: IBM PC/AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/737,560A  
; FILING DATE: 13-NOV-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: KR 95-8176  
; FILING DATE: 08-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:

; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 363 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; OTHER INFORMATION: 1 to 324 bp 4B4-1-1 light chain  
; OTHER INFORMATION: variable region  
; OTHER INFORMATION: 70 to 102 bp hypervariable region CDR1  
; OTHER INFORMATION: 148 to 168 bp hypervariable region CDR2  
; OTHER INFORMATION: 265 to 291 bp hypervariable region CDR3  
; OTHER INFORMATION: 325 to 363 bp 4B4-1-1 light chain constant region  
US-08-737-560A-8

Query Match 77.1%; Score 16.2; DB 2; Length 363;  
Best Local Similarity 85.7%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatcgttccagtcctctct 21  
||| ||||| ||||| |||||  
Db 148 TATGCTTCCCAATCCATCTCT 168

RESULT 11  
US-09-247-352-6  
; Sequence 6, Application US/09247352  
; Patent No. 6312693  
; GENERAL INFORMATION:  
; APPLICANT: Aruffo, Alejandro A.  
; APPLICANT: Siadak, Anthony W.  
; APPLICANT: Berry, Karen K.  
; APPLICANT: Harris, Linda  
; APPLICANT: Thorne, Barbara A.  
; APPLICANT: Bajorath, Jurgen  
; APPLICANT: Huse, William D.  
; APPLICANT: Wu, Herren  
; APPLICANT: Watkins, Jeffry D.  
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40  
; FILE REFERENCE: DB2a SEQUENCE  
; CURRENT APPLICATION NUMBER: US/09/247,352  
; CURRENT FILING DATE: 1999-02-10  
; EARLIER FILING DATE: 1998-02-19  
; EARLIER FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 8858  
; TYPE: DNA  
; ORGANISM: Human and Mouse  
US-09-247-352-6

Query Match 77.1%; Score 16.2; DB 4; Length 8858;  
Best Local Similarity 85.7%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tatcgtccagtcacatct 21  
||| ||||| ||||| |||||  
Db 1212 tatcgtccagtcacatct 1232

## RESULT 12

US-09-094-103-3/c  
; Sequence 3, Application US/09094103  
; Patent No. 6140061  
; GENERAL INFORMATION:  
; APPLICANT: Wallis, Nicola G.  
; APPLICANT: Zalacain, Magdalena  
; APPLICANT: Throup, John  
; APPLICANT: Biswas, Sanjoy  
; TITLE OF INVENTION: Response regulator  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert, Price & Rhoads  
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-2793  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/094,103  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/050,332  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Falk, Stephen T  
; REGISTRATION NUMBER: 36,795  
; REFERENCE/DOCKET NUMBER: GM10016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-994-2488  
; TELEFAX: 215-994-2222  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1100 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

US-09-094-103-3

Query Match 75.2%; Score 15.8; DB 3; Length 1100;  
Best Local Similarity 89.5%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgtccagtcacatct 19  
||| | ||||| |||||  
Db 45 TATCGCTCCAGTCCATCT 27

## RESULT 13

US-09-094-103-1/c  
; Sequence 1, Application US/09094103  
; Patent No. 6140061  
; GENERAL INFORMATION:  
; APPLICANT: Wallis, Nicola G.  
; APPLICANT: Zalacain, Magdalena  
; APPLICANT: Throup, John

; APPLICANT: Biswas, Sanjoy  
; TITLE OF INVENTION: Response regulator  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dechert, Price & Rhoads  
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-2793  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/094,103  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/050,332  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Falk, Stephen T  
; REGISTRATION NUMBER: 36,795  
; REFERENCE/DOCKET NUMBER: GM10016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-994-2488  
; TELEFAX: 215-994-2222  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1172 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

US-09-094-103-1

Query Match 75.2%; Score 15.8; DB 3; Length 1172;  
Best Local Similarity 89.5%; Pred. No. 41;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tatcgtccagtcacatct 19  
||| | ||||| |||||  
Db 117 TATCGCTCCAGTCCATCT 99

## RESULT 14

US-09-036-987A-1/c  
; Sequence 1, Application US/09036987A  
; Patent No. 6143526  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H.  
; APPLICANT: Broughton, Mary C.  
; APPLICANT: Crawford, Kathryn P.  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Merlo, Donald J.  
; APPLICANT: Treadway, Patti J.  
; APPLICANT: Turner, Jan R.  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dow Agrosciences LLC Patent Department  
; STREET: 9330 Zionsville Road  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: USA  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/036,987A  
; FILING DATE: 09-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stuart, Donald R  
; REGISTRATION NUMBER: 28,479  
; REFERENCE/DOCKET NUMBER: 50,608  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317)337-4816  
; TELEFAX: (317)337-4847  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80161 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-036-987A-1

Query Match 72.4%; Score 15.2; DB 3; Length 80161;  
Best Local Similarity 85.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 atcggtcccgagtcacatctct 21  
||||| ||||| ||||| |||||  
Db 59135 ATCGCTCCGAGTCCACATCT 59116

RESULT 15  
US-09-370-700-1/c  
; Sequence 1, Application US/09370700  
; Patent No. 6274350  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H  
; APPLICANT: Broughton, Mary C  
; APPLICANT: Crawford, Kathryn P  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Treadway, Patti J  
; APPLICANT: Turner, Jan R  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; FILE REFERENCE: 50489 DIV1  
; CURRENT APPLICATION NUMBER: US/09/370,700  
; CURRENT FILING DATE: 1999-08-09  
; EARLIER APPLICATION NUMBER: US 09/36987  
; EARLIER FILING DATE: 1998-03-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 80161  
; TYPE: DNA  
; ORGANISM: Saccharopolyspora spinosa  
US-09-370-700-1

Query Match 72.4%; Score 15.2; DB 4; Length 80161;  
Best Local Similarity 85.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 atcggtcccgagtcacatctct 21  
||||| ||||| ||||| |||||  
Db 59135 ATCGCTCCGAGTCCACATCT 59116

Search completed: August 21, 2002, 10:52:27  
Job time: 9667 sec